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 OM nucleic - nucleic search, using sw model
 Run on: March 8, 2006, 20:59:06 ; Search time 72.1262 Seconds
 (without alignments)
 468.258 Million cell updates/sec

Title: US-10-829-474-1
 Perfect score: 19
 Sequence: 1 cccttgatgcggctaatc 19

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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 Listing first 500 summaries

Database : Issued Patents NA:
 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:
 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:
 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	19	100.0	27	US-09-724-678D-9	Sequence 9, Appli
2	19	100.0	628	US-08-387-845-5	Sequence 5, Appli
3	19	100.0	628	US-08-778-275-5	Sequence 5, Appli
4	19	100.0	628	US-08-867-352-5	Sequence 5, Appli
5	19	100.0	1220	US-09-116-032-2	Sequence 2, Appli
6	19	100.0	1560	US-09-724-678D-16	Sequence 16, Appli
7	19	100.0	2320	US-09-202-904A-10	Sequence 10, Appli
8	19	100.0	7400	US-09-116-032-1	Sequence 1, Appli
9	19	100.0	7441	US-09-284-349B-1	Sequence 1, Appli
10	18	94.7	25	US-09-311-260-105	Sequence 105, App
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C 250	13.2	69.5	252	3	US-09-513-998C-31381	Sequence 31381, A	C 323	13.2	69.5	672	3	US-08-906-769-16	Sequence 16, Appl
C 251	13.2	69.5	264	3	US-08-956-171E-4483	Sequence 4483, Ap	C 324	13.2	69.5	672	3	US-08-906-769-16	Sequence 16, Appl
C 252	13.2	69.5	264	3	US-08-781-986A-4483	Sequence 4483, Ap	C 325	13.2	69.5	672	3	US-08-817-795-16	Sequence 16, Appl
C 253	13.2	69.5	265	3	US-09-919-039-181	Sequence 181, Ap	C 326	13.2	69.5	672	3	US-08-485-443B-16	Sequence 16, Appl
C 254	13.2	69.5	278	3	US-09-313-294A-6858	Sequence 6858, Ap	C 327	13.2	69.5	672	3	US-08-639-075A-16	Sequence 16, Appl
C 255	13.2	69.5	279	3	US-08-956-171E-4455	Sequence 4455, Ap	C 328	13.2	69.5	672	3	US-09-012-431-16	Sequence 16, Appl
C 256	13.2	69.5	279	3	US-08-781-986A-4455	Sequence 4455, Ap	C 329	13.2	69.5	672	3	US-09-012-431-16	Sequence 16, Appl
C 257	13.2	69.5	321	3	US-09-025-762B-54	Sequence 54, Appl	C 330	13.2	69.5	672	3	US-08-906-769-16	Sequence 16, Appl
C 258	13.2	69.5	321	3	US-09-490-070A-54	Sequence 54, Appl	C 331	13.2	69.5	672	6	PCT-US95-1442A-2201	Sequence 2201, Ap
C 259	13.2	69.5	321	3	US-09-490-153-54	Sequence 54, Appl	C 332	13.2	69.5	777	3	US-09-107-532A-2201	Sequence 2201, Ap
C 260	13.2	69.5	321	3	US-09-490-153-54	Sequence 54, Appl	C 333	13.2	69.5	848	2	US-07-998-636-1	Sequence 1, Appl
C 261	13.2	69.5	324	3	US-08-956-171E-4279	Sequence 4279, Ap	C 334	13.2	69.5	884	3	US-09-774-639-23	Sequence 23, Appl
C 262	13.2	69.5	324	3	US-08-781-986A-4279	Sequence 4279, Ap	C 335	13.2	69.5	891	3	US-09-602-787A-273	Sequence 273, Appl
C 263	13.2	69.5	372	3	US-09-270-767-1879	Sequence 1879, Ap	C 336	13.2	69.5	891	4	US-09-605-703B-945	Sequence 945, Appl
C 264	13.2	69.5	400	3	US-08-956-171E-17161	Sequence 17161, A	C 337	13.2	69.5	891	4	US-09-605-703B-947	Sequence 947, Appl
C 265	13.2	69.5	400	3	US-08-956-171E-3899	Sequence 3899, Ap	C 338	13.2	69.5	975	3	US-09-252-991A-5370	Sequence 5370, Ap
C 266	13.2	69.5	400	3	US-08-956-171E-3901	Sequence 3901, Ap	C 339	13.2	69.5	989	3	US-09-906-393A-19	Sequence 19, Appl
C 267	13.2	69.5	400	3	US-08-956-171E-4429	Sequence 4429, Ap	C 340	13.2	69.5	990	3	US-09-976-594-565	Sequence 565, Appl
C 268	13.2	69.5	400	3	US-08-781-986A-3899	Sequence 3899, Ap	C 341	13.2	69.5	990	3	US-09-919-039-224	Sequence 224, Appl
C 269	13.2	69.5	400	3	US-08-781-986A-3901	Sequence 3901, Ap	C 342	13.2	69.5	1008	3	US-08-235-836C-130	Sequence 130, Appl
C 270	13.2	69.5	400	3	US-08-781-986A-4429	Sequence 4429, Ap	C 343	13.2	69.5	1011	3	US-08-235-836C-131	Sequence 131, Appl
C 271	13.2	69.5	402	3	US-09-118-554-28	Sequence 28, Appl	C 344	13.2	69.5	1086	3	US-09-328-352-99	Sequence 99, Appl
C 272	13.2	69.5	402	3	US-09-118-627-28	Sequence 28, Appl	C 345	13.2	69.5	1182	3	US-09-489-039A-4766	Sequence 4766, Ap
C 273	13.2	69.5	402	3	US-09-602-877A-28	Sequence 28, Appl	C 346	13.2	69.5	1188	3	US-08-712-363-18	Sequence 18, Appl
C 274	13.2	69.5	426	3	US-09-252-991A-5382	Sequence 5382, Ap	C 347	13.2	69.5	1200	3	US-09-252-991A-5386	Sequence 5386, Ap
C 275	13.2	69.5	439	3	US-09-513-998C-1208	Sequence 1208, Ap	C 348	13.2	69.5	1236	3	US-09-758-759-50	Sequence 50, Appl
C 276	13.2	69.5	455	3	US-09-621-976-12457	Sequence 12457, A	C 349	13.2	69.5	1248	3	US-09-614-221A-439	Sequence 439, Appl
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C 278	13.2	69.5	458	3	US-08-781-986A-1219	Sequence 1219, Ap	C 351	13.2	69.5	1283	3	US-09-956-004-72	Sequence 72, Appl
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C 282	13.2	69.5	564	3	US-09-252-991A-6135	Sequence 6135, Ap	C 355	13.2	69.5	1482	3	US-10-267-311-18	Sequence 18, Appl
C 283	13.2	69.5	601	3	US-09-949-016-19024	Sequence 19024, A	C 356	13.2	69.5	1517	3	US-09-270-767-12029	Sequence 12029, A
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C 285	13.2	69.5	601	3	US-09-949-016-27785	Sequence 27785, A	C 358	13.2	69.5	1805	3	US-08-016-434-1086	Sequence 1086, Ap
C 286	13.2	69.5	601	3	US-09-949-016-27786	Sequence 27786, A	C 359	13.2	69.5	1805	3	US-09-949-016-851	Sequence 851, Appl
C 287	13.2	69.5	601	3	US-09-949-016-27787	Sequence 27787, A	C 360	13.2	69.5	1805	3	US-09-949-016-3817	Sequence 3817, Ap
C 288	13.2	69.5	601	3	US-09-949-016-43042	Sequence 43042, A	C 361	13.2	69.5	2034	3	US-09-489-847-83	Sequence 83, Appl
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C 291	13.2	69.5	601	3	US-09-949-016-55403	Sequence 55403, A	C 364	13.2	69.5	2103	3	US-08-489-039A-6292	Sequence 6292, Ap
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C 294	13.2	69.5	601	3	US-09-949-016-104752	Sequence 104752, A	C 367	13.2	69.5	2493	3	US-09-252-991A-12390	Sequence 12390, A
C 295	13.2	69.5	601	3	US-09-949-016-107955	Sequence 107955, A	C 368	13.2	69.5	2682	3	US-09-489-039A-6956	Sequence 6956, Ap
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C 297	13.2	69.5	601	3	US-09-949-016-110156	Sequence 110156, A	C 370	13.2	69.5	3024	3	US-08-252-991A-12202	Sequence 12202, A
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C 299	13.2	69.5	601	3	US-09-949-016-129194	Sequence 129194, A	C 372	13.2	69.5	3997	3	US-09-345-236B-145	Sequence 145, Appl
C 300	13.2	69.5	601	3	US-09-949-016-129195	Sequence 129195, A	C 373	13.2	69.5	3997	3	US-09-345-236B-146	Sequence 146, Appl
C 301	13.2	69.5	601	3	US-09-949-016-131028	Sequence 131028, A	C 374	13.2	69.5	4029	3	US-08-956-171E-301	Sequence 301, Appl
C 302	13.2	69.5	601	3	US-09-949-016-140363	Sequence 140363, A	C 375	13.2	69.5	4029	3	US-08-781-986A-301	Sequence 301, Appl
C 303	13.2	69.5	601	3	US-09-949-016-172153	Sequence 172153, A	C 376	13.2	69.5	4308	3	US-09-634-228-182	Sequence 182, Appl
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C 305	13.2	69.5	601	3	US-09-949-016-202288	Sequence 202288, A	C 378	13.2	69.5	4415	3	US-09-486-580A-1	Sequence 1, Appl
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C 309	13.2	69.5	601	3	US-09-949-002-2054	Sequence 2054, Ap	C 382	13.2	69.5	5806	3	US-09-949-016-15559	Sequence 15559, A
C 310	13.2	69.5	601	3	US-09-949-002-2055	Sequence 2055, Ap	C 383	13.2	69.5	5838	2	US-08-578-096A-1	Sequence 1, Appl
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C 313	13.2	69.5	636	3	US-09-736-457-1530	Sequence 1530, Ap	C 386	13.2	69.5	7585	3	US-09-949-016-14641	Sequence 14641, A
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C 316	13.2	69.5	636	3	US-09-658-824-1530	Sequence 1530, Ap	C 389	13.2	69.5	9901	3	US-09-949-016-16834	Sequence 16834, A

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C 332	13.2	69.5	12687	3	US-08-981-459-1	Sequence 1, Appli
C 333	13.2	69.5	12687	3	US-09-063-431A-1	Sequence 1, Appli
C 334	13.2	69.5	15363	3	US-08-961-527-139	Sequence 139, App
C 335	13.2	69.5	15572	3	US-09-902-540-1131	Sequence 1131, Ap
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C 339	13.2	69.5	20513	3	US-09-949-016-13930	Sequence 13930, A
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C 405	13.2	69.5	32654	3	US-10-345-198-3	Sequence 3, Appli
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C 407	13.2	69.5	38078	3	US-09-949-016-12429	Sequence 12429, A
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C 415	13.2	69.5	45833	3	US-09-949-016-14333	Sequence 14333, A
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C 452	13.2	69.5	131332	3	US-09-949-016-15535	Sequence 15535, A
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C 454	13.2	69.5	166698	3	US-09-949-016-16038	Sequence 16038, A
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C 460	13.2	69.5	209210	3	US-09-949-016-15094	Sequence 15094, A
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C 462	13.2	69.5	209632	3	US-09-949-002-802	Sequence 802, App
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C 466	13.2	69.5	285478	3	US-09-949-016-13362	Sequence 13362, A
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C 470	13.2	69.5	312957	3	US-09-949-001-31	Sequence 31, Appl
C 471	13.2	69.5	312972	3	US-09-949-001-34	Sequence 34, Appl
C 472	13.2	69.5	312972	3	US-09-949-001-34	Sequence 34, Appl
C 473	13.2	69.5	330890	3	US-09-949-016-14720	Sequence 14720, A
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C 475	13.2	69.5	1230025	3	US-09-438-185A-1	Sequence 1, Appli
C 476	13	68.4	466	3	US-09-910-430-15	Sequence 15, Appl
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C 479	13	68.4	601	3	US-09-949-016-57837	Sequence 57837, A
C 480	13	68.4	601	3	US-09-949-016-61181	Sequence 61181, A
C 481	13	68.4	954	3	US-10-043-238-2	Sequence 2, Appli
C 482	13	68.4	1038	3	US-09-543-681A-368	Sequence 368, App
C 483	13	68.4	1393	6	PCT-US93-07261-12	Sequence 12, Appl
C 484	13	68.4	1670	3	US-09-910-430-17	Sequence 17, Appl
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C 487	13	68.4	6663	3	US-09-335-011-15	Sequence 15, Appl
C 488	13	68.4	7223	3	US-09-335-011-8	Sequence 8, Appli
C 489	13	68.4	15164	3	US-09-949-016-11759	Sequence 11759, A
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C 492	13	68.4	31720	3	US-09-949-016-16947	Sequence 16947, A
C 493	13	68.4	109690	3	US-09-949-016-13525	Sequence 13525, A
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C 495	13	68.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 496	12.8	67.4	18	3	US-09-422-978-8815	Sequence 8815, Ap
C 497	12.8	67.4	20	3	US-07-998-289B-18	Sequence 18, Appl
C 498	12.8	67.4	25	3	US-09-396-196G-38020	Sequence 38020, A
C 499	12.8	67.4	25	3	US-09-396-196G-38021	Sequence 38021, A
C 500	12.8	67.4	25	3	US-09-396-196G-38022	Sequence 38022, A
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RESULT 1						
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; APPLICANT: Tseng, Yang-Yuan						
; APPLICANT: Wang, Yih-Weng						
; APPLICANT: Wang, Shing-Hwan						
; TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses and the p						
; TITLE OF INVENTION: and Probes Therefor						
; FILE REFERENCE: TAI 316						
; CURRENT APPLICATION NUMBER: US/09/724,678D						
; CURRENT FILING DATE: 2000-11-28						
; NUMBER OF SEQ ID NOS: 16						
; SOFTWARE: PatentIn version 3.1						
; SEQ ID NO 9						
; LENGTH: 27						
; TYPE: DNA						
; ORGANISM: Artificial Sequence						
; FEATURE:						
; OTHER INFORMATION: Artificial Sequence is Synthesized						
; Patent No. 6818397						
US-09-724-678D-9						
Query Match 100.0%; Score 19; DB 3; Length 27;						
Best Local Similarity 100.0%; Pred. No. 0.71;						
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						

Qy 1 CCCCTGAATGCGGCTAATC 19
 Db 9 CCCCTGAATGCGGCTAATC 27

RESULT 2

US-08-387-845-5
 ; Sequence 5, Application US/08387845
 ; Patent No. 5685567
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
 ; TITLE OF INVENTION: bicistronic vector system in mammalian cells
 ; NUMBER OF SEQUENCES: 16
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/387,845
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 628 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; ORIGINAL SOURCE:
 ; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
 ; IMMEDIATE SOURCE:
 ; CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 1..628
 ; OTHER INFORMATION: /note= "shown are the first
 ; OTHER INFORMATION: 628 nt of the 5' non-translated region of
 ; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 610
 ; OTHER INFORMATION: /note= "non-authentic sequence
 ; OTHER INFORMATION: due to a base pair substitution from C to G
 ; OTHER INFORMATION: at position 610"
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Sarnow, P.
 ; JOURNAL: J. Virol.
 ; VOLUME: 63
 ; PAGES: 467-470
 ; DATE: 1989
 ; US-08-387-845-5

Query Match 100.0%; Score 19; DB 2; Length 628;

Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
 Db 451 CCCCTGAATGCGGCTAATC 469

RESULT 3

US-08-778-275-5
 ; Sequence 5, Application US/08778275
 ; Patent No. 5935819
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
 ; TITLE OF INVENTION: bicistronic vector system in mammalian cells
 ; NUMBER OF SEQUENCES: 16
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/778,275
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/387,845
 FILING DATE:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 628 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ORIGINAL SOURCE:
 ORGANISM: Poliovirus Typ 1 (Mahoney strain)
 IMMEDIATE SOURCE:
 CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..628
 OTHER INFORMATION: /note= "shown are the first
 OTHER INFORMATION: 628 nt of the 5' non-translated region of
 OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
 FEATURE:
 NAME/KEY: -
 LOCATION: 610
 OTHER INFORMATION: /note= "non-authentic sequence
 OTHER INFORMATION: due to a base pair substitution from C to G
 OTHER INFORMATION: at position 610"
 PUBLICATION INFORMATION:
 AUTHORS: Sarnow, P.
 JOURNAL: J. Virol.
 VOLUME: 63
 PAGES: 467-470
 DATE: 1989
 US-08-778-275-5

Query Match 100.0%; Score 19; DB 2; Length 628;

Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
 Db 451 CCCCTGAATGCGGCTAATC 469

RESULT 4

US-08-867-352-5
 ; Sequence 5, Application US/08867352
 ; Patent No. 6060273
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Multicistronic expression units and their use
 ; NUMBER OF SEQUENCES: 25
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/867,352
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/387,847
 ; FILING DATE:
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 628 base pairs
 ; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
; IMMEDIATE SOURCE:
; CLONE: pGEM3-5-Polio (M) (4708 bp), (Sarnow, 1989)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..628 /note= "shown are the first
; OTHER INFORMATION: 628 nt of the 5' non-translated region of
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
; FEATURE:
; NAME/KEY: -
; LOCATION: 610
; OTHER INFORMATION: /note= "non-authentic sequence
; OTHER INFORMATION: due to a base pair substitution from C to G
; OTHER INFORMATION: at Location 610"
; PUBLICATION INFORMATION:
; AUTHORS: Sarnow, P.
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-867-352-5

Query Match 100.0%; Score 19; DB 3; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||
Db 451 CCCCTGAATGGCGCTAATC 469

RESULT 5
US-09-116-032-2
; Sequence 2, Application US/09116032
; Patent No. 6200576
; GENERAL INFORMATION:
; APPLICANT: HWONG, CHING LONG
; APPLICANT: LO, CHENG-KAI
; APPLICANT: YANG, YING-CHUAN
; APPLICANT: JENG, KING-SONG
; APPLICANT: CHANG, EDWARD L.
; APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY
; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
; FILE REFERENCE: 9751.79US01
; CURRENT APPLICATION NUMBER: US/09/116,032
; EARLIER APPLICATION NUMBER: 1998-07-15
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1220
; TYPE: DNA
; ORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-2

Query Match 100.0%; Score 19; DB 3; Length 1220;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||
Db 454 CCCCTGAATGGCGCTAATC 472

RESULT 6
US-09-724-678D-16
; Sequence 16, Application US/09724678D

; Patent No. 6818397
; GENERAL INFORMATION:
; APPLICANT: Lee, Kang-Hung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Tseng, Yang-Yuan
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Wang, Shing-Hwan
; TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses and the P
; FILE REFERENCE: TAI 316
; CURRENT APPLICATION NUMBER: US/09/724,678D
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-09-724-678D-16

Query Match 100.0%; Score 19; DB 3; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||
Db 456 CCCCTGAATGGCGCTAATC 474

RESULT 7

US-09-202-904A-10
; Sequence 10, Application US/09202904A
; Patent No. 6395471
; GENERAL INFORMATION:
; APPLICANT: Kang, Sung Key
; APPLICANT: Hahn, Bumsuk
; TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing
; TITLE OF INVENTION: the Activity of Hepatitis C Virus Protease, a Recombinant
; FILE REFERENCE: A32210-PCT-USA 072944.0104
; CURRENT APPLICATION NUMBER: US/09/202,904A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/KR97/00120
; PRIOR FILING DATE: 1997-06-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Genetically engineered virus derived from
; OTHER INFORMATION: poliovirus and hepatitis C virus
US-09-202-904A-10

Query Match 100.0%; Score 19; DB 3; Length 2320;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||
Db 451 CCCCTGAATGGCGCTAATC 469

RESULT 8

US-09-116-032-1
; Sequence 1, Application US/09116032
; Patent No. 6200576
; GENERAL INFORMATION:
; APPLICANT: HWONG, CHING LONG
; APPLICANT: LO, CHENG-KAI
; APPLICANT: YANG, YING-CHUAN
; APPLICANT: JENG, KING-SONG

APPLICANT: CHANG, EDWARD L.
APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY
TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
FILE REFERENCE: 9751.79US01
CURRENT APPLICATION NUMBER: US/09/116,032
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: CHINA 86105814
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 7400
TYPE: DNA
ORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-1

Query Match 100.0%; Score 19; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 454 CCCCTGAATGCGGCTAATC 472

RESULT 9
US-09-284-349B-1
Sequence 1, Application US/09284349B
Patent No. 6696289
GENERAL INFORMATION:
APPLICANT: Yong Soo, Bae
APPLICANT: Jung, Hye Rhan
TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain
FILE REFERENCE: Docket No. 6696289; 4220-109 US
CURRENT APPLICATION NUMBER: US/09/284,349B
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: PCT/KR98/00242
PRIOR FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: KR 97/37812
PRIOR FILING DATE: 1997-07-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 7441
TYPE: DNA
ORGANISM: Human poliovirus 1
US-09-284-349B-1

Query Match 100.0%; Score 19; DB 3; Length 7441;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 451 CCCCTGAATGCGGCTAATC 469

RESULT 10
US-09-311-260-105
Sequence 105, Application US/09311260
Patent No. 6214555
GENERAL INFORMATION:
APPLICANT: Leushner, James
APPLICANT: Hui, May
APPLICANT: Dunn, James M.
APPLICANT: Lacroix, Jean-Michel
TITLE OF INVENTION: METHOD, COMPOSITIONS AND KIT FOR DETECTION OF
TITLE OF INVENTION: MICROORGANISMS AND BI-DIRECTIONAL SEQUENCING OF NUCLEIC ACID
TITLE OF INVENTION: POLYMERS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson LLP

STREET: P.O. Box 5270
CITY: Frisco
STATE: CO
COUNTRY: US
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/311,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-058-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2082
TELEX:
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
US-09-311-260-105

Query Match 94.7%; Score 18; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAAT 18
Db 8 CCCCTGAATGCGGCTAAT 25

RESULT 11
US-09-061-273-9
Sequence 9, Application US/09061273
Patent No. 6258570
GENERAL INFORMATION:
APPLICANT: Glustein, Joseph Z.
APPLICANT: Ehrlich, Garth D.
APPLICANT: Zhang, Yingze
TITLE OF INVENTION: PCR Assay For Bacterial and
TITLE OF INVENTION: Viral Meningitis
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Pittsburgh
STREET: Office of Technology Transfer
STREET: 911 William Pitt Union
CITY: Pittsburgh
STATE: Pennsylvania
COUNTRY: USA
ZIP: 15260
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" high density diskette
COMPUTER: IBM PC or compatibles
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,273
FILING DATE: 17-APR-1998

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6258570 applicable
; FILING DATE: No. 6258570 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary-Elizabeth Buckles
; REGISTRATION NUMBER: 31,907
; REFERENCE/DOCKET NUMBER: 017917/20132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/414-3267
; TELEFAX: 202/414/9299
; TELEX: 64711
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: synthetic DNA
US-09-061-273-9

Query Match          94.7%; Score 18; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
   |||||
Db 8 CCCCTGAATCGGCTAAT 25

RESULT 12
US-09-313-221A-114
; Sequence 114, Application US/09313221A
; Patent No. 6468743
; GENERAL INFORMATION:
; APPLICANT: Thomas L. Romick (Inventor)
; APPLICANT: Mark S. Fraser (Inventor)
; TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
; TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS
; FILE REFERENCE: HUNT-042784
; CURRENT APPLICATION NUMBER: US/09/313,221A
; CURRENT FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/086,025
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Related to Entoviruses
US-09-313-221A-114

Query Match          94.7%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
   |||||
Db 8 CCCCTGAATCGGCTAAT 25

RESULT 13
US-07-852-260-1
; Sequence 1, Application US/07852260
; Patent No. 5525715
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatam, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
; TITLE OF INVENTION: CDNA
```

```
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/852,260
; FILING DATE: 19920619
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-B-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
US-07-852-260-1

Query Match          94.7%; Score 18; DB 2; Length 7432;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
   |||||
Db 454 CCCCTGAATCGGCTAAT 471

RESULT 14
US-08-461-503-1
; Sequence 1, Application US/08461503
; Patent No. 5834302
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatam, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
; TITLE OF INVENTION: FROM CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,503
```

;; FILING DATE: 5-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 278-0400
;; TELEFAX: (212) 391-0525
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7432 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 743..7361
US-08-461-503-1

Query Match 94.7%; Score 18; DB 2; Length 7432;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAAT 18
|||||
DB 454 CCCCTGAATGGCGCTAAT 471

RESULT 15
US-08-465-250-1
; Sequence 1, Application US/08465250
; Patent No. 6136570
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatem, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,250
; FILING DATE: 6-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-E-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 743..7361
US-08-465-250-1

Query Match 94.7%; Score 18; DB 3; Length 7432;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAAT 18
|||||
DB 454 CCCCTGAATGGCGCTAAT 471

RESULT 16
US-08-221-816B-31
; Sequence 31, Application US/08221816B
; Patent No. 5738985
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-221-816B-31

Query Match 91.6%; Score 17.4; DB 2; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19
|||||
DB 457 CCCUGAUGCGGUAAACC 475

RESULT 17

US-10-112-547-31
; Sequence 31, Application US/10112547
; Patent No. 6579674
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,547
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-112-547-31

Query Match 91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
||||:||||:||||:|
Db 457 CCCUGAAGCGCUAAC 475

RESULT 18

US-10-112-241-31
; Sequence 31, Application US/10112241
; Patent No. 6623961
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,241
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-112-241-31

Query Match 91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
||||:||||:||||:|
Db 457 CCCUGAAGCGCUAAC 475

RESULT 19

US-10-104-611-31
; Sequence 31, Application US/10104611
; Patent No. 6667152
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/104,611
; FILING DATE: 22-Mar-2002

```
;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31

Query Match          91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCCTGAATGCGGCTAATC 19
DB      457 CCCUGAAGCGGUAACC 475

RESULT 20
US-10-109-368-31
; Sequence 31, Application US/10109368
; Patent No. 677179
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31

Query Match          91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCCTGAATGCGGCTAATC 19
DB      457 CCCUGAAGCGGUAACC 475

RESULT 20
US-10-109-368-31
; Sequence 31, Application US/10109368
; Patent No. 677179
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31
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;
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-109-368-31

Query Match          91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCCTGAATGCGGCTAATC 19
DB      457 CCCUGAAGCGGUAACC 475

RESULT 21
US-09-724-380-31
; Sequence 31, Application US/09724380
; Patent No. 6824976
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,380
; FILING DATE: 01-APR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-724-380-31

Query Match          91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCCTGAATGCGGCTAATC 19
DB      457 CCCUGAAGCGGUAACC 475
```

```
Db 457 CCCUGAUGCGGCUAAC 475

RESULT 22
US-08-246-373-1
; Sequence 1, Application US/08246373
; Patent No. 5550018
; GENERAL INFORMATION:
; APPLICANT: LEVENBOOK, Inessa
; APPLICANT: CHUMAKOV, Konstantin
; APPLICANT: POWERS, Laurie
; APPLICANT: RONINSON, Igor
; TITLE OF INVENTION: "TEST FOR VIRULENT REVERTANTS IN
; TITLE OF INVENTION: ATTENUATED LIVE VACCINES"
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 No. 5550018th Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246.373
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/607,742
; FILING DATE: No. 5550018ember 6, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald M. Murphy, Jr.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1173-234P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 241-1300
; TELEFAX: (703) 241-0369
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: sense strand PCR primer
; ANTI-SENSE: (N)
;
US-08-246-373-1
Query Match 86.3%; Score 16.4; DB 2; Length 32;
Best Local Similarity 94.4%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAAT 18
Db 15 CCCCTGAATGCGGCTGAT 32

RESULT 23
5340713-1
; Patent No. 5340713
; APPLICANT: TORGENSEN, HELGE;SKERN, TIMOTHY;BLAAS, DIETER
; TITLE OF INVENTION: PROCESS FOR THE CHARACTERIZATION OF
; HUMAN RHINOVIRUSES
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/541.907
; FILING DATE: 22-JUN-1990
; SEQ ID NO:1:

;
LENGTH: 250
5340713-1

Query Match 83.2%; Score 15.8; DB 9; Length 250;
Best Local Similarity 89.5%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 202 CCCCTGAATGTGGCTAACC 220

RESULT 24
US-09-489-039A-5242
; Sequence 5242, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5242
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
;
US-09-489-039A-5242
Query Match 81.1%; Score 15.4; DB 3; Length 1269;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
Db 1067 CGCTGAATGCGGCTAAT 1083

RESULT 25
US-09-949-016-15436
; Sequence 15436, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15436
; LENGTH: 199945
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-15436
Query Match 81.1%; Score 15.4; DB 3; Length 199945;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
Db 168571 CCCTGAATGCGGCTAAT 168587
```

RESULT 26
US-08-361-337-36
; Sequence 36, Application US/08361337
; Patent No. 5728519
; GENERAL INFORMATION:
; APPLICANT: Levenbook, Inessa S.
; APPLICANT: Chumakov, Konstantin M.
; APPLICANT: No. 5728519wood, Laurie P.
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.337
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.634
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-361-337-36
Query Match 78.9%; Score 15; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCT 15
Db 21 CCCCTGAATGCGGCT 35

RESULT 27
US-08-361-337-38
; Sequence 38, Application US/08361337
; Patent No. 5728519
; GENERAL INFORMATION:
; APPLICANT: Levenbook, Inessa S.
; APPLICANT: Chumakov, Konstantin M.
; APPLICANT: No. 5728519wood, Laurie P.
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA

ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.337
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.634
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-361-337-38

Query Match 78.9%; Score 15; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGCGGCTAATC 19
Db 1 TGAATGCGGCTAATC 15

RESULT 28
US-09-949-016-34646
; Sequence 34646, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34646
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-34646

Query Match 77.9%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
Db 393 CCCTGAATGCGGCTGATC 410

RESULT 29
US-09-949-016-146512/c
; Sequence 146512, Application US/09949016
; Patent No. 6812339

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146512
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-146512

Query Match          77.9%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCCCTGAATGCGGCTAAT 18
        |||||
Db      580 CCCCTGAATGCAACTAAT 563

RESULT 30
US-09-949-016-170260
; Sequence 170260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170260
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-170260

Query Match          77.9%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCTGAATGCGGCTAATC 19
        |||||
Db      393 CCCTGAATGCGGCTAATC 410

RESULT 31
US-09-270-767-13998/c
; Sequence 13998, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
```

```
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13998
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13998

Query Match          77.9%; Score 14.8; DB 3; Length 678;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCTGAATGCGGCTAATC 19
        |||||
Db      299 CTCTGAATGTGGCTAATC 282

RESULT 32
US-09-270-767-13244
; Sequence 13244, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13244
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13244

Query Match          77.9%; Score 14.8; DB 3; Length 960;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCTGAATGCGGCTAATC 19
        |||||
Db      689 CTCTGAATGTGGCTAATC 706

RESULT 33
US-09-614-221A-478/c
; Sequence 478, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 478
; LENGTH: 4086
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-478

Query Match          77.9%; Score 14.8; DB 3; Length 4086;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCTGAATGCGGCTAATC 19
        |||||
```

Db 408 CCTGATGCGGAGATC 391

RESULT 34

US-09-453-702B-194
; Sequence 194, Application US/09453702B
; Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 194:

SEQUENCE CHARACTERISTICS:

LENGTH: 9057

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 194:

US-09-453-702B-194

Query Match 77.9%; Score 14.8; DB 3; Length 9057;

Best Local Similarity 88.9%; Pred. No. 2.8e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGATGCGGCTAATC 19

Db 4504 CACTGATGCGGCTAATC 4521

RESULT 35

US-10-114-170-194

; Sequence 194, Application US/10114170

; Patent No. 6855814

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod

TITLE OF INVENTION: No. 6855814el Sequences of E. coli 0157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,170

FILING DATE: 01-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/453,702

FILING DATE: 03-DEC-1999

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 194:

SEQUENCE CHARACTERISTICS:

LENGTH: 9057

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 194:

US-10-114-170-194

Query Match 77.9%; Score 14.8; DB 3; Length 9057;

Best Local Similarity 88.9%; Pred. No. 2.8e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGATGCGGCTAATC 19

Db 4504 CACTGATGCGGCTAATC 4521

RESULT 36

US-08-611-280-4/c

; Sequence 4, Application US/08611280

; Patent No. 5891666

GENERAL INFORMATION:

APPLICANT: Matsuyama, Toshifumi

APPLICANT: Grossman, Alex

APPLICANT: Richardson, Christopher D.

TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Canada Inc.

STREET: 6733 Mississauga Road, Suite 303

CITY: Mississauga

STATE: Ontario

COUNTRY: Canada

ZIP: L5N 6J8

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/611,280

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-611-280-4

Query Match 77.9%; Score 14.8; DB 2; Length 12537;
Best Local Similarity 88.9%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 2 CCCTGAATGCGGCTAATC 19
|||||
Db 1565 CCCTGAATGCTGCTAACC 1548

RESULT 37

US-09-195-940-4/c
Sequence 4, Application US/09195940
Patent No. 6258935
GENERAL INFORMATION:

APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP: L5N 6J8

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,940
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/611,280
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 12537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-195-940-4

Query Match 77.9%; Score 14.8; DB 3; Length 12537;
Best Local Similarity 88.9%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 2 CCCTGAATGCGGCTAATC 19
|||||
Db 1565 CCCTGAATGCTGCTAACC 1548

RESULT 38

US-09-562-466-4/c
Sequence 4, Application US/09562466
Patent No. 6369202
GENERAL INFORMATION:

APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP: L5N 6J8

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,466
FILING DATE: 01-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/195,940
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-562-466-4
Query Match 77.9%; Score 14.8; DB 3; Length 12537;
Best Local Similarity 88.9%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 2 CCCTGAATGCGGCTAATC 19
|||||
Db 1565 CCCTGAATGCTGCTAACC 1548

RESULT 39

US-09-949-016-17245/c
Sequence 17245, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17245
LENGTH: 16083
TYPE: DNA

ORGANISM: Human
US-09-949-016-17245

Query Match 77.9%; Score 14.8; DB 3; Length 16083;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGCGCTAAT 18
|||||
Db 15339 CCCTGAATGGCGCGAAT 15322

RESULT 40

US-10-164-230-2/c
; Sequence 2, Application US/10164230
; Patent No. 6933118
; GENERAL INFORMATION:
; APPLICANT: Inoko, Hidetoshi
; APPLICANT: Tamiya, Gen
; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
; FILE REFERENCE: 06501-112US1
; CURRENT APPLICATION NUMBER: US/10/164,230
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: PCT/JP00/08624
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11/346867
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 25235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)....(420)
; NAME/KEY: exon
; LOCATION: (1282)....(1405)
; NAME/KEY: exon
; LOCATION: (1602)....(1702)
; NAME/KEY: exon
; LOCATION: (1602)....(1631)
; NAME/KEY: exon
; LOCATION: (2352)....(2364)
; NAME/KEY: exon
; LOCATION: (6287)....(6509)
; NAME/KEY: exon
; LOCATION: (10417)....(10493)
; NAME/KEY: exon
; LOCATION: (14244)....(14407)
; NAME/KEY: exon
; LOCATION: (14244)....(14344)
; NAME/KEY: exon
; LOCATION: (25190)....(25235)

Query Match 77.9%; Score 14.8; DB 3; Length 25235;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGCGCTAAT 18
|||||
Db 18057 CCCTGAATGGCGCTAAT 18040

RESULT 41

US-09-949-016-16549
; Sequence 16549, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16549
; LENGTH: 47555
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16549

Query Match 77.9%; Score 14.8; DB 3; Length 47555;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAATC 19
|||||
Db 30940 CCCTGAATGGCGCTGATC 30957

RESULT 42

US-09-949-016-12598
; Sequence 12598, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12598
; LENGTH: 49673
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12598

Query Match 77.9%; Score 14.8; DB 3; Length 49673;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAATC 19
|||||
Db 30940 CCCTGAATGGCGCTGATC 30957

RESULT 43

US-09-949-016-17433/c
; Sequence 17433, Application US/09949016
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17433
; LENGTH: 101349
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17433

Query Match          77.9%; Score 14.8; DB 3; Length 101349;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCTGAATGCGGCTAATC 19
      ||||| ||||| ||||| |||||
Db      79405 CCCTGAAGGCGAGCTAATC 79388

RESULT 44
US-09-949-016-13765
; Sequence 13765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13765
; LENGTH: 128470
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13765

Query Match          77.9%; Score 14.8; DB 3; Length 128470;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCTGAATGCGGCTAATC 19
      ||||| ||||| ||||| |||||
Db      6099 CCCTGAATGCTTCTAATC 6116

RESULT 45
US-09-949-016-15890/c
; Sequence 15890, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15890
; LENGTH: 144922
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15890

Query Match          77.9%; Score 14.8; DB 3; Length 144922;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCTGAATGCGGCTAATC 19
      ||||| ||||| ||||| |||||
Db      70425 CCCTGAATGCGTCCAATC 70408

RESULT 46
US-09-949-016-15858
; Sequence 15858, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15858
; LENGTH: 145320
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15858

Query Match          77.9%; Score 14.8; DB 3; Length 145320;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCCTGAATGCGGCTAAT 18
      ||||| ||||| ||||| |||||
Db      30228 CCCTGAATGCACTAAT 30245

RESULT 47
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
```

```
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 3; Length 4403765;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAATC 19
|||
Db 1547708 CCTGAATGCGGGAATC 1547691

RESULT 48
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 3; Length 4411529;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAATC 19
|||
Db 1547869 CCTGAATGCGGGAATC 1547852

RESULT 49
US-09-702-705-1724
; Sequence 1724, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833

; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 3; Length 4403765;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAATC 19
|||
Db 1547708 CCTGAATGCGGGAATC 1547691

RESULT 48
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 3; Length 4411529;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAATC 19
|||
Db 1547869 CCTGAATGCGGGAATC 1547852

RESULT 49
US-09-702-705-1724
; Sequence 1724, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1724
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-1724

Query Match
Best Local Similarity 75.8%; Score 14.4; DB 3; Length 145;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAAT 18
|||
Db 116 CCATGNATGCGGCTAAT 132

RESULT 50
US-09-736-457-1724
; Sequence 1724, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1724
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-1724

Query Match
Best Local Similarity 75.8%; Score 14.4; DB 3; Length 145;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAAT 18
|||
Db 116 CCATGNATGCGGCTAAT 132

RESULT 51
US-09-671-325-1724
; Sequence 1724, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
```

; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1724
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-671-325-1724

Query Match 75.8%; Score 14.4; DB 3; Length 145;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
||| ||||| ||||| |||||
Db 116 CCATGNATGCGGCTAAT 132

RESULT 52
US-09-658-824-1724

; Sequence 1724, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1724
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-658-824-1724

Query Match 75.8%; Score 14.4; DB 3; Length 145;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
||| ||||| ||||| |||||
Db 116 CCATGNATGCGGCTAAT 132

RESULT 53
US-10-017-754-1724

; Sequence 1724, Application US/10017754
; Patent No. 6858204
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Ronger, Gary R.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: AND DIAGNOSIS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1724
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4, 12, 27, 32, 45, 47, 48, 59, 61, 65, 93, 98, 103, 121
; OTHER INFORMATION: n = A,T,C or G
US-10-017-754-1724

Query Match 75.8%; Score 14.4; DB 3; Length 145;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
||| ||||| ||||| |||||
Db 116 CCATGNATGCGGCTAAT 132

RESULT 54

US-09-270-767-27427
; Sequence 27427, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27427
; LENGTH: 671
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-27427

Query Match 75.8%; Score 14.4; DB 3; Length 671;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGAATGCGGCTAATC 19
||| ||||| ||||| |||||
Db 79 CTGAATGCGGCTAATC 94

RESULT 55

US-09-902-540-8469
; Sequence 8469, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.

```

; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8469
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8469

Query Match      75.8%; Score 14.4; DB 3; Length 1494;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTA 16
DB 535 CCCCTGAATGGCGGTA 550

RESULT 56
US-09-221-017B-461/c
; Sequence 461, Application US/09221017B
; Patent No. 644799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Montoy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 461:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1660 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

```

```

; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORYPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...1660
US-09-221-017B-461

Query Match      75.8%; Score 14.4; DB 3; Length 1660;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGAATGGCGCTAATC 19
DB 327 CTGAATGGCGCTAAGC 312

RESULT 57
US-09-270-767-11790
; Sequence 11790, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11790
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-11790

Query Match      75.8%; Score 14.4; DB 3; Length 2058;
Best Local Similarity 93.8%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGAATGGCGCTAATC 19
DB 79 CTGAATGGCGGTAATC 94

RESULT 58
US-09-902-540-891
; Sequence 891, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 891
; LENGTH: 6380
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-891

Query Match      75.8%; Score 14.4; DB 3; Length 6380;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;

```

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTA 16
 |||||
 Db 1168 CCCCTGAATGCGGCTA 1183

RESULT 59

US-09-524-101D-18
 ; Sequence 18, Application US/09524101D
 ; Patent No. 6762291
 ; GENERAL INFORMATION:
 ; APPLICANT: EXELIXIS, INC.
 ; TITLE OF INVENTION: INSECT P53 TUMOR SUPPRESSOR GENES AND PROTEINS
 ; FILE REFERENCE: EX00015C FIRST AMENDMENT
 ; CURRENT APPLICATION NUMBER: US/09/524,101D
 ; CURRENT FILING DATE: 2000-03-13
 ; PRIOR APPLICATION NUMBER: US 09/268,969
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: US 60/184,373
 ; PRIOR FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 18
 ; LENGTH: 27425
 ; TYPE: DNA
 ; ORGANISM: Drosophila melanogaster
 US-09-524-101D-18

Query Match 75.8%; Score 14.4; DB 3; Length 27425;
 Best Local Similarity 93.8%; Pred. No. 5.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGAATGCGGCTAATC 19
 |||||
 Db 3535 CTGAATGCGGCTAATC 3550

RESULT 60

US-09-949-016-12008/c
 ; Sequence 12008, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12008
 ; LENGTH: 331814
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(331814)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-12008

Query Match 75.8%; Score 14.4; DB 3; Length 331814;
 Best Local Similarity 93.8%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18
 |||||

Db 79048 CCTTAATGCGGCTAAT 79033

RESULT 61

US-09-949-016-17056/c
 ; Sequence 17056, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17056
 ; LENGTH: 331814
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(331814)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-17056

Query Match 75.8%; Score 14.4; DB 3; Length 331814;
 Best Local Similarity 93.8%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18
 |||||

Db 79048 CCTTAATGCGGCTAAT 79033

RESULT 62

US-09-513-999C-30496
 ; Sequence 30496, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; FILE REFERENCE: 59.US2.REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.Pm
 ; SEQ ID NO 30496
 ; LENGTH: 403
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 371
 ; OTHER INFORMATION: n=a, g, c or t
 US-09-513-999C-30496

Query Match 74.7%; Score 14.2; DB 3; Length 403;
 Best Local Similarity 84.2%; Pred. No. 4.1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19

; GENERAL INFORMATION:
 ; APPLICANT: Randy M. Berka

; APPLICANT: Michael W. Rey
 ; APPLICANT: Jeffrey R. Shuster
 ; APPLICANT: Sakari Kauppinen
 ; APPLICANT: Ib Groth Clausen
 ; APPLICANT: Peter Bjørke Olsen
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 ; FILE REFERENCE: 5849.200-US
 ; CURRENT APPLICATION NUMBER: US/09/533,559
 ; EARLIER FILING DATE: 2000-03-22
 ; PRIOR FILING DATE: 1999-03-22
 ; NUMBER OF SEQ ID NOS: 7860
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1622
 ; LENGTH: 608
 ; TYPE: DNA
 ; ORGANISM: Fusarium venenatum
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(608)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-533-559-1622

Query Match 74.7%; Score 14.2; DB 3; Length 608;
 Best Local Similarity 84.2%; Pred. No. 4.3e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 ||| ||||| ||||| |||||
 Db 208 CCCAAGAATCGGCTAATC 226

RESULT 68
 US-09-489-039A-5060
 ; Sequence 5060, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 5060
 ; LENGTH: 1020
 ; TYPE: DNA
 ; ORGANISM: Klebsiella pneumoniae
 ; US-09-489-039A-5060

Query Match 74.7%; Score 14.2; DB 3; Length 1020;
 Best Local Similarity 84.2%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 ||| ||||| ||||| |||||
 Db 508 CCGCTGATTGAGGCTAATC 526

RESULT 69
 US-10-029-180-61/c
 ; Sequence 61, Application US/10029180
 ; Patent No. 6806082
 ; GENERAL INFORMATION:
 ; APPLICANT: Cali, Brian M.
 ; APPLICANT: Holtzman, Doug
 ; APPLICANT: Madden, Kevin T.
 ; APPLICANT: Milna, G. Todd
 ; APPLICANT: Sherman, Amir
 ; APPLICANT: Silva, Jeffrey C.

; APPLICANT: Trueheart, Josh
 ; APPLICANT: Zhang, Lixin
 ; TITLE OF INVENTION: No. 6806082el Regulators of Fungal Gene Expression
 ; FILE REFERENCE: MIC-004
 ; CURRENT APPLICATION NUMBER: US/10/029,180
 ; CURRENT FILING DATE: 2001-12-22
 ; PRIOR APPLICATION NUMBER: US 60/257,431
 ; PRIOR FILING DATE: 2000-12-22
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 61
 ; LENGTH: 1095
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fungal gene
 ; US-10-029-180-61

Query Match 74.7%; Score 14.2; DB 3; Length 1095;
 Best Local Similarity 84.2%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 ||| ||||| ||||| |||||
 Db 418 CCTCTGAATACGGCTCATC 400

RESULT 70
 US-09-602-777A-393/c
 ; Sequence 393, Application US/09602777A
 ; Patent No. 6831165
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
 ; INVOLVED IN HOMEOSTASIS AND ADAPTATION
 ; FILE REFERENCE: BGI-128CP
 ; CURRENT APPLICATION NUMBER: US/09/602,777A
 ; CURRENT FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 60/141031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: DE 19931636.8
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19932125.6
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932126.4
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932127.2
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932128.0
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932129.9
 ; PRIOR FILING DATE: 1999-07-19
 ; PRIOR APPLICATION NUMBER: DE 19932226.0
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932920.6
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932922.2
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932924.9
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932928.1
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932930.3
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932933.8
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932935.4
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932973.7

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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 393
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1195)
; OTHER INFORMATION: RXN00136
US-09-602-777A-393

Query Match          74.7%; Score 14.2; DB 3; Length 1218;
Best Local Similarity 84.2%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CCCCTGAATGCGGTAATC 19
Db      1150 CCCCTGAATGCGGTAACC 1132

RESULT 71
US-08-426-236-1
; Sequence 1, Application US/08426236
; Patent No. 5629188
; GENERAL INFORMATION:
; APPLICANT: Shiba, Kiyotaka
; APPLICANT: Schimmel, Paul R.
; APPLICANT: Ripmaster, Tracy L.
; TITLE OF INVENTION: Human Alanyl-tRNA Synthetase Proteins,
; TITLE OF INVENTION: Nucleic Acids and Tester Strains Comprising Same
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,236
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPI94-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 111..3014
US-08-426-236-1

Query Match          74.7%; Score 14.2; DB 2; Length 3344;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CCCCTGAATGCGGTAATC 19
Db      2826 CCCCAATGCGGCAATC 2844

RESULT 72
US-09-220-132-73
; Sequence 73, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OTHER INFORMATION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 3344
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-73

Query Match          74.7%; Score 14.2; DB 3; Length 3344;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CCCCTGAATGCGGTAATC 19
Db      2826 CCCCAATGCGGCAATC 2844

RESULT 73
US-09-949-016-4054
; Sequence 4054, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4054
```

; LENGTH: 3344
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4054

Query Match 74.7%; Score 14.2; DB 3; Length 3344;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| |||||
Db 2826 CCCAGAATGAGCCAAATC 2844

RESULT 74
US-09-566-921-63
; Sequence 63, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 63
; LENGTH: 3505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 263336.12
US-09-566-921-63

Query Match 74.7%; Score 14.2; DB 3; Length 3505;
Best Local Similarity 84.2%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| |||||
Db 2847 CCCAGAATGAGCCAAATC 2865

RESULT 75
US-09-949-016-16816
; Sequence 16816, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16816
; LENGTH: 8165
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16816

Query Match 74.7%; Score 14.2; DB 3; Length 8165;
Best Local Similarity 84.2%; Pred. No. 6e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| |||||
Db 1339 CCCCTGAACGCGGCCAAGC 1357

RESULT 76
US-09-949-016-13284/c
; Sequence 13284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13284
; LENGTH: 9962
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13284

Query Match 74.7%; Score 14.2; DB 3; Length 9962;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| |||||
Db 1051 CCCCTTAATGTGCTAATC 1033

RESULT 77
US-09-949-016-13659/c
; Sequence 13659, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13659
; LENGTH: 23105
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13659

Query Match 74.7%; Score 14.2; DB 3; Length 23105;
Best Local Similarity 84.2%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| |||||
Db 13327 CCCCTGAATGTGGCTAAAC 13309

```
RESULT 78
US-09-949-016-12582/c
; Sequence 12582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12582
; LENGTH: 23108
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12582

Query Match          74.7%; Score 14.2; DB 3; Length 23108;
Best Local Similarity 84.2%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGAATGCGGCTAATC 19
   |||||
DB 13330 CCCTGAATGCGGTAAC 13312

RESULT 79
US-08-311-731A-124
; Sequence 124, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36033 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-124

Query Match          74.7%; Score 14.2; DB 3; Length 36033;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGAATGCGGCTAATC 19
   |||||
DB 13061 CGCTGAACGCGGCTAATC 13079

RESULT 80
US-09-949-016-12532/c
; Sequence 12532, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12532
; LENGTH: 49407
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(49407)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12532

Query Match          74.7%; Score 14.2; DB 3; Length 49407;
Best Local Similarity 84.2%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGAATGCGGCTAATC 19
   |||||
DB 26300 CTCTGAATGCTGGTAATC 26282

RESULT 81
US-09-949-016-17045/c
; Sequence 17045, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
```

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17045
; LENGTH: 49408
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(49408)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17045

Query Match 74.7%; Score 14.2; DB 3; Length 49408;
Best Local Similarity 84.2%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 26300 CTCCTGAATCGGCTAATC 26282

RESULT 82

US-09-949-016-16339
; Sequence 16339, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16339
; LENGTH: 79578
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16339

Query Match 74.7%; Score 14.2; DB 3; Length 79578;
Best Local Similarity 84.2%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 45634 CCCCTGAATCGGCTAACC 45652

RESULT 83

US-09-585-858-1
; Sequence 1, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjørleifsdóttir
; APPLICANT: Guðmundur O. Hreggvidsson
; APPLICANT: Olafur H. Friðjónsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/09/585,858
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02

; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 129908
; TYPE: DNA
; ORGANISM: Bacteriophage RM378
US-09-585-858-1

Query Match 74.7%; Score 14.2; DB 3; Length 129908;
Best Local Similarity 84.2%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 34425 CCCCTGAATCGGTTTGATC 34443

RESULT 84

US-10-270-878-1
; Sequence 1, Application US/10270878
; Patent No. 6818425
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjørleifsdóttir
; APPLICANT: Guðmundur O. Hreggvidsson
; APPLICANT: Olafur H. Friðjónsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,878
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 129908
; TYPE: DNA
; ORGANISM: Bacteriophage RM378
US-10-270-878-1

Query Match 74.7%; Score 14.2; DB 3; Length 129908;
Best Local Similarity 84.2%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 34425 CCCCTGAATCGGTTTGATC 34443

RESULT 85

US-09-949-016-16476
; Sequence 16476, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16476
; LENGTH: 141560
; TYPE: DNA

```
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(141560)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16476

Query Match      74.7%; Score 14.2; DB 3; Length 141560;
Best Local Similarity 84.2%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| ||||| |||||
DB 42787 CCCCTAATGTCGCTCATC 42805

RESULT 86
US-09-949-016-15868
; Sequence 15868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15868
; LENGTH: 374159
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15868

Query Match      74.7%; Score 14.2; DB 3; Length 374159;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| ||||| |||||
DB 357750 CCCCTGAATGTCGCTAGTC 357768

RESULT 87
US-08-956-171E-136/c
; Sequence 136, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
US-08-949-016-15868

Query Match      74.7%; Score 14; DB 3; Length 11823;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGAATGCGGCTAAT 18
||||| ||||| ||||| |||||
DB 4156 TGAATGCGGCTAAT 4143

RESULT 88
US-08-781-986A-136/c
; Sequence 136, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11823 base pairs
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; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11823 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-08-956-171E-136

Query Match      73.7%; Score 14; DB 3; Length 11823;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGAATGCGGCTAAT 18
||||| ||||| ||||| |||||
DB 4156 TGAATGCGGCTAAT 4143

RESULT 88
US-08-781-986A-136/c
; Sequence 136, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11823 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-136

Query Match      73.7%; Score 14; DB 3; Length 11823;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGGCGCTAAT 18
   |||||
Db 4156 TGAATGGCGCTAAT 4143

RESULT 89
US-09-270-767-8260
; Sequence 8260, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8260
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8260

Query Match      72.6%; Score 13.8; DB 3; Length 300;
Best Local Similarity 88.2%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAAT 18
   |||||
Db 231 CCCAGATGGCGCTGAT 247

RESULT 90
US-09-270-767-23542
; Sequence 23542, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23542
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23542

Query Match      72.6%; Score 13.8; DB 3; Length 300;
Best Local Similarity 88.2%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAAT 18
   |||||
Db 231 CCCAGATGGCGCTGAT 247

RESULT 91
US-09-270-767-5089
; Sequence 5089, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
```

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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5089
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5089

Query Match      72.6%; Score 13.8; DB 3; Length 506;
Best Local Similarity 88.2%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCTGAATGGCGCTAATC 19
   |||||
Db 456 CCTGAATGGCGCTAGTC 472

RESULT 92
US-09-270-767-20371
; Sequence 20371, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20371
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20371

Query Match      72.6%; Score 13.8; DB 3; Length 506;
Best Local Similarity 88.2%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCTGAATGGCGCTAATC 19
   |||||
Db 456 CCTGAATGGCGCTAGTC 472

RESULT 93
US-07-998-289B-9/c
; Sequence 9, Application US/07998289B
; Patent No. 6027876
; GENERAL INFORMATION:
; APPLICANT: Black, Bruce C
; APPLICANT: Taylor, Martin
; APPLICANT: Heckel, David G
; TITLE OF INVENTION: Method for Monitoring Pesticide
; TITLE OF INVENTION: Resistance
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/07/998,289B
FILING DATE: 30-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, JOSEPH R
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/OA939
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-998-289B-9

Query Match 72.6%; Score 13.8; DB 3; Length 521;
Best Local Similarity 88.2%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
Db 17 CCCTGATGCGGCTCAT 1

RESULT 94

US-07-998-289B-2/c
Sequence 2, Application US/07998289B
Patent No. 6027876
GENERAL INFORMATION:

APPLICANT: Black, Bruce C
APPLICANT: Taylor, Martin
APPLICANT: Heckel, David G
TITLE OF INVENTION: Method for Monitoring Pesticide
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,289B
FILING DATE: 30-DEC-1992
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, JOSEPH R
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/OA939
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-998-289B-2

Query Match 72.6%; Score 13.8; DB 3; Length 567;
Best Local Similarity 88.2%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
Db 63 CCCTGATGCGGCTCAT 47

RESULT 95

US-09-949-016-25349/c
Sequence 25349, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25349
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-25349

Query Match 72.6%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
Db 283 CCCTGATGCTCTAAT 267

RESULT 96

US-09-949-016-69732/c
Sequence 69732, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69732
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-69732

Query Match 72.6%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18

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Db      283  CCCTGAATGTGCTAAT 267
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RESULT 97
US-09-540-3264/c
; Sequence 3264, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3264
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3264

Query Match      72.6%; Score 13.8; DB 3; Length 642;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3  CCTGAATCGCGCTAATC 19
|||||
Db      19  CCTGAACGCGCCCAATC 3

RESULT 98
US-09-533-559-6637/c
; Sequence 6637, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6637
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(672)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-6637

Query Match      72.6%; Score 13.8; DB 3; Length 672;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  CCCTGAATCGCGCTAAT 18
|||||
Db      163 CCCTCAATGTGCTAAT 147
|||||

```

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RESULT 99
US-09-134-000C-3216/c
; Sequence 3216, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3216
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3216

Query Match      72.6%; Score 13.8; DB 3; Length 738;
Best Local Similarity 88.2%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  CCCCTGAATCGCGCTAA 17
|||||
Db      95  CCAATGAATCGCGCTAA 79
|||||

RESULT 100
US-08-945-038-5
; Sequence 5, Application US/08945038
; Patent No. 6762295
; GENERAL INFORMATION:
; APPLICANT: Doidge, Christopher V.
; APPLICANT: Lee, Adrian
; APPLICANT: Radcliff, Fiona J.
; APPLICANT: Hocking, Dianna M.
; APPLICANT: Webb, Elizabeth A.
; TITLE OF INVENTION: PROTECTIVE HELICOBACTER ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,038
; FILING DATE: 23-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU96/00225
; FILING DATE: 19-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN2575
; FILING DATE: 21-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN3931
; FILING DATE: 03-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN7565
; FILING DATE: 16-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768

```

REFERENCE/DOCKET NUMBER: 017227/0133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
IMMEDIATE SOURCE:
CLONE: Clone G3.8
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1299
US-08-945-038-5

Query Match 72.6%; Score 13.8; DB 3; Length 1302;
Best Local Similarity 88.2%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAA 17
Db 421 CTCTTGAATGGCGCTAA 437

Search completed: March 8, 2006, 21:06:49
Job time : 107.126 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:06:59 ; Search time 190.369 Seconds
(without alignments)
665.178 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19

Sequence: 1 ccctgaatggcgtaatc 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	10	ACF04788 Tissue ce
2	19	100.0	27	8	ACD26709 Enterovir
3	19	100.0	27	13	ADU47462 p1 probe
4	19	100.0	30	6	ABL53132 Micro-org
5	19	100.0	30	6	ABL53128 Micro-org
6	19	100.0	30	6	ABL53130 Micro-org
7	19	100.0	35	2	AAV23434 Polioviru
8	19	100.0	119	14	ABE56836 Human cox
9	19	100.0	173	14	ABE56856 Human ech
10	19	100.0	173	14	ABE56855 Human ech
11	19	100.0	176	3	AAZ58488 Recombina
12	19	100.0	180	14	ABE56834 Human cox
13	19	100.0	198	14	ABE56865 Human ech
14	19	100.0	198	14	ABE56853 Human ech
15	19	100.0	198	14	ABE56860 Human ech
16	19	100.0	198	14	ABE56854 Human ech
17	19	100.0	237	14	ABE56837 Human cox
18	19	100.0	237	14	ABE56848 Human cox
19	19	100.0	237	14	ABE56879 Human pol

20	19	100.0	237	14	ABE56875	Ab556875 Human pol
21	19	100.0	237	14	ABE56876	Ab556876 Human pol
22	19	100.0	237	14	ABE56877	Ab556877 Human pol
23	19	100.0	237	14	ABE56861	Ab556861 Human ech
24	19	100.0	237	14	ABE56857	Ab556857 Human ech
25	19	100.0	237	14	ABE56871	Ab556871 Human ent
26	19	100.0	237	14	ABE56872	Ab556872 Human pol
27	19	100.0	238	14	ABE56840	Ab556840 Human cox
28	19	100.0	238	14	ABE56850	Ab556850 Human cox
29	19	100.0	238	14	ABE56878	Ab556878 Human pol
30	19	100.0	238	14	ABE56849	Ab556849 Human cox
31	19	100.0	238	14	ABE56839	Ab556839 Human cox
32	19	100.0	238	14	ABE56846	Ab556846 Human cox
33	19	100.0	238	14	ABE56847	Ab556847 Human cox
34	19	100.0	238	14	ABE56838	Ab556838 Human cox
35	19	100.0	238	14	ABE56842	Ab556842 Human cox
36	19	100.0	238	14	ABE56832	Ab556832 Human cox
37	19	100.0	238	14	ABE56835	Ab556835 Human cox
38	19	100.0	238	14	ABE56851	Ab556851 Human cox
39	19	100.0	238	14	ABE56852	Ab556852 Human cox
40	19	100.0	238	14	ABE56874	Ab556874 Human pol
41	19	100.0	238	14	ABE56829	Ab556829 Consensus
42	19	100.0	238	14	ABE56843	Ab556843 Human cox
43	19	100.0	238	14	ABE56845	Ab556845 Human cox
44	19	100.0	238	14	ABE56870	Ab556870 Human ech
45	19	100.0	238	14	ABE56830	Ab556830 Human cox
46	19	100.0	238	14	ABE56833	Ab556833 Human cox
47	19	100.0	238	14	ABE56877	Ab556877 Human pol
48	19	100.0	238	14	ABE56859	Ab556859 Human ech
49	19	100.0	238	14	ABE56841	Ab556841 Human cox
50	19	100.0	238	14	ABE56831	Ab556831 Human cox
51	19	100.0	238	14	ABE56867	Ab556867 Human ech
52	19	100.0	238	14	ABE56844	Ab556844 Human cox
53	19	100.0	238	14	ABE56866	Ab556866 Human ech
54	19	100.0	238	14	ABE56882	Ab556882 Human pol
55	19	100.0	497	8	ABX12446	Abx12446 Cxsackie
56	19	100.0	502	8	ABX12451	Abx12451 Cxsackie
57	19	100.0	514	3	AAZ58487	AAZ58487 Polioviru
58	19	100.0	520	6	ABL53112	AbL53112 Micro-org
59	19	100.0	521	6	ABL53111	AbL53111 Micro-org
60	19	100.0	525	6	ABL53113	AbL53113 Micro-org
61	19	100.0	548	8	ABX12448	Abx12448 Cxsackie
62	19	100.0	551	8	ABX12453	Abx12453 Cxsackie
63	19	100.0	552	8	ABX12452	Abx12452 Cxsackie
64	19	100.0	554	8	ABX12457	Abx12457 Cxsackie
65	19	100.0	556	8	ABX12449	Abx12449 Cxsackie
66	19	100.0	556	8	ABX12450	Abx12450 Cxsackie
67	19	100.0	559	8	ABX12456	Abx12456 Cxsackie
68	19	100.0	560	8	ABX12447	Abx12447 Cxsackie
69	19	100.0	562	8	ABX12454	Abx12454 Cxsackie
70	19	100.0	567	8	ABX12455	Abx12455 Cxsackie
71	19	100.0	628	2	AAQ58715	AAQ58715 Polioviru
72	19	100.0	628	2	AAQ58726	AAQ58726 Polioviru
73	19	100.0	639	12	ADP74707	ADP74707 Novel bic
74	19	100.0	646	4	AAAC85153	AAc85153 Echo viru
75	19	100.0	654	4	AAAC85173	AAc85173 Cxsackie
76	19	100.0	660	4	AAAC85174	AAc85174 Cxsackie
77	19	100.0	660	14	ABE56828	Ab556828 Cxsackie
78	19	100.0	682	13	ADU77356	ADU77356 Prima7 vi
79	19	100.0	709	14	AEA00424	AEa00424 Enterovir
80	19	100.0	743	14	ADW37919	ADw37919 Polioviru
81	19	100.0	745	4	AAAC85152	AAc85152 Cxsackie
82	19	100.0	745	8	AAAC48197	AAc48197 Polioviru
83	19	100.0	810	12	ADP82873	ADp82873 Human cox
84	19	100.0	1560	13	ADU47469	ADu47469 Enterovir
85	19	100.0	2076	6	ABK14791	ABk14791 Platelet-
86	19	100.0	4148	5	AAH20890	AAh20890 Vector co
87	19	100.0	5252	12	ADAO07652	ADo07652 Triclatro
88	19	100.0	7185	12	ADP74699	ADp74699 Novel bic
89	19	100.0	7185	12	ADP74701	ADp74701 Novel bic
90	19	100.0	7235	12	ADP74714	ADp74714 Novel bic
91	19	100.0	7235	12	ADP74715	ADp74715 Novel bic
92	19	100.0	7235	12	ADP74700	ADp74700 Novel bic

93	19	100.0	7235	12	ADP74713	Adp74713 Novel bic	15.4	81.1	32187	9	ADB60819	Adb60819 Connectiv
94	19	100.0	7392	8	ABX12440	Abx12440 Diabetoge	15.4	81.1	32193	4	ABK42662	Abk42662 Genomic s
95	19	100.0	7399	2	RAQ11816	Raq11816 RNA encod	15.4	81.1	32193	9	ADB60818	Adb60818 Connectiv
96	19	100.0	7399	10	ABV76134	Abv76134 Cxsackie	15.4	81.1	39353	4	AAK67232	Aak67232 Human imm
97	19	100.0	7400	3	AAZ98719	Aaz98719 Swine ves	15.4	81.1	39353	4	AAK65396	Aak65396 Human imm
98	19	100.0	7400	3	AAZ98717	Aaz98717 Swine ves	15.4	81.1	39358	4	AAK65397	Aak65397 Human imm
99	19	100.0	7400	3	AAZ98718	Aaz98718 Swine ves	15.4	81.1	39358	4	AAK67233	Aak67233 Human imm
100	19	100.0	7400	3	AAZ29863	Aaz29863 Swine ves	15	78.9	20	14	ADZ76560	Adz76560 Enterovir
101	19	100.0	7421	3	AAZ98720	Aaz98720 Swine ves	15	78.9	24	13	ADU61148	Adu61148 Polioviru
102	19	100.0	7431	2	AAQ30148	Aaq30148 Attenuate	15	78.9	35	2	AAV23435	Aav23435 Polioviru
103	19	100.0	7440	1	AAZ20042	Aaz20042 Sequence	15	78.9	35	2	AAV23437	Aav23437 Polioviru
104	19	100.0	7441	2	AAZ26152	Aaz26152 DNA sequ	15	78.9	534	8	ACA32459	Aca32459 Prokaryot
105	19	100.0	7441	2	AAZ26152	Aaz26152 DNA sequ	15	78.9	534	8	ACA32459	Aca32459 Prokaryot
106	19	100.0	7925	12	ADP74702	Adp74702 Novel bic	15	78.9	2780	5	AAZ93777	Aaz93777 DNA encod
107	19	100.0	7943	8	ACC43139	Acc43139 Nucleotid	14.8	77.9	293	6	ABN77120	Abn77120 Human ORF
108	19	100.0	8298	2	AAV18096	Aav18096 pMCDHAP	14.8	77.9	582	10	ACF70262	Acf70262 Phototrab
109	19	100.0	10448	6	ABK86535	Abk86535 EIAV base	14.8	77.9	688	10	ADD17643	Add17643 DNA (Seq)
110	19	100.0	10633	12	ADO07660	Ado07660 Viral vec	14.8	77.9	688	10	ADD16044	Add16044 cDNA (Seq)
111	19	100.0	11058	6	ABK86536	Abk86536 EIAV base	14.8	77.9	708	4	ABA89900	Abas89900 Escherich
112	19	100.0	11326	2	AAV12373	Aav12373 Chimeric	14.8	77.9	767	10	ADI22436	Adi22436 Rat liver
113	19	100.0	11746	12	ADO07659	Ado07659 Viral vec	14.8	77.9	925	4	ABL10205	Abli10205 Drosophil
114	19	100.0	38246	12	ADO07662	Ado07662 Viral vec	14.8	77.9	1208	2	AAZ84058	Aaz84058 DNA encod
115	18	94.7	25	2	AAQ06254	Aaq06254 Primer fo	14.8	77.9	1468	10	ADC35635	Adc35635 Wheat SSE
116	18	94.7	25	2	AAZ37545	Aaz37545 Enterovir	14.8	77.9	2000	10	ACC61482	Acc61482 Gene sequ
117	18	94.7	25	3	AAZ57426	Aaz57426 Blood typ	14.8	77.9	2000	10	ADK64645	Adk64645 Disease t
118	18	94.7	25	4	AAH03941	Aah03941 PCR prime	14.8	77.9	2534	4	ABL25378	Abli25378 Drosophil
119	18	94.7	25	4	AAH03081	Aah03081 Microorga	14.8	77.9	2833	4	ABL22734	Abli22734 Drosophil
120	18	94.7	25	9	ADA27505	Ada27505 Microorga	14.8	77.9	3631	4	ABL10204	Abli10204 Drosophil
121	18	94.7	25	10	ADC55468	Adc55468 Primer sp	14.8	77.9	6357	4	ABL11914	Abli11914 Drosophil
122	18	94.7	44	3	AAZ49429	Aaz49429 Enterohae	14.8	77.9	9057	9	ACD19181	Acad19181 E. coli 0
123	18	94.7	195	10	ABZ69931	Abz69931 Polioviru	14.8	77.9	9972	6	ABS79000	Abs79000 E. coli C
124	18	94.7	237	14	ABE56881	Abe56881 Human pol	14.8	77.9	9972	10	ADH80567	Adh80567 Escherich
125	18	94.7	237	14	ABE56880	Abe56880 Human pol	14.8	77.9	9974	4	ABA88897	Aba88897 Escherich
126	18	94.7	7432	2	AAQ22965	Aaq22965 True type	14.8	77.9	12537	12	AAAT41705	Aaat41705 Lymphocy
127	17.4	91.6	198	14	ABE56858	Abe56858 Human ech	14.8	77.9	15755	12	ADM66947	Adm66947 Murine ad
128	17.4	91.6	198	14	ABE56863	Abe56863 Human ech	14.8	77.9	25235	4	AAH45310	Aah45310 Human SEE
129	17.4	91.6	237	14	ABE56862	Abe56862 Human ech	14.8	77.9	25235	4	AAH45310	Aah45310 Human SEE
130	17.4	91.6	238	14	ABE56864	Abe56864 Human ech	14.8	77.9	37672	8	AAZ56120	Aaz56120 Mouse lrf
131	17.4	91.6	248	2	AAQ10172	Aaq10172 5' non-co	14.8	77.9	37672	9	ADA02483	Ada02483 Mouse lrf
132	17.4	91.6	608	5	AAZ93057	Aaz93057 Human rhi	14.8	77.9	37672	10	ADB72221	Adb72221 Mouse lrf
133	17.4	91.6	627	8	ABX11923	Abx11923 Human rhi	14.8	77.9	55050	6	ABQ75680	Abq75680 Human SEE
134	17.4	91.6	627	8	ABX11971	Abx11971 Human rhi	14.8	77.9	93483	9	ADA03083	Ada03083 Mouse mCG
135	17.4	91.6	627	10	ADB84230	Adb84230 Rhinoviru	14.8	77.9	93483	11	ADL27161	Adl27161 Mouse mCG
136	17.4	91.6	627	10	ADA15642	Ada15642 Human rhi	14.8	77.9	93483	11	ADL27161	Adl27161 Mouse gen
137	17.4	91.6	627	14	ADV78854	Adv78854 Novel anc	14.8	77.9	110000	4	AAI99682_15	AAI99682_15 o
138	17.4	91.6	627	14	ADW171616	Adw171616 Human rhi	14.8	77.9	110000	4	AAI99683_15	AAI99683_15 o
139	17.4	91.6	7227	1	AAZ60194	Aaz60194 Sequence	14.8	77.9	110000	10	ACF65385_4	ACF65385_4 o
140	17	89.5	24	14	ADY39812	Ady39812 Enterovir	14.8	77.9	110000	10	ACF67367_33	ACF67367_33 o
141	16.4	86.3	19	14	AEA22931	Aea22931 Meningiti	14.8	77.9	110000	12	ADQ97328_2	ADQ97328_2 o
142	16.4	86.3	32	2	AAZ45153	Aaz45153 PCR prime	14.8	77.9	160921	11	ACN44962_2	ACN44962_2 o
143	16	84.2	103	2	AAQ06807	Aaq06807 Mutagenis	14.8	77.9	161334	11	ACN44962_2	ACN44962_2 o
144	15.8	83.2	250	2	AAQ01071	Aaq01071 5' non-co	14.8	77.9	161334	11	ACN44962_2	ACN44962_2 o
145	15.8	83.2	610	1	AAZ81398	Aaz81398 Sequence	14.8	77.9	263852	13	ADS99460	Ads99460 Murine ki
146	15.8	83.2	618	1	AAZ81397	Aaz81397 Sequence	14.8	77.9	342748	14	ADZ13793	Adz13793 Human can
147	15.8	83.2	1024	14	ABE65545	Abe65545 Rice geno	14.4	75.8	145	6	ABK39676	Abk39676 cDNA enco
148	15.8	83.2	1326	8	ACA31960	Aca31960 Prokaryot	14.4	75.8	145	8	ACA12005	Aca12005 Human lun
149	15.8	83.2	7100	2	AAQ03360	Aaq03360 Complete	14.4	75.8	145	8	ACA03191	Aca03191 Lung canc
150	15.8	83.2	7100	2	AAQ03360	Aaq03360 Complete	14.4	75.8	145	10	ADH47243	Adh47243 Human lun
151	15.8	83.2	7102	1	AAZ60044	Aaz60044 Sequence	14.4	75.8	145	10	ADJ21162	Adj21162 Human lun
152	15.8	83.2	7102	1	AAZ81393	Aaz81393 Rhinoviru	14.4	75.8	482	11	ADW22162	Adw22162 Rat hepat
153	15.8	83.2	7102	1	AAZ81390	Aaz81390 Sequence	14.4	75.8	663	4	AAF26362	Aaf26362 P. putida
154	15.8	83.2	7152	1	AAZ81390	Aaz81390 Sequence	14.4	75.8	810	8	ACA25005	Aca25005 Prokaryot
155	15.8	83.2	7152	1	AAZ81390	Aaz81390 Sequence	14.4	75.8	1389	5	AAZ87543	Aaz87543 DNA encod
156	15.4	81.1	21	2	AAQ26920	Aaq26920 PCR Prime	14.4	75.8	1494	14	ACL72006	Acl72006 M. xanthu
157	15.4	81.1	21	10	ADE37350	Ade37350 Enterovir	14.4	75.8	1957	13	ADX60014	Adx60014 Plant ful
158	15.4	81.1	743	6	ABK78684	Abk78684 Bacillus	14.4	75.8	2307	4	ABL23687	Abli23687 Drosophil
159	15.4	81.1	1269	11	ACH99447	Ach99447 Klebsiell	14.4	75.8	2614	4	ABL01962	Abli01962 Drosophil
160	15.4	81.1	1633	2	AAZ14567	Aaz14567 H. pylori	14.4	75.8	3889	10	ADB53544	Adb53544 Primaty r
161	15.4	81.1	1707	1	AAZ50411	Aaz50411 Secretion	14.4	75.8	5479	4	ABL23686	Abli23686 Drosophil
162	15.4	81.1	1720	11	ACL38298	Acl38298 Rice stre	14.4	75.8	6380	14	ACL64428	Acl64428 M. xanthu
163	15.4	81.1	1943	14	AEA49129	Aea49129 L. rhamno	14.4	75.8	7784	13	ADT04771	Adt04771 Escherich
164	15.4	81.1	2000	11	ACL36559	Acl36559 Rice stre	14.4	75.8	7800	3	AAZ53860	Aaz53860 Neisseria
165	15.4	81.1	32187	4	ABK42663	Abk42663 Genomic s	14.4	75.8	8112	8	ACA42054	Aca42054 Prokaryot
									8397	8	ACA41510	Aca41510 Prokaryot

239	14.4	75.8	27425	3	AA533978	Aaa533978 DWP53 tum	312	14.2	74.7	3090	6	ABN79827	Abn79827 Fungal 2B
240	14.4	49914	3	AA381471	Aaa81471 N. mening	313	14.2	74.7	3111	11	ACL26227	ACL26227 Rice abio	
241	14.4	70549	12	ADQ97436	Adq97436 Mouse can	c 314	14.2	74.7	3165	11	ADM02816	Adm02816 Human cDN	
242	14.4	75.8	110000	3	AA811490_05	Continuation (6 of	315	14.2	74.7	3344	2	AA71086	Aa71086 Human ala
243	14.4	75.8	110000	4	AA199682_20	Continuation (21 o	316	14.2	74.7	3344	2	AA339683	Aax339683 Renal can
244	14.4	75.8	110000	14	AD213747_0	Ad213747 Human can	317	14.2	74.7	3344	10	ADB31357	Adb31357 Bicalucam
245	14.4	75.8	347814	12	ADQ53440_0	Adq53440 Human can	318	14.2	74.7	3344	10	ABX74491	Abx74491 Human cDN
246	14.4	75.8	349980	3	AA21607	Aaf21607 Neisseria	319	14.2	74.7	3344	13	ADR24775	Adr24775 Breast ca
247	14.4	74.7	60	6	ABN41848	Abn41848 Bifidobac	320	14.2	74.7	3344	13	ACN40037	Acn40037 Tumor-as
248	14.2	74.7	387	13	ACN26421	Acn26421 Human spl	321	14.2	74.7	3344	13	ADP23085	Adp23085 Puro poly
249	14.2	74.7	403	3	AA266436	Aac266436 Human sec	322	14.2	74.7	3344	14	ADY14359	Ady14359 DNA encod
250	14.2	74.7	467	6	ABX66436	Abx66436 Helicobac	323	14.2	74.7	3344	14	ADZ75432	Adz75432 Human ala
251	14.2	74.7	468	9	ACH28819	Ach28819 Human adu	324	14.2	74.7	3505	12	ADI61695	Adi61695 Human cDN
252	14.2	74.7	481	3	AA411440	Aac411440 Zea maye	325	14.2	74.7	3810	4	ABE43860	Aea43860 Human cDN
253	14.2	74.7	512	6	ABN63232	Abn63232 Human can	c 326	14.2	74.7	3814	4	ABL05406	Abi05406 Drosophi
254	14.2	74.7	487	6	ABN64886	Abn64886 Human can	c 327	14.2	74.7	3814	4	ABL21026	Abi21026 Drosophi
255	14.2	74.7	524	13	ACN57786	Acn57786 Cotton gy	328	14.2	74.7	4007	10	ADG42134	Adg42134 Human bra
256	14.2	74.7	530	13	ACN62066	Acn62066 Cotton gy	329	14.2	74.7	4281	4	ABL02573	Abi02573 Drosophi
257	14.2	74.7	583	4	AAU36607	Aal36607 Human mus	c 330	14.2	74.7	4381	9	AAU62526	Aal62526 Human tra
258	14.2	74.7	583	8	ABX59595	Abx59595 cDNA enco	c 331	14.2	74.7	4519	8	AAU47360	Aad47360 Human tra
259	14.2	74.7	583	12	ADJ30345	Adj30345 Human mus	c 332	14.2	74.7	4603	12	ADP99221	Adp99221 Human tra
260	14.2	74.7	586	13	ACN61703	Acn61703 Cotton gy	333	14.2	74.7	4664	12	ADJ96595	Adj96595 Human tyr
261	14.2	74.7	586	4	AAU18216	Aal18216 Human bre	c 334	14.2	74.7	4771	4	ABL07514	Abi07514 Drosophi
262	14.2	74.7	597	13	ACN50736	Acn50736 Cotton an	c 335	14.2	74.7	5237	12	ADQ64500	Adq64500 Novel hum
263	14.2	74.7	608	3	AAU09099	Aaf09099 Fusarium	336	14.2	74.7	5549	8	ACC57740	Acc57740 Human pro
264	14.2	74.7	608	13	ADU53140	Adu53140 Fusarium	337	14.2	74.7	5549	10	ADE38362	Ad38362 Human hepatic s
265	14.2	74.7	608	14	ADZ91143	Adz91143 Fusarium	338	14.2	74.7	5677	10	ADG91195	Adg91195 Hepatic s
266	14.2	74.7	710	2	AAV32991	Aav32991 Human top	339	14.2	74.7	6587	4	ABL02572	Abi02572 Drosophi
267	14.2	74.7	774	10	ACF66321	Acf66321 Photorhab	c 340	14.2	74.7	7005	4	ABL15355	Abi15355 Drosophi
268	14.2	74.7	781	10	ACF66296	Acf66296 Photorhab	c 341	14.2	74.7	7005	13	ADQ89655	Adq89655 Antagonis
269	14.2	74.7	792	10	ACF67636	Acf67636 Photorhab	c 342	14.2	74.7	8201	6	ABL34510	Abi34510 Human met
270	14.2	74.7	817	10	ADT94569	Adt94569 Colon can	c 343	14.2	74.7	8201	6	ABL70539	Abi70539 Chemical
271	14.2	74.7	817	11	ADT94569	Adt94569 Colon can	c 344	14.2	74.7	8201	7	ADJ99771	Adj99771 Bisulphit
272	14.2	74.7	817	11	ADX41051	Adx41051 Human cDN	c 345	14.2	74.7	9407	4	AA559606	Aa559606 Propionib
273	14.2	74.7	866	4	ABL12071	Abi12071 Drosophi	346	14.2	74.7	9407	8	ACF64535	Acf64535 Propionib
274	14.2	74.7	895	6	ABX66710	Abx66710 Helicobac	347	14.2	74.7	10685	13	ADR84250	Adr84250 Aspergill
275	14.2	74.7	912	10	ACF68830	Acf68830 Photorhab	c 348	14.2	74.7	13075	4	ABL15354	Abi15354 Drosophi
276	14.2	74.7	926	5	AA593956	Aa593956 DNA encod	c 349	14.2	74.7	16929	4	AAK72509	Aak72509 Human imm
277	14.2	74.7	939	8	ACA34971	Aca34971 Prokaryot	c 350	14.2	74.7	16929	12	ADJ12871	Adj12871 DNA fragm
278	14.2	74.7	981	6	ABT11491	Abt11491 Yeast sel	c 351	14.2	74.7	19802	4	ABL12950	Abi12950 Drosophi
279	14.2	74.7	985	6	ABS62890	Abs62890 Selected	c 352	14.2	74.7	22111	12	ADJ46536	Adj46536 Human req
280	14.2	74.7	985	6	ABT11464	Abt11464 Yeast sel	c 353	14.2	74.7	22111	12	ADJ46536	Adj46536 Human req
281	14.2	74.7	1020	11	ACH9265	Ach9265 Klebsiell	c 354	14.2	74.7	22933	13	ABD33416	Abd33416 Murine ca
282	14.2	74.7	1095	5	AAH66756	Aah66756 C Glutami	c 355	14.2	74.7	22933	13	ABD33416	Abd33416 Murine ca
283	14.2	74.7	1095	8	ABQ94247	Abq94247 FLO11 gen	c 356	14.2	74.7	32572	6	AA517820	Aa517820 PadV-5 HN
284	14.2	74.7	1099	8	ACA22772	Ac22772 Prokaryot	c 357	14.2	74.7	33393	13	ABD33323	Abd33323 Human can
285	14.2	74.7	1101	3	AA533703	Aac533703 Arabidops	c 358	14.2	74.7	36033	10	ADB74375	Adb74375 Mycobacte
286	14.2	74.7	1104	6	ABO88741	Ab088741 Breast sp	c 359	14.2	74.7	69770	10	ADC86870	Adc86870 Human GPC
287	14.2	74.7	1117	6	ABT11357	Abt11357 Yeast sel	c 360	14.2	74.7	75782	12	ADQ97795	Adq97795 Mouse can
288	14.2	74.7	1135	8	ACA22522	Ac22522 Prokaryot	c 361	14.2	74.7	96597	10	ADC85340	Adc85340 Human lmo
289	14.2	74.7	1218	4	AAF71334	Aaf71334 Corynebac	c 362	14.2	74.7	96598	9	ADA02861	Ada02861 Mouse itp
290	14.2	74.7	1503	3	AA595495	Aac595495 Human sec	c 363	14.2	74.7	96598	12	ADM74456	Adm74456 Murine ca
291	14.2	74.7	1503	3	AA595495	Aac595495 Human sec	c 364	14.2	74.7	96598	12	ADM74456	Adm74456 Murine ca
292	14.2	74.7	1593	3	AA490507	Aac490507 Arabidops	c 365	14.2	74.7	110000	10	ACF65383_1	Acf65383_1 Continuation (2 of
293	14.2	74.7	1612	4	ABL05407	Abi05407 Drosophi	c 366	14.2	74.7	110000	10	ACF67367_02	Acf67367_02 Continuation (3 of
294	14.2	74.7	1665	8	ADA26542	Ada26542 Arabidops	c 367	14.2	74.7	110000	14	ACF67367_16	Acf67367_16 Continuation (17 o
295	14.2	74.7	1755	4	ABL21027	Abi21027 Drosophi	c 368	14.2	74.7	110000	14	AEA61163_3	Aea61163_3 Continuation (4 of
296	14.2	74.7	1985	12	ADJ10845	Adj10845 Recombina	c 369	14.2	74.7	110000	14	AEA61163_4	Aea61163_4 Continuation (5 of
297	14.2	74.7	2063	3	ABQ88742	Abq88742 Breast sp	370	14.2	74.7	119057	13	ABD33460	Abd33460 Murine ca
298	14.2	74.7	2136	3	ACA44709	Aca44709 Arabidops	371	14.2	74.7	130480	4	AAF25833	Aaf25833 R. marinu
299	14.2	74.7	2136	6	AB212398	Ab212398 Arabidops	372	14.2	74.7	132544	13	ADV99887	Adv99887 Nanchangm
300	14.2	74.7	2136	8	ADA68489	Ada68489 Arabidops	373	14.2	74.7	146733	12	ADQ97410	Adq97410 Mouse can
301	14.2	74.7	2423	2	AAQ51237	Aaq51237 Plant NAD	374	14.2	74.7	164772	10	ADL13904	Adl13904 Oseleorath
302	14.2	74.7	2445	13	AD082137	Ad082137 Plant ful	375	14.2	74.7	166181	12	ADQ20461	Adq20461 Human sof
303	14.2	74.7	2592	6	ABK36053	Abk36053 cDNA sequ	376	14.2	74.7	166181	12	ADQ18633	Adq18633 Human sof
304	14.2	74.7	2668	4	ABL25154	Abi25154 Drosophi	377	14.2	74.7	203132	13	ABD33364	Abd33364 Murine ca
305	14.2	74.7	2907	13	ADQ89887	Adq89887 Antagonis	378	14.2	74.7	203132	14	ADZ13443	Adz13443 Murine ca
306	14.2	74.7	2910	10	ADAS2971	Ada2971 Human cod	c 379	14.2	74.7	249878	10	ACF65381	Acf65381 Photorhab
307	14.2	74.7	2927	3	ACA76720	Aac76720 Human ORF	380	14.2	74.7	349980	5	AAH68529	Aah68529 C Glutami
308	14.2	74.7	2944	4	ABL12070	Abi12070 Drosophi	381	14.2	73.7	14	2	AAQ50709	Aaq50709 ERM picor
309	14.2	74.7	3036	13	ADX62298	Adx62298 Plant ful	382	14.2	73.7	14	14	AEB56764	Aeb56764 Enterovir
310	14.2	74.7	3080	4	ABL04732	Abi04732 Drosophi	383	14.2	73.7	19	8	ABZ68824	Abz68824 Primer us
311	14.2	74.7	3084	4	ABL05392	Abi05392 Drosophi	384	14.2	73.7	591	6	ABK62210	Abk62210 Rat seque

385	14	73.7	647	10	ACF66435	Acf66435 Phototrab	c 458	13.8	72.6	889	4	ABA07991	AbA07991 Human ova
386	14	73.7	966	8	ACA53923	Aca53923 Prokaryot	c 459	13.8	72.6	889	4	ABA07990	AbA07990 Human ova
387	14	73.7	966	10	ACF69113	Acf69113 Phototrab	c 460	13.8	72.6	935	3	AAC42055	Aac42055 Arabidops
388	14	73.7	1356	8	ACA43171	Aca43171 Prokaryot	c 461	13.8	72.6	935	13	AD845749	Ad845749 Bacterial
389	14	73.7	1473	4	AAS52034	Aas52034 Staphyloc	c 462	13.8	72.6	993	6	ABL40772	AbL40772 Human pro
390	14	73.7	1512	8	ACF74373	Acf74373 Staphyloc	c 463	13.8	72.6	993	10	ADC26676	Adc26676 Human lip
391	14	73.7	1515	4	AAS54957	Aas54957 Staphyloc	c 464	13.8	72.6	1034	5	AAS70584	Aas70584 DNA encod
392	14	73.7	1536	8	ACA20374	Aca20374 Prokaryot	c 465	13.8	72.6	1053	5	AAS92608	Aas92608 DNA encod
393	14	73.7	1641	10	ACF68994	Acf68994 Phototrab	c 466	13.8	72.6	1085	12	ADP29016	Adp29016 Human sec
394	14	73.7	1660	10	ADBS8863	Adbs8863 Toxicity-	c 467	13.8	72.6	1099	8	ACA52166	Aca52166 Prokaryot
395	14	73.7	1660	14	ADZ60815	Adz60815 Rat Hadhs	c 468	13.8	72.6	1102	6	ABK75380	Abk75380 Bacillus
396	14	73.7	2254	12	ADP72855	Adp72855 Renal tox	c 469	13.8	72.6	1103	8	ACA49232	Aca49232 Prokaryot
397	14	73.7	2465	4	ABL18148	AbL18148 Drosophil	c 470	13.8	72.6	1155	13	ADX31948	Adx31948 Plant ful
398	14	73.7	4467	2	AXX19253	Axx19253 Corn dihy	c 471	13.8	72.6	1218	8	ACA23053	Aca23053 Prokaryot
399	14	73.7	11823	2	AAV74447	Aav74447 Staphyloc	c 472	13.8	72.6	1218	8	ACA31564	Aca31564 Prokaryot
400	14	73.7	92076	13	ABD33368	Abd33368 Murine ca	c 473	13.8	72.6	1281	4	AAF56025	Aaf56025 Lactobaci
401	14	73.7	110000	2	AZ01425_09	Continuation (10 o	c 474	13.8	72.6	1302	2	AAT43045	Aat43045 Helicobac
402	14	73.7	110000	10	ACF67367_18	Continuation (21 o	c 475	13.8	72.6	1314	2	AAT68169	Aat68169 H. pylori
403	14	73.7	110000	10	ACF67367_20	Continuation (24 o	c 476	13.8	72.6	1326	8	ACA35579	Aca35579 Prokaryot
404	14	73.7	110000	10	ACF67367_23	Continuation (25 o	c 477	13.8	72.6	1356	4	ABL2679	AbL2679 Drosophil
405	14	73.7	110000	10	ACF67367_24	Continuation (5 of	c 478	13.8	72.6	1356	4	AAS57125	Aas57125 cDNA enco
406	14	73.7	210710	10	ACF65380	Acf65380 Phototrab	c 479	13.8	72.6	1356	10	ADC35828	Adc35828 Drosophil
407	14	73.7	210710	10	ACF65380	Acf65382 Phototrab	c 480	13.8	72.6	1356	13	ADQ89757	Adq89757 Antagonis
408	14	73.7	243072	10	ACF65382	Adv02873 Human BAC	c 481	13.8	72.6	1356	13	ADQ89757	Adq89757 Antagonis
409	13.8	72.6	29	5	ADV02873	Adv02873 Human BAC	c 482	13.8	72.6	1395	13	ADT45153	Adt45153 Bacterial
410	13.8	72.6	100	8	ACD75161	AcD75161 E. coli K	c 483	13.8	72.6	1404	5	AAH49409	Aah49409 D. melano
411	13.8	72.6	129	10	ADJ37814	Adj37814 Rat strok	c 484	13.8	72.6	1425	11	ACH98878	Ach98878 Klebsiell
412	13.8	72.6	129	12	ADI30602	Adi30602 Rat strok	c 485	13.8	72.6	1431	11	ACH95521	Ach95521 Klebsiell
413	13.8	72.6	254	7	ADS65209	AdS65209 Corn seed	c 486	13.8	72.6	1435	4	AAF56001	Aaf56001 Lactobaci
414	13.8	72.6	295	3	AAA42360	Aaa42360 Human sec	c 487	13.8	72.6	1451	5	AAS05853	Aas05853 Fruit fly
415	13.8	72.6	296	2	AAL12608	Aal12608 Human gen	c 488	13.8	72.6	1451	10	AD814541	Ad814541 DNA encod
416	13.8	72.6	298	6	ABL75616	AbL75616 Corn tass	c 489	13.8	72.6	1451	11	ADL83389	Adl83389 Drosophil
417	13.8	72.6	387	10	ACF70133	Acf70133 Phototrab	c 490	13.8	72.6	1451	12	ADR03109	Adr03109 Drosophil
418	13.8	72.6	404	6	ABS98328	Abs98328 Human lac	c 491	13.8	72.6	1452	9	AAD57458	Aad57458 Fruit fly
419	13.8	72.6	423	10	ADF81229	Adf81229 Leukaemia	c 492	13.8	72.6	1452	9	AAD57458	Aad57458 Fruit fly
420	13.8	72.6	430	4	AAI62598	Aai62598 Human bre	c 493	13.8	72.6	1532	6	ABL40774	AbL40774 Human pro
421	13.8	72.6	430	4	AAI03781	Aai03781 Human rep	c 494	13.8	72.6	1532	6	ABL40774	AbL40774 Human pro
422	13.8	72.6	445	10	ADE59275	Ades9275 Rat gene	c 495	13.8	72.6	1532	6	ABL40773	AbL40773 Human pro
423	13.8	72.6	457	13	ACF82308	Acf82308 Human SIR	c 496	13.8	72.6	1554	13	ADO82643	Ado82643 Plant ful
424	13.8	72.6	462	9	ACH13619	Ach13619 Human adu	c 497	13.8	72.6	1554	5	AAS71295	Aas71295 DNA encod
425	13.8	72.6	469	9	ACH19903	Ach19903 Human adu	c 498	13.8	72.6	1589	11	ACN45015	Acn45015 Human mRN
426	13.8	72.6	488	6	ABL40781	AbL40781 Human pro	c 499	13.8	72.6	1630	12	ADO57322	Ado57322 DNA encod
427	13.8	72.6	519	6	ABK74169	Abk74169 Bacillus	c 500	13.8	72.6	1665	5	AAS92765	Aas92765 DNA encod
428	13.8	72.6	549	10	ACD94383	AcD94383 Human col							
429	13.8	72.6	558	4	AAH34783	Aah34783 Human col							
430	13.8	72.6	558	10	ADK52783	Adk52783 Plant DNA							
431	13.8	72.6	567	2	AAQ71201	Aaq71201 scd72, a							
432	13.8	72.6	583	12	ADL83910	Adl83910 DNA up-re							
433	13.8	72.6	583	12	ADL83911	Adl83911 DNA up-re							
434	13.8	72.6	603	3	AAZ47454	Aaz47454 Glutathio							
435	13.8	72.6	642	14	ACL66801	AcL66801 M. xanthu							
436	13.8	72.6	645	10	ADK53443	Adk53443 Plant DNA							
437	13.8	72.6	654	4	AAH34361	Aah34361 Human col							
438	13.8	72.6	660	10	ADF82599	Adf82599 Leukaemia							
439	13.8	72.6	672	3	AAF14114	Aaf14114 Aspergill							
440	13.8	72.6	672	13	ADU58155	Adu58155 Aspergill							
441	13.8	72.6	672	14	ADZ36158	Adz36158 Aspergill							
442	13.8	72.6	673	4	AAO16669	Aao16669 Human rep							
443	13.8	72.6	673	4	ABA07589	AbA07589 Human ova							
444	13.8	72.6	693	2	AAT67402	Aat67402 H. pylori							
445	13.8	72.6	694	10	ACF66756	Acf66756 Phototrab							
446	13.8	72.6	697	10	ACF66728	Acf66728 Phototrab							
447	13.8	72.6	704	13	ADSG1386	Adsg1386 Bacterial							
448	13.8	72.6	705	10	ADK55596	Adk55596 Plant DNA							
449	13.8	72.6	719	6	ABQ68564	Abq68564 Listeria							
450	13.8	72.6	735	10	ADK59361	Adk59361 Plant DNA							
451	13.8	72.6	737	4	AAH70463	Aah70463 Human cer							
452	13.8	72.6	738	10	ADH85331	Adh85331 Enterococ							
453	13.8	72.6	759	6	ABL40776	AbL40776 Human pro							
454	13.8	72.6	846	8	ACA43170	Aca43170 Prokaryot							
455	13.8	72.6	872	13	ADX32098	Adx32098 Plant ful							
456	13.8	72.6	889	4	AAI05672	Aai05672 Human rep							
457	13.8	72.6	889	4	AAI05673	Aai05673 Human rep							

ALIGNMENTS

RESULT 1

ACF04788
ID ACF04788 standard; DNA; 19 BP.

XX ACF04788;
AC ACF04788;

XX 18-DEC-2003 (first entry)
DT 18-DEC-2003 (first entry)

XX Tissue cell culture procedure enterovirus control PCR primer #2.
DE Tissue cell culture procedure enterovirus control PCR primer #2.

XX RNA detection; crude cell lysate; human; tissue culture; PCR; primer;
KW probe; ss.
XX Enterovirus.

XX WO2003064605-A2.
XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002439.
XX 28-JAN-2002; 2002US-0352402P.

XX (AMBI-) AMBION INC.
XX

PI Paskloske BL;
 XX WPI; 2003-748084/70.
 XX
 PT Producing cDNA from one or more biological units, useful for detecting a
 PT specific sequence of RNA in a cell or tissue sample, comprises preparing
 PT an admixture of the biological unit and the catabolic enzyme.
 XX
 PS Example 1; Page 41; 46pp; English.
 XX
 CC The present invention relates to a method of producing cDNA from one or
 CC more biological units, comprising preparing an admixture of the
 CC biological unit and the catabolic enzyme. This involves preparing cDNA
 CC from one or more biological units by obtaining at least one biological
 CC unit, obtaining at least one catabolic enzyme, preparing an admixture of
 CC the biological unit and the catabolic enzyme and incubating the admixture
 CC at a temperature where the catabolic enzyme is active and with reverse
 CC transcriptase under conditions to allow reverse transcription. The method
 CC is useful for detecting a specific sequence of RNA in a cell or tissue
 CC sample, and for enzymatically manipulating the RNA in a crude cell
 CC lysate. The kit is useful for producing cDNA in a biological unit. The
 CC present sequence is a PCR primer/probe used in the exemplification of the
 CC invention
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 10; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGGCTAATC 19
 |||||
 DB 1 CCCCTGAATGGGCTAATC 19

RESULT 2
 ACD26709
 ID ACD26709 standard; DNA; 27 BP.
 XX
 AC ACD26709;
 XX

DT 11-SEP-2003 (first entry)
 XX
 DE Enterovirus detection method associated primer #9.
 XX

KW Enterovirus detection; primer; ss.
 XX

OS Enterovirus.
 XX

FN CN1366066-A.
 XX

PD 28-AUG-2002.
 XX

PF 15-JAN-2001; 2001CN-00100622.
 XX

PR 15-JAN-2001; 2001CN-00100622.
 XX

PA (JING-) JINGYU BIOLOGIC SCI TECHNOLOGY IND CO LT.
 XX

PI Li G, Bai Q, Zeng Y;
 XX

DR WPI; 2003-230558/23.
 XX

PT Process, primer and probe for detecting and discriminating enterovirus.
 XX

PS Claim 5; Page 1; 33pp; Chinese.
 XX

CC The invention describes the application of nucleotide primer to detecting
 CC enterovirus. The detection method and the reagent kit are disclosed. This
 CC sequence represents an enterovirus detection method associated primer
 XX

SQ Sequence 27 BP; 4 A; 11 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGGCTAATC 19
 |||||
 DB 9 CCCCTGAATGGGCTAATC 27

RESULT 3
 ADU47462
 ID ADU47462 standard; DNA; 27 BP.
 XX
 AC ADU47462;
 XX

DT 27-JAN-2005 (first entry)
 XX

DE p1 probe used to detect enterovirus type 71 (EV71) in a sample.
 XX

KW Detection; enterovirus type 71; probe; ss.
 XX

OS Enterovirus.
 XX

FN US6818397-B1.
 XX

PD 16-NOV-2004.
 XX

PF 28-NOV-2000; 2000US-00724678.
 XX

PR 28-NOV-2000; 2000US-00724678.
 XX

PA (CHIP-) CHIP BIOTECHNOLOGY INC.
 XX

PI Lee X, Bair C, Tseng Y, Wang Y, Wang S;
 XX

DR WPI; 2004-793563/78.
 XX

PT New kit comprising a pair of oligonucleotide primers for nucleic acid
 PT amplification, useful in detecting and differentiating an enterovirus in
 PT a sample.
 XX

PS Claim 1; SEQ ID NO 9; 14pp; English.
 XX

CC The invention provides a method and a kit for detecting and
 CC differentiating an enterovirus type 71 (EV71) in a sample. The method
 CC involves contacting nucleic acids in the sample with a pair of primers to
 CC form an amplification product; contacting the amplification product with
 CC at least one synthetic nucleotide sequence fixed on a solid substrate and
 CC detecting hybridisation. The present sequence is a probe used to detect
 CC and differentiate enterovirus type 71 (EV71) in a sample.
 XX

SQ Sequence 27 BP; 4 A; 11 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 13; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGGCTAATC 19
 |||||
 DB 9 CCCCTGAATGGGCTAATC 27

RESULT 4
 ABL53132
 ID ABL53132 standard; DNA; 30 BP.
 XX
 AC ABL53132;
 XX

DT 29-AUG-2003 (revised)
 XX

DT 25-JUN-2002 (first entry)
 XX

DE Micro-organism detection probe #74.
 XX

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KW Probe; microorganism detection; microbiological quality;
XX water purification; ss.
XX
OS Human echovirus 12.
XX
XX WO200202811-A2.
XX
XX 10-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-FR002191.
XX
XX 06-JUL-2000; 2000FR-00008839.
XX
XX (INMR ) BIO MERIEUX.
XX
XX Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;
XX Armand M, Laffaire P;
XX
XX WPI; 2002-148021/19.
XX
XX Monitoring microbiological quality of water, useful particularly for
XX controlling water purification, uses oligonucleotide probes to detect at
XX least three representative microbes.
XX
XX Claim 24; Page 80; 85pp; French.
XX
XX The present invention relates to a method for monitoring microbiological
XX quality of an aqueous environmental medium that potentially contains many
XX different microorganisms. A reference set of at least three
XX microorganisms is chosen that, separately or collectively, represent
XX microbiological quality. The test medium is treated, then any
XX microorganisms, or their fragments, in the treated medium is contacted
XX with a set of at least three probes for specific identification and
XX multiple determination of selected microorganisms. This determination
XX represents the level of microbiological quality. The method is useful for
XX identifying and quantifying microorganisms in water and provides results
XX that are used to control water purification/production processes. The
XX present sequence is a probe which was used to illustrate the invention.
XX (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 30 BP; 5 A; 12 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 6; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 2;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCCCTGAATGGGCTAATC 19
XX 11 CCCCTGAATGGGCTAATC 29
XX
XX Db 11 CCCCTGAATGGGCTAATC 29
XX
XX RESULT 5
XX ABL53128
XX ID ABL53128 standard; DNA; 30 BP.
XX
XX AC ABL53128;
XX
XX XX 29-AUG-2003 (revised)
XX DT 25-JUN-2002 (first entry)
XX
XX DE Micro-organism detection probe #70.
XX
XX KW Probe; microorganism detection; microbiological quality;
XX KW water purification; ss.
XX
XX OS Human poliovirus 2.
XX
XX XX WO200202811-A2.
XX
XX PD 10-JAN-2002.
XX
XX PF 06-JUL-2001; 2001WO-FR002191.
XX
XX XX
XX
XX

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PR 06-JUL-2000; 2000FR-00008839.
XX
XX (INMR ) BIO MERIEUX.
XX
XX Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;
XX Armand M, Laffaire P;
XX
XX WPI; 2002-148021/19.
XX
XX Monitoring microbiological quality of water, useful particularly for
XX controlling water purification, uses oligonucleotide probes to detect at
XX least three representative microbes.
XX
XX Claim 24; Page 79; 85pp; French.
XX
XX The present invention relates to a method for monitoring microbiological
XX quality of an aqueous environmental medium that potentially contains many
XX different microorganisms. A reference set of at least three
XX microorganisms is chosen that, separately or collectively, represent
XX microbiological quality. The test medium is treated, then any
XX microorganisms, or their fragments, in the treated medium is contacted
XX with a set of at least three probes for specific identification and
XX multiple determination of selected microorganisms. This determination
XX represents the level of microbiological quality. The method is useful for
XX identifying and quantifying microorganisms in water and provides results
XX that are used to control water purification/production processes. The
XX present sequence is a probe which was used to illustrate the invention.
XX (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 30 BP; 6 A; 12 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 6; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 2;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCCCTGAATGGGCTAATC 19
XX 7 CCCCTGAATGGGCTAATC 25
XX
XX Db 7 CCCCTGAATGGGCTAATC 25
XX
XX RESULT 6
XX ABL53130
XX ID ABL53130 standard; DNA; 30 BP.
XX
XX AC ABL53130;
XX
XX XX 29-AUG-2003 (revised)
XX DT 25-JUN-2002 (first entry)
XX
XX DE Micro-organism detection probe #72.
XX
XX KW Probe; microorganism detection; microbiological quality;
XX KW water purification; ss.
XX
XX OS Human coxsackievirus A21.
XX
XX XX WO200202811-A2.
XX
XX XX 10-JAN-2002.
XX
XX PF 06-JUL-2001; 2001WO-FR002191.
XX
XX PR 06-JUL-2000; 2000FR-00008839.
XX
XX PA (INMR ) BIO MERIEUX.
XX
XX Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;
XX Armand M, Laffaire P;
XX
XX WPI; 2002-148021/19.
XX
XX Monitoring microbiological quality of water, useful particularly for
XX controlling water purification, uses oligonucleotide probes to detect at
XX least three representative microbes.
XX
XX PF 06-JUL-2001; 2001WO-FR002191.
XX
XX XX
XX
XX

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PT least three representative microbes.

PS Claim 24; Page 79; 85pp; French.

XX The present invention relates to a method for monitoring microbiological
 CC quality of an aqueous environmental medium that potentially contains many
 CC different microorganisms. A reference set of at least three
 CC microorganisms is chosen that, separately or collectively, represent
 CC microbiological quality. The test medium is treated, then any
 CC microorganisms, or their fragments, in the treated medium is contacted
 CC with a set of at least three probes for specific identification and
 CC multiple determination of selected microorganisms. This determination
 CC represents the level of microbiological quality. The method is useful for
 CC identifying and quantifying microorganisms in water and provides results
 CC that are used to control water purification/production processes. The
 CC present sequence is a probe which was used to illustrate the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 30 BP; 6 A; 12 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
 |||||
 Db 6 CCCCTGAATGCGGCTAATC 24

RESULT 7

AAV23434/c

ID AAV23434 standard; DNA; 35 BP.

XX

AC AAV23434;

XX 08-JUL-1998 (first entry)

DE Poliovirus DNA primer 438 used in method of the invention.

XX PCR primer; vaccine classification; poliovirus type 2 vaccine;
 KW attenuated poliovirus vaccine; neurovirulence; ss.

XX Synthetic.

OS Poliovirus.

XX US5728519-A.

XX 17-MAR-1998.

XX 21-DEC-1994; 94US-00361337.

XX 06-NOV-1990; 90US-00607742.

XX 18-MAY-1994; 94US-00246373.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Roninson I, Chumakov KM, Levenbook IS, Norwood LP;

XX WPI; 1998-270433/24.

XX Determining acceptability of poliovirus vaccines - based on mutation

XX reversion(s) and comparison to World Health Organisation standard.

XX Example; Col 23-24; 38pp; English.

XX This sequence represents a primer used in the method of the invention.

XX The method is for classifying an unclassified live poliovirus type 2

XX vaccine (attenuated by a G to A substitution at nucleotide position 481)

XX as having an acceptable or unacceptable level of neurovirulence, and

XX comprises, prior to vaccine administration: (a) selectively amplifying a

XX region (I) of the poliovirus genome containing nucleotide position 481

XX using selectively mismatched primers to introduce a site-specific

XX mutation to create a restriction endonuclease (RE) site which includes

CC nucleotide position 481; (b) digesting an amount of (I) with a RE that
 CC specifically cleaves the amplified sequences in revertant viruses which
 CC contain an A to G reversion at nucleotide position 481; (c) digesting an
 CC amount of (I) with a RE that specifically cleaves the amplified sequences
 CC in non-revertant viruses which contain an A at nucleotide position 481;
 CC (d) quantifying the percentage of revertant viruses in the unclassified
 CC vaccine; and (e) comparing the percentage of revertant viruses in the
 CC unclassified vaccine to the percentage of revertant viruses in an
 CC accepted reference vaccine which can pass the monkey neurovirulence test
 CC utilised by the World Health Organisation, an unclassified vaccine with a
 CC higher percentage of A to G revertant viruses than in the reference
 CC vaccine being classified as unacceptable and an unclassified vaccine with
 CC an equal or lower percentage of A to G revertant viruses than in the
 CC reference vaccine classified as acceptable. The test can also be used to
 CC identify cells that are suitable for the culture of attenuated
 CC polioviruses

SQ Sequence 35 BP; 8 A; 8 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
 |||||
 Db 22 CCCCTGAATGCGGCTAATC 4

RESULT 8

AEBS6836

ID AEBS6836 standard; DNA; 119 BP.

XX

AC AEBS6836;

XX 22-SEP-2005 (first entry)

DE Human coxsackievirus B2 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human coxsackievirus B2.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN//) TSANG S.

XX (PRIC//) PRICE J A.

XX (HELL//) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; Y09512.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

XX target binding sequence of an oligonucleotide chosen from any one of the

XX 10 selected sequences of AEB56771; and (b) a sequence required for

XX selected amplification or detection reaction. Also described: (1) a kit

XX (K1) comprising (I), and one or more container that contains (I); and (2)

XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying

XX the target sequence using first amplification primer having a sequence

XX consisting essentially of target binding sequence of any one of AEB56764

XX to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 119 BP; 26 A; 28 C; 36 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 119;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
 |||||
 Db 47 CCCCTGAATGGGCTAATC 65

RESULT 9
 AEB56856
 ID AEB56856 standard; DNA; 173 BP.
 XX AC AEB56856;
 XX DT 22-SEP-2005 (first entry)
 XX DE Human echovirus 5 5' untranslated polynucleotide sequence.
 XX KW DNA detection; enteroviral detection; ds.
 XX OS Human echovirus 5.
 XX FN US2005158710-A1.
 XX PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.
 PR 16-JAN-2004; 2004US-00760048.
 XX (TSAN//) TSANG S.
 XX (PRIC//) PRICE J A.
 XX (HELL//) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 DR GENBANK; AF188359.

PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence,
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771; and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 173 BP; 36 A; 44 C; 45 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 173;
 Best Local Similarity 100.0%; Pred. No. 2.5; 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
 |||||
 Db 47 CCCCTGAATGGGCTAATC 65

RESULT 10
 AEB56855
 ID AEB56855 standard; DNA; 173 BP.
 XX AC AEB56855;
 XX DT 22-SEP-2005 (first entry)
 XX DE Human echovirus 5 5' untranslated polynucleotide sequence.
 XX KW DNA detection; enteroviral detection; ds.
 XX OS Human echovirus 5.
 XX FN US2005158710-A1.
 XX PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.
 PR 16-JAN-2004; 2004US-00760048.
 XX (TSAN//) TSANG S.
 XX (PRIC//) PRICE J A.
 XX (HELL//) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 DR GENBANK; AF188358.

PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771; and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

SQ Sequence 173 BP; 36 A; 45 C; 45 G; 47 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 173;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
 |||||
 Db 47 CCCCTGAATGGGCTAATC 65

RESULT 11
AAZ58488
ID AAZ58488 standard; RNA; 176 BP.
XX AC AAZ58488;
XX
XX 15-SEP-2003 (revised)
DT 23-MAY-2000 (first entry)
XX
XX Recombinant poliovirus PVI(pr) IRES domain V-VI region.
XX
XX Internal ribosomal entry site; IRES; picornavirus; PVI(pr); tumour;
KW cancer; glioblastoma multiforme; medulloblastoma; mammary carcinoma;
KW prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;
KW bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.
XX
XX Human poliovirus 1.
OS Human rhinovirus sp; type 2.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH stem_loop 1..109
FT /*tag= a
FT /note= "domain V"
FT 138..176
FT /*tag= b
FT /note= "domain VI"
XX
XX WO200008166-A1.
XX
XX 17-FEB-2000.
XX
XX 09-APR-1999; 99WO-US007839.
XX
XX 05-AUG-1998; 98US-00129686.
XX (UUNY) UNIV NEW YORK STATE RES FOUND.
XX
XX Gromeier M, Wimmer E;
XX
XX WPI; 2000-205717/18.
XX
XX Chimeric recombinant poliovirus useful for treating malignant tumors
PT comprises internal ribosomal entry site derived from picornaviruses.
XX
XX Example 6; Fig 7; 99pp; English.
XX
XX This sequence represents domains V-VI of the internal ribosomal entry
CC site (IRES) of PVI(pr), a recombinant, non-pathogenic oncolytic
CC poliovirus that carries the IRES of poliovirus type 1 Mahoney where the
CC terminal loop of regions of domain V and domain VI are substituted with
CC the corresponding fragments of human rhinovirus type 2 (HRV2). PVI(pr)
CC was characterized by a loss of neuropathogenicity, demonstrated by its
CC reduced ability to propagate within cells of neuronal origin and failure
CC to cause neurological disease in Cd155 tg mice. Oncolytic potential was
CC demonstrated against a panel of malignant cell lines. PVI(pr) is an
CC example of novel recombinant polioviruses (I) of the invention in which
CC the IRES of wild-type poliovirus is exchanged with the IRES of another
CC picornavirus, such as HRV2, and optionally the P1, P3 or 3' untranslated
CC region is exchanged with that of Sabin poliovirus. (I) are useful for
CC treating malignant tumors such as glioblastoma multiforme,
CC medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial
CC and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to
XX standardise OS field)
XX
XX Sequence 176 BP; 42 A; 43 C; 40 G; 0 T; 51 U; 0 Other;
Query Match 100.0%; Score 19; DB 3; Length 176;
Best Local Similarity 78.9%; Pred. No. 2.5;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCCTGAATGCGGCTAATC 19

|||||:||||:||||:||||:
4 CCCUGAAGCGCGUAUC 22
Db
RESULT 12
AEB56834
ID AEB56834 standard; DNA; 180 BP.
XX AC AEB56834;
XX
XX 22-SEP-2005 (first entry)
DT
XX Human coxsackievirus B1 5' untranslated polynucleotide sequence.
DE
XX DNA detection; enteroviral detection; ds.
KW
XX Human coxsackievirus B1.
OS
XX US2005158710-A1.
PN
XX 21-JUL-2005.
PD
XX 16-JAN-2004; 2004US-00760048.
PF
XX 16-JAN-2004; 2004US-00760048.
PR
XX (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
PI
XX WPI; 2005-512251/52.
DR
XX GENBANK; S76767.
DR
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
PT
XX Disclosure; Fig 1A-D; 34pp; English.
PS
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX Sequence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 19; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCCTGAATGCGGCTAATC 19
|||||:||||:||||:||||:
45 CCCCTGAATGCGGCTAATC 63
Db
RESULT 13
AEB56865
ID AEB56865 standard; DNA; 198 BP.
XX AC AEB56865;
XX

XX 22-SEP-2005 (first entry)
 XX Human echovirus 12 5' untranslated polynucleotide sequence.
 DE DNA detection; enteroviral detection; ds.
 KW Human echovirus 12.
 OS US2005158710-A1.
 PN 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 FI WPI; 2005-512251/52.
 XX GENBANK; U11706.
 DR Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 19; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCCCTGAATCGGCTAATC 19
 Db 7 CCCCTGAATCGGCTAATC 25
 RESULT 14
 AEB56853
 ID AEB56853 standard; DNA; 198 BP.
 AC AEB56853;
 XX 22-SEP-2005 (first entry)
 DT Human echovirus 2 5' untranslated polynucleotide sequence.
 DE DNA detection; enteroviral detection; ds.
 KW Human echovirus 2.
 OS US2005158710-A1.
 PN 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 FI WPI; 2005-512251/52.
 XX GENBANK; U11706.
 DR Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 19; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCCCTGAATCGGCTAATC 19
 Db 7 CCCCTGAATCGGCTAATC 25
 RESULT 14
 AEB56853
 ID AEB56853 standard; DNA; 198 BP.
 AC AEB56853;
 XX 22-SEP-2005 (first entry)
 DT Human echovirus 2 5' untranslated polynucleotide sequence.
 DE DNA detection; enteroviral detection; ds.
 KW Human echovirus 2.
 OS US2005158710-A1.
 PN 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.

PN US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 FI WPI; 2005-512251/52.
 XX GENBANK; U11707.
 DR Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX Sequence 198 BP; 42 A; 53 C; 51 G; 52 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 19; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCCCTGAATCGGCTAATC 19
 Db 7 CCCCTGAATCGGCTAATC 25
 RESULT 15
 AEB56860
 ID AEB56860 standard; DNA; 198 BP.
 XX AEB56860;
 AC AEB56860;
 XX 22-SEP-2005 (first entry)
 DT Human echovirus 9 5' untranslated polynucleotide sequence.
 DE DNA detection; enteroviral detection; ds.
 KW Human echovirus 9.
 OS US2005158710-A1.
 PN 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.

PA (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 PI Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; U11710.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
 XX Sequence 198 BP; 39 A; 49 C; 52 G; 58 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 19; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGGGCTAATC 19
 DB 7 CCCCTGAATGGGCTAATC 25
 RESULT 16
 AEB56854
 ID AEB56854 standard; DNA; 198 BP.
 AC AEB56854;
 XX 22-SEP-2005 (first entry)
 XX Human echovirus 4 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human echovirus 4.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; U11708.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
 XX Sequence 198 BP; 43 A; 48 C; 50 G; 57 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 19; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGGGCTAATC 19
 DB 7 CCCCTGAATGGGCTAATC 25
 RESULT 17
 AEB56837
 ID AEB56837 standard; DNA; 237 BP.
 AC AEB56837;
 XX 22-SEP-2005 (first entry)
 XX Human coxsackievirus B2 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human coxsackievirus B2.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; AF081485.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (1), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (1), (M1) and
CC specifically and selectively recognizes the enterovirus genome. (1)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX
SQ Sequence 237 BP; 46 A; 54 C; 66 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | | | | | | |
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 18
AEB56848
ID AEB56848 standard; DNA; 237 BP.
XX
AC AEB56848;
XX
XX
XX 22-SEP-2005 (first entry)
XX
XX Human coxsackievirus B5 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.

XX Human coxsackievirus B5.
XX US2005158710-A1.
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; AF114383.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (1), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (1)
XX specifically and selectively recognizes the enterovirus genome. (1)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX
SQ Sequence 237 BP; 48 A; 52 C; 66 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | | | | | | |
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 19
AEB56879
ID AEB56879 standard; DNA; 237 BP.
XX
XX AEB56879;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human poliovirus 3 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 3.
XX US2005158710-A1.
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; K01392.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (1), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (1)
XX specifically and selectively recognizes the enterovirus genome. (1)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.

XX
XX
SQ Sequence 237 BP; 54 A; 57 C; 65 G; 61 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
 |||||
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 20

AEBS6875
 ID AEBS6875 standard; DNA; 237 BP.

XX AC AEBS6875;
 XX XX

DT 22-SEP-2005 (first entry)

DE Human poliovirus 1 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

PN US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

PA (PRIC/) PRICE J A.

PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

DR GENBANK; V01149.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains: (1) a kit
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

SQ Sequence 237 BP; 57 A; 54 C; 62 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
 |||||
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 21

AEBS6876
 ID AEBS6876 standard; DNA; 237 BP.

XX

AC AEBS6876;
 XX 22-SEP-2005 (first entry)
 XX Human poliovirus 1 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

PN US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

PA (PRIC/) PRICE J A.

PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

DR GENBANK; V01150.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains: (1) a kit
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

SQ Sequence 237 BP; 56 A; 54 C; 63 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
 |||||
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 22

AEBS6873

ID AEBS6873 standard; DNA; 237 BP.

XX AC AEBS6873;

XX 22-SEP-2005 (first entry)

XX Human poliovirus 1 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; AJ132961.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (I), and one or more container that contains (I); and (2)
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 XX specifically and selectively recognizes the enterovirus genome. (I)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The
 XX present sequence represents a viral 5' untranslated polynucleotide
 XX sequence given in the exemplification of the present invention.
 XX Sequence 237 BP; 54 A; 57 C; 63 G; 63 T; 0 U; 0 Other;
 XX Query Match 100.0%; Score 19; DB 14; Length 237;
 XX Best Local Similarity 100.0%; Pred. No. 2.6;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 CCCCTGAATCGGCTAATC 19
 XX |||||
 XX Db 47 CCCCTGAATCGGCTAATC 65
 XX
 XX RESULT 23
 XX AEB56861
 XX ID AEB56861 standard; DNA; 237 BP.
 XX AC AEB56861;
 XX 22-SEP-2005 (first entry)
 XX Human echovirus 9 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human echovirus 9.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; AF083069.
 XX

PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; X84981.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (I), and one or more container that contains (I); and (2)
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 XX specifically and selectively recognizes the enterovirus genome. (I)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The
 XX present sequence represents a viral 5' untranslated polynucleotide
 XX sequence given in the exemplification of the present invention.
 XX Sequence 237 BP; 48 A; 54 C; 65 G; 70 T; 0 U; 0 Other;
 XX Query Match 100.0%; Score 19; DB 14; Length 237;
 XX Best Local Similarity 100.0%; Pred. No. 2.6;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 CCCCTGAATCGGCTAATC 19
 XX |||||
 XX Db 46 CCCCTGAATCGGCTAATC 64
 XX
 XX RESULT 24
 XX AEB56857
 XX ID AEB56857 standard; DNA; 237 BP.
 XX AC AEB56857;
 XX 22-SEP-2005 (first entry)
 XX Human echovirus 5 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human echovirus 5.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; AF083069.
 XX

PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 49 A; 59 C; 63 G; 66 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
 |||||
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 25
 AEB56871
 ID AEB56871 standard; DNA; 237 BP.
 AC AEB56871;
 XX
 XX 22-SEP-2005 (first entry)
 XX Human enterovirus 70 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human enterovirus 70.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.

(TSAN/) TSANG S.
 (PRIC/) PRICE J A.
 (HELL/) HELLYER T J.
 TSANG S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 GENBANK; D00820.
 Novel oligonucleotide comprising sequences for binding and amplifying or
 detecting target, useful for detecting enterovirus nucleic acids.

Disclosure; Fig 1A-D; 34pp; English.
 The invention relates to an oligonucleotide (I) consisting of: (a) the
 target binding sequence of an oligonucleotide chosen from any one of the
 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 54 A; 52 C; 60 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
 |||||
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 26
 AEB56872
 ID AEB56872 standard; DNA; 237 BP.
 AC AEB56872;
 XX
 XX 22-SEP-2005 (first entry)

XX Human poliovirus 1 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human poliovirus 1.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.

(TSAN/) TSANG S.
 (PRIC/) PRICE J A.
 (HELL/) HELLYER T J.
 TSANG S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 GENBANK; AJ132960.
 Novel oligonucleotide comprising sequences for binding and amplifying or
 detecting target, useful for detecting enterovirus nucleic acids.

Disclosure; Fig 1A-D; 34pp; English.
 The invention relates to an oligonucleotide (I) consisting of: (a) the
 target binding sequence of an oligonucleotide chosen from any one of the
 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 237 BP; 54 A; 56 C; 64 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
 |||||
 Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 27
 AEB56840
 ID AEB56840 standard; DNA; 238 BP.
 XX
 AC AEB56840;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human coxsackievirus B3.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.
 XX
 PF 16-JAN-2004; 2004US-00760048.
 XX
 PR 16-JAN-2004; 2004US-00760048.
 XX
 PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 PI Tsang S, Price JA, Hellyer TJ;
 XX
 WPI; 2005-512251/52.
 DR GENBANK; AH008164.
 XX

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (I), and one or more container that contains: (1) a kit
 XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequences. (I), (MI) and
 XX (K1) are useful for detecting enterovirus target sequences. (I)
 XX specifically and selectively recognizes the enterovirus genome. (I)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The
 XX present sequence represents a viral 5' untranslated polynucleotide
 XX sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
 |||||
 Db 47 CCCCTGAATGCGGCTAATC 65

Qy 1 CCCCTGAATGCGGCTAATC 19
 |||||
 Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 28
 AEB56850
 ID AEB56850 standard; DNA; 238 BP.
 XX
 AC AEB56850;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human coxsackievirus B6 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human coxsackievirus B6.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.
 XX
 PF 16-JAN-2004; 2004US-00760048.
 XX
 PR 16-JAN-2004; 2004US-00760048.
 XX
 PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 PI Tsang S, Price JA, Hellyer TJ;
 XX
 WPI; 2005-512251/52.
 DR GENBANK; AF039205.
 XX

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (I), and one or more container that contains: (1) a kit
 XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequences. (I), (MI) and
 XX (K1) are useful for detecting enterovirus target sequences. (I)
 XX specifically and selectively recognizes the enterovirus genome. (I)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The
 XX present sequence represents a viral 5' untranslated polynucleotide
 XX sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 52 A; 59 C; 64 G; 63 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
 |||||
 Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 29
 AEB56878
 ID AEB56878 standard; DNA; 238 BP.

XX AC AEB56878;
 XX XX 22-SEP-2005 (first entry)
 XX XX Human poliovirus 2 5' untranslated polynucleotide sequence.
 XX DE DNA detection; enteroviral detection; ds.
 XX KW Human poliovirus 2.
 XX OS US2005158710-A1.
 XX PN 21-JUL-2005.
 XX PD 16-JAN-2004; 2004US-00760048.
 XX PF 16-JAN-2004; 2004US-00760048.
 XX PR (TSAN/) TSANG S.
 XX PA (PRIC/) PRICE J A.
 XX PA (HELL/) HELLYER T J.
 XX PI Tsang S, Price JA, Hellyer TJ;
 XX XX WPI; 2005-512251/52.
 XX DR GENBANK; X00595.
 XX XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX PT detecting target, useful for detecting enterovirus nucleic acids.
 XX PS Disclosure; Fig 1A-D; 34pp; English.
 XX XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 238 BP; 56 A; 53 C; 66 G; 63 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 Db 47 CCCCTGAATGCGGCTAATC 65
 RESULT 30
 AEB56849
 ID AEB56849 standard; DNA; 238 BP.
 XX AC AEB56849;
 XX XX 22-SEP-2005 (first entry)
 XX DE Human coxsackievirus B5 5' untranslated polynucleotide sequence.
 XX KW DNA detection; enteroviral detection; ds.
 XX XX

OS Human coxsackievirus B5.
 XX US2005158710-A1.
 XX PN 21-JUL-2005.
 XX PD 16-JAN-2004; 2004US-00760048.
 XX PF 16-JAN-2004; 2004US-00760048.
 XX PR (TSAN/) TSANG S.
 XX PA (PRIC/) PRICE J A.
 XX PA (HELL/) HELLYER T J.
 XX PI Tsang S, Price JA, Hellyer TJ;
 XX XX WPI; 2005-512251/52.
 XX DR GENBANK; X67706.
 XX XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX PT detecting target, useful for detecting enterovirus nucleic acids.
 XX PS Disclosure; Fig 1A-D; 34pp; English.
 XX XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 238 BP; 53 A; 57 C; 61 G; 67 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 Db 47 CCCCTGAATGCGGCTAATC 65
 RESULT 31
 AEB56839
 ID AEB56839 standard; DNA; 238 BP.
 XX AC AEB56839;
 XX XX 22-SEP-2005 (first entry)
 XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 XX KW DNA detection; enteroviral detection; ds.
 XX OS Human coxsackievirus B3.
 XX XX US2005158710-A1.
 XX PN 21-JUL-2005.
 XX PD 16-JAN-2004; 2004US-00760048.
 XX PF 16-JAN-2004; 2004US-00760048.
 XX PR

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XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX WPI; 2005-512251/52.
XX DR GENBANK; AF169670.
XX DR
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC comprising (I), and one or more container that contains (I); and (2)
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 52 A; 54 C; 63 G; 69 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGGCGCTAATC 19
Db 47 CCCCTGAATGGCGCTAATC 65
RESULT 12
AEB56846
ID AEB56846 standard; DNA; 238 BP.
XX AC AEB56846;
XX XX 22-SEP-2005 (first entry)
XX DT Human coxsackievirus B4 5' untranslated polynucleotide sequence.
XX DE DNA detection; enteroviral detection; ds.
XX KW Human coxsackievirus B4.
XX OS US2005158710-A1.
XX PN 21-JUL-2005.
XX PD 16-JAN-2004; 2004US-00760048.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX WPI; 2005-512251/52.
XX DR GENBANK; D00149.
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC comprising (I), and one or more container that contains (I); and (2)
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 52 A; 54 C; 63 G; 69 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGGCGCTAATC 19
Db 47 CCCCTGAATGGCGCTAATC 65
RESULT 33
AEB56847
ID AEB56847 standard; DNA; 238 BP.
XX AC AEB56847;
XX XX 22-SEP-2005 (first entry)
XX DT Human coxsackievirus B4 5' untranslated polynucleotide sequence.
XX DE DNA detection; enteroviral detection; ds.
XX KW Human coxsackievirus B4.
XX OS US2005158710-A1.
XX PN 21-JUL-2005.
XX PD 16-JAN-2004; 2004US-00760048.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX WPI; 2005-512251/52.
XX DR GENBANK; X05690.
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

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CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CCCCTGAATGCGGCTAATC 19
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 34
 AEB56838
 ID AEB56838 standard; DNA; 238 BP.
 AC AEB56838;
 DT 22-SEP-2005 (first entry)
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 DE DNA detection; enteroviral detection; ds.
 OS Human coxsackievirus B3.
 PN US2005158710-A1.
 PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.
 PR 16-JAN-2004; 2004US-00760048.
 PA (TSAN//) TSANG S.
 PA (PRIC//) PRICE J A.
 PA (HELL//) HELLYER T J.
 PI Tsang S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 DR GENBANK; AF169665.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CCCCTGAATGCGGCTAATC 19
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 35
 AEB56842
 ID AEB56842 standard; DNA; 238 BP.
 AC AEB56842;
 DT 22-SEP-2005 (first entry)
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 DE DNA detection; enteroviral detection; ds.
 OS Human coxsackievirus B3.
 PN US2005158710-A1.
 PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.
 PR 16-JAN-2004; 2004US-00760048.
 PA (TSAN//) TSANG S.
 PA (PRIC//) PRICE J A.
 PA (HELL//) HELLYER T J.
 PI Tsang S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 DR GENBANK; M16572.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;


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XX OS Human coxsackievirus B6.
XX PA US2005158710-A1.
XX FN 21-JUL-2005.
XX PD 16-JAN-2004; 2004US-00760048.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX FI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX DR GENBANK; AF105342.
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX CC (K1) are useful for detecting enterovirus target sequences. (I)
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 52 A; 59 C; 64 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 39
AEB56852
ID AEB56852 standard; DNA; 238 BP.
XX AC AEB56852;
XX DT 22-SEP-2005 (first entry)
XX DE Human coxsackievirus B6 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human coxsackievirus B6.
XX PA US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX FI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX DR 16-JAN-2004; 2004US-00760048.

Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 40
AEB56874
ID AEB56874 standard; DNA; 238 BP.
XX AC AEB56874;
XX DT 22-SEP-2005 (first entry)
XX DE Human poliovirus 1 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human poliovirus 1.
XX PA US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX FI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX DR 16-JAN-2004; 2004US-00760048.

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DR GENBANK; V01148.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a consensus viral 5' untranslated
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCCCTGAATGCGGCTAATC 19
 Db 47 CCCCTGAATGCGGCTAATC 65
 RESULT 41
 AEB56829
 ID AEB56829 standard; DNA; 238 BP.
 XX
 AC AEB56829;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Consensus viral 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Synthetic.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.
 XX
 PF 16-JAN-2004; 2004US-00760048.
 XX
 PR 16-JAN-2004; 2004US-00760048.
 XX
 PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 PI Tsang S, Price JA, Hellyer TJ;
 XX
 DR WPI; 2005-512251/52.
 XX
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCCCTGAATGCGGCTAATC 19
 Db 47 CCCCTGAATGCGGCTAATC 65
 RESULT 42
 AEB56843
 ID AEB56843 standard; DNA; 238 BP.
 XX
 AC AEB56843;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human coxsackievirus B3.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.
 XX
 PF 16-JAN-2004; 2004US-00760048.
 XX
 PR 16-JAN-2004; 2004US-00760048.
 XX
 PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 PI Tsang S, Price JA, Hellyer TJ;
 XX
 DR WPI; 2005-512251/52.
 XX
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 SQ Sequence 238 BP; 53 A; 58 C; 64 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATGGCGCTAATC 19
 |||||
 Db 47 CCCCTGAATGGCGCTAATC 65

RESULT 43

AEB56845
 ID AEB56845 standard; DNA; 238 BP.

XX AC AEB56845;
 XX XX

DT 22-SEP-2005 (first entry)

DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 XX XX

KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B3.
 XX XX

PN US2005158710-A1.
 XX XX

PD 21-JUL-2005.
 XX XX

PF 16-JAN-2004; 2004US-00760048.
 XX XX

PR 16-JAN-2004; 2004US-00760048.
 XX XX

PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;
 XX XX

DR WPI; 2005-512251/52.
 DR GENBANK; U57056.

PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX XX

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I) (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX XX

SQ Sequence 238 BP; 54 A; 57 C; 62 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;

Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATGGCGCTAATC 19
 |||||
 Db 47 CCCCTGAATGGCGCTAATC 65

RESULT 44

AEB56870
 ID AEB56870 standard; DNA; 238 BP.

XX AC AEB56870;
 XX XX

DT 22-SEP-2005 (first entry)

DE Human echovirus 30 5' untranslated polynucleotide sequence.
 XX XX

KW DNA detection; enteroviral detection; ds.

XX OS Human echovirus 30.
 XX XX

PN US2005158710-A1.
 XX XX

PD 21-JUL-2005.
 XX XX

PF 16-JAN-2004; 2004US-00760048.
 XX XX

PR 16-JAN-2004; 2004US-00760048.
 XX XX

PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;
 XX XX

DR WPI; 2005-512251/52.
 DR GENBANK; AF162711.

PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX XX

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I) (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX XX

SQ Sequence 238 BP; 51 A; 56 C; 61 G; 70 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATGGCGCTAATC 19
 |||||
 Db 47 CCCCTGAATGGCGCTAATC 65

RESULT 45

```

AEB56830
ID AEB56830 standard; DNA; 238 BP.
XX
AC AEB56830;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human coxsackievirus A9 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Human coxsackievirus A9.
OS
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
XX
XX GENBANK; D00627.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX Sequence 238 BP; 50 A; 58 C; 66 G; 64 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 2.6;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCCCTGAATCGGCTAATC 19
XX |||||
XX Db 47 CCCCTGAATCGGCTAATC 65
XX
XX RESULT 46
XX AEB56833
XX ID AEB56833 standard; DNA; 238 BP.
XX
XX AC AEB56833;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human coxsackievirus A24 5' untranslated polynucleotide sequence.
XX
XX

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KW DNA detection; enteroviral detection; ds.
XX Human coxsackievirus A24.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
XX
XX GENBANK; D90457.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX Sequence 238 BP; 53 A; 54 C; 64 G; 67 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 2.6;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCCCTGAATCGGCTAATC 19
XX |||||
XX Db 47 CCCCTGAATCGGCTAATC 65
XX
XX RESULT 47
XX AEB56877
XX ID AEB56877 standard; DNA; 238 BP.
XX
XX AC AEB56877;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human poliovirus 2 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Human poliovirus 2.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX

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XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; M12197.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (I), and one or more container that contains (I); and (2)
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 XX (K1) are useful for detecting enterovirus target sequences. (I) and
 XX specifically and selectively recognizes the enterovirus genome. (I)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The
 XX present sequence represents a viral 5' untranslated polynucleotide
 XX sequence given in the exemplification of the present invention.
 XX Sequence 238 BP; 56 A; 56 C; 63 G; 63 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 DB 47 CCCCTGAATGCGGCTAATC 65
 RESULT 48
 AEB56859
 ID AEB56859 standard; DNA; 238 BP.
 XX AEB56859;
 XX 22-SEP-2005 (first entry)
 XX Human echovirus 6 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human echovirus 6.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; M74567.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the

DR WPI; 2005-512251/52.
 DR GENBANK; U16283.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (I), and one or more container that contains (I); and (2)
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 XX (K1) are useful for detecting enterovirus target sequences. (I) and
 XX specifically and selectively recognizes the enterovirus genome. (I)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The
 XX present sequence represents a viral 5' untranslated polynucleotide
 XX sequence given in the exemplification of the present invention.
 XX Sequence 238 BP; 47 A; 53 C; 66 G; 72 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 DB 47 CCCCTGAATGCGGCTAATC 65
 RESULT 49
 AEB56841
 ID AEB56841 standard; DNA; 238 BP.
 XX AEB56841;
 XX 22-SEP-2005 (first entry)
 XX Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human coxsackievirus B3.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; M74567.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains: (1) a kit
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 52 A; 58 C; 65 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. NO. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 |||||
 Db 47 CCCCTGAATCGGCTAATC 65

RESULT 50

AEB56831
 ID AEB56831 standard; DNA; 238 BP.

XX AC AEB56831;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus A16 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus A16.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.
 XX PA (PRIC/) PRICE J A.
 XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.
 XX DR GENBANK; U05876.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains: (1) a kit
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. NO. 2.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 |||||
 Db 47 CCCCTGAATCGGCTAATC 65

RESULT 51

AEB56867
 ID AEB56867 standard; DNA; 238 BP.

XX AC AEB56867;

XX DT 22-SEP-2005 (first entry)

XX DE Human echovirus 12 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human echovirus 12.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.
 XX PA (PRIC/) PRICE J A.
 XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.
 XX DR GENBANK; X79047.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains: (1) a kit
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
|||||
Db 47 CCCCTGAATGGGCTAATC 65

RESULT 52

AEBS6844
ID AEBS6844 standard; DNA; 238 BP.
XX
AC AEBS6844;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Human coxsackievirus B3.
XX
PN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PF 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
DR GENBANK; M88483.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
|||||
Db 47 CCCCTGAATGGGCTAATC 65

RESULT 53

AEBS6866
ID AEBS6866 standard; DNA; 238 BP.
XX
AC AEBS6866;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human echovirus 12 5' untranslated polynucleotide sequence.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Human echovirus 12.
XX
PN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PF 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
DR GENBANK; X77708.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
|||||
Db 47 CCCCTGAATGGGCTAATC 65

RESULT 54

AEBS6882
ID AEBS6882 standard; DNA; 238 BP.
XX
AC AEBS6882;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human poliovirus 3 5' untranslated polynucleotide sequence.

```

XX DNA detection; enteroviral detection; ds.
KW Human poliovirus 3.
OS
XX
XX US2005158710-A1.
XX PN
XX
XX 21-JUL-2005.
XX PD
XX
XX 16-JAN-2004; 2004US-00760048.
XX PF
XX
XX 16-JAN-2004; 2004US-00760048.
XX PR
XX
XX (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX PI
XX WPI; 2005-512251/52.
XX DR
XX GENBANK; X04468.
XX DR
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX FT
XX Disclosure; Fig 1A-D; 34pp; English.
XX PS
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of ABB56764
XX CC to ABB56771; and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX CC (K1) are useful for detecting enterovirus target sequences. (I)
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX
XX Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
| | | | | | | | | | | | | | |
Db 47 CCCCTGAATGGGCTAATC 65
| | | | | | | | | | | | | | |

RESULT 55
ABX12446
ID ABX12446 standard; DNA; 497 BP.
XX
XX ABX12446;
XX
XX 10-MAY-2003 (first entry)
XX DT
XX
XX Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #1.
XX DE
XX
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX KW renal failure; leg amputation; ds.
XX
XX Cocksackievirus.
XX OS
XX WO2002103060-A2.
XX PN

XX 27-DEC-2002.
XX PD
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX PF
XX
XX 20-JUN-2001; 2001SE-00002198.
XX PR
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX PA
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX XX
XX WPI; 2003-278229/27.
XX DR
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX PT the diabetogenic coxsackie B virus-4 strain VD2921.
XX FT
XX Disclosure; Page 72; 79pp; English.
XX PS
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX CC strain VD2921, particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX CC P3C and P3D nucleic acids). The methods and primers are used for the
XX CC detection of CBV-4 strain VD2921 which is associated with diabetes
XX CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX CC cells, can improve prognosis by allowing treatment e.g. with antiviral
XX CC drugs, to prevent further loss of beta cells and severe long term
XX CC consequences of diabetes including blindness, renal failure and leg
XX CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX CC (CBV-4) strain VD2921 associated polynucleotide
XX
XX Sequence 497 BP; 119 A; 134 C; 129 G; 115 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 19; DB 8; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
| | | | | | | | | | | | | | |
Db 365 CCCCTGAATGGGCTAATC 383
| | | | | | | | | | | | | | |

RESULT 56
ABX12451
ID ABX12451 standard; DNA; 502 BP.
XX
XX ABX12451;
XX
XX 10-MAY-2003 (first entry)
XX DT
XX
XX Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #6.
XX DE
XX
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX KW renal failure; leg amputation; ds.
XX
XX Cocksackievirus.
XX OS
XX WO2002103060-A2.
XX PN

XX 27-DEC-2002.
XX PD
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX PF
XX
XX 20-JUN-2001; 2001SE-00002198.
XX PR
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX PA
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX XX
XX WPI; 2003-278229/27.
XX DR
XX

```

PT Polymerase chain reaction and primers for detecting nucleic acids from
 XX the diabetogenic coxsackie B virus-4 strain VD2921.
 XX
 PS Disclosure; Page 73; 79pp; English.
 XX
 CC The invention describes a polymerase chain reaction (PCR) and primers for
 CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
 CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
 CC P3C and P3D nucleic acids). The methods and primers are used for the
 CC detection of CBV-4 strain VD2921 which is associated with diabetes
 CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
 CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
 CC cells, can improve prognosis by allowing treatment e.g. with antiviral
 CC drugs, to prevent further loss of beta cells and severe long term
 CC consequences of diabetes including blindness, renal failure and leg
 CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
 CC (CBV-4) strain VD2921 associated polynucleotide
 XX
 SQ Sequence 502 BP; 120 A; 132 C; 128 G; 122 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 8; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 DB 368 CCCCTGAATGCGGCTAATC 386
 RESULT 57
 AAZ58487
 ID AAZ58487 standard; RNA; 514 BP.
 XX
 AC AAZ58487;
 DT 15-SEP-2003 (revised)
 DT 23-MAY-2000 (first entry)
 XX
 DE Poliovirus IRES domain II-VI region.
 XX
 KW Internal ribosomal entry site; IRES; poliovirus; tumour; cancer;
 KW glioblastoma multiforme; medulloblastoma; mammary carcinoma;
 KW prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;
 KW bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.
 XX
 OS Human poliovirus 1.
 XX
 FH Key Location/Qualifiers
 FT stem_loop 25..63
 FT /*tag= a
 FT /note= "domain II"
 FT stem_loop 70..83
 FT /*tag= b
 FT stem_loop 84..120
 FT /*tag= c
 FT /note= "domain III"
 FT stem_loop 132..338
 FT /*tag= d
 FT /note= "domain IV"
 FT stem_loop 183..209
 FT /*tag= e
 FT /note= "domain V"
 FT stem_loop 273..292
 FT /*tag= f
 FT stem_loop 346..454
 FT /*tag= g
 FT /note= "domain VI"
 FT stem_loop 481..513
 FT /*tag= h
 FT /note= "domain VI"
 XX
 PN WO200008166-A1.
 XX
 PD 17-FEB-2000.

XX 09-APR-1999; 99WO-US007839.
 XX
 XX 05-AUG-1998; 98US-00129686.
 XX
 XX (UUNY) UNIV NEW YORK STATE RES FOUND.
 XX
 XX Gromeier M, Wimmer E;
 XX
 XX WPI; 2000-205717/18.
 XX
 XX Chimeric recombinant poliovirus useful for treating malignant tumors
 XX comprises internal ribosomal entry site derived from picornaviruses.
 XX
 XX Disclosure; Fig 2; 99pp; English.
 XX
 CC This sequence represents domains II-VI of the internal ribosomal entry
 CC site (IRES) of wild-type poliovirus type 1 Mahoney. The invention
 CC provides non-pathogenic, oncolytic, recombinant polioviruses (I) in which
 CC the IRES of the wild-type poliovirus is exchanged with the IRES of
 CC another picornavirus, such as human rhinovirus type 2, and optionally the
 CC P1, P3 or 3' untranslated region is exchanged with that of Sabin
 CC poliovirus. (I) may contain a composite IRES encompassing IRES domains
 CC from both wild-type poliovirus and from another virus. (I) are useful for
 CC treating malignant tumors such as glioblastoma multiforme,
 CC medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial
 CC and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 514 BP; 122 A; 134 C; 132 G; 0 T; 126 U; 0 Other;
 Query Match 100.0%; Score 19; DB 3; Length 514;
 Best Local Similarity 78.9%; Pred. No. 2.8;
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 DB 349 CCCCTGAATGCGGCTAATC 367
 RESULT 58
 ABL53112
 ID ABL53112 standard; DNA; 520 BP.
 XX
 AC ABL53112;
 DT 07-AUG-2003 (revised)
 DT 25-JUN-2002 (first entry)
 XX
 XX Micro-organism detection probe #54.
 XX
 KW Probe; microorganism detection; microbiological quality;
 KW water purification; ss.
 XX
 OS Coxsackievirus.
 XX
 PN WO200202811-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 06-JUL-2001; 2001WO-FR002191.
 XX
 PR 06-JUL-2000; 2000FR-00008839.
 XX
 XX (INNR) BIO MERIEUX.
 XX
 XX Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;
 XX Armand M, Laffaire P;
 XX
 XX WPI; 2002-148021/19.
 XX
 XX Monitoring microbiological quality of water, useful particularly for
 XX controlling water purification, uses oligonucleotide probes to detect at

PT least three representative microbes.
XX
PS Claim 24; Page 75-76 ; 85pp; French.
XX
CC The present invention relates to a method for monitoring microbiological
CC quality of an aqueous environmental medium that potentially contains many
CC different microorganisms. A reference set of at least three
CC microorganisms is chosen that, separately or collectively, represent
CC microbiological quality. The test medium is treated, then any
CC microorganisms, or their fragments, in the treated medium is contacted
CC with a set of at least three probes for specific identification and
CC multiple determination of selected microorganisms. This determination
CC represents the level of microbiological quality. The method is useful for
CC identifying and quantifying microorganisms in water and provides results
CC that are used to control water purification/production processes. The
CC present sequence is a probe which was used to illustrate the invention.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 520 BP; 113 A; 141 C; 131 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGTAATC 19
Db 386 CCCCTGAATGGCGTAATC 404

RESULT 59
ABL53111
ID ABL53111 standard; DNA; 521 BP.
XX
AC ABL53111;
XX
XX 07-AUG-2003 (revised)
DT 25-JUN-2002 (first entry)
XX
XX Micro-organism detection probe #53.
DE
XX Probe; microorganism detection; microbiological quality;
KW water purification; ss.
XX
XX Poliovirus.
OS
XX
XX Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;
FN Armand M, Laffaire P;
XX
XX WO200202811-A2.
PD
XX 10-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-FR002191.
PF
XX 06-JUL-2000; 2000FR-00008839.
PR
XX (INNR) BIO MERIEUX.
PA
XX
XX Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;
PI Armand M, Laffaire P;
XX
XX WPI; 2002-148021/19.
DR
XX
XX Monitoring microbiological quality of water, useful particularly for
PT controlling water purification, uses oligonucleotide probes to detect at
PT least three representative microbes.
XX
XX Claim 24; Page 75; 85pp; French.
PS
XX
XX The present invention relates to a method for monitoring microbiological
CC quality of an aqueous environmental medium that potentially contains many
CC different microorganisms. A reference set of at least three
CC microorganisms is chosen that, separately or collectively, represent
CC microbiological quality. The test medium is treated, then any
CC microorganisms, or their fragments, in the treated medium is contacted
CC with a set of at least three probes for specific identification and

CC multiple determination of selected microorganisms. This determination
CC represents the level of microbiological quality. The method is useful for
CC identifying and quantifying microorganisms in water and provides results
CC that are used to control water purification/production processes. The
CC present sequence is a probe which was used to illustrate the invention.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 521 BP; 113 A; 140 C; 138 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 521;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGTAATC 19
Db 387 CCCCTGAATGGCGTAATC 405

RESULT 60
ABL53113
ID ABL53113 standard; DNA; 525 BP.
XX
AC ABL53113;
XX
XX 07-AUG-2003 (revised)
DT 25-JUN-2002 (first entry)
XX
XX Micro-organism detection probe #55.
DE
XX Probe; microorganism detection; microbiological quality;
KW water purification; ss.
XX
XX Echovirus sp.
OS
XX
XX WO200202811-A2.
FN
XX 10-JAN-2002.
PD
XX
XX 06-JUL-2001; 2001WO-FR002191.
PF
XX 06-JUL-2000; 2000FR-00008839.
PR
XX (INNR) BIO MERIEUX.
PA
XX
XX Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;
FI Armand M, Laffaire P;
XX
XX WPI; 2002-148021/19.
DR
XX
XX Monitoring microbiological quality of water, useful particularly for
PT controlling water purification, uses oligonucleotide probes to detect at
PT least three representative microbes.
XX
XX Claim 24; Page 76; 85pp; French.
PS
XX
XX The present invention relates to a method for monitoring microbiological
CC quality of an aqueous environmental medium that potentially contains many
CC different microorganisms. A reference set of at least three
CC microorganisms is chosen that, separately or collectively, represent
CC microbiological quality. The test medium is treated, then any
CC microorganisms, or their fragments, in the treated medium is contacted
CC with a set of at least three probes for specific identification and
CC multiple determination of selected microorganisms. This determination
CC represents the level of microbiological quality. The method is useful for
CC identifying and quantifying microorganisms in water and provides results
CC that are used to control water purification/production processes. The
CC present sequence is a probe which was used to illustrate the invention.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 525 BP; 117 A; 142 C; 135 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.8;

```
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
Db 391 CCCCTGAATGGGCTAATC 409

RESULT 61
ABX12448
ID ABX12448 standard; DNA; 548 BP.
AC ABX12448;
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #3.
XX
KW Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #3.
XX
KW Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
DT 27-DEC-2002.
XX
PF 19-JUN-2002; 2002WO-IB003278.
XX
PR 20-JUN-2001; 2001SE-00002198.
XX
PA (INNO-) INNOVENTUS PROJECT AB.
XX
PI Tuvemo HT, Frisk GE, Yin H;
XX
DR WPI; 2003-278229/27.
XX
PT Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetogenic coxsackie B virus-4 strain VD2921.
XX
PS Disclosure; Page 72; 79pp; English.
XX
CC The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX
SQ Sequence 548 BP; 124 A; 145 C; 144 G; 135 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 8; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
Db 358 CCCCTGAATGGGCTAATC 376

RESULT 62
ABX12453
ID ABX12453 standard; DNA; 551 BP.
AC ABX12453;
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #7.
XX
KW Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
```

```
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #8.
XX
KW Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
DT 27-DEC-2002.
XX
PF 19-JUN-2002; 2002WO-IB003278.
XX
PR 20-JUN-2001; 2001SE-00002198.
XX
PA (INNO-) INNOVENTUS PROJECT AB.
XX
PI Tuvemo HT, Frisk GE, Yin H;
XX
DR WPI; 2003-278229/27.
XX
PT Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetogenic coxsackie B virus-4 strain VD2921.
XX
PS Disclosure; Page 74; 79pp; English.
XX
CC The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX
SQ Sequence 551 BP; 130 A; 147 C; 140 G; 134 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 8; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
Db 364 CCCCTGAATGGGCTAATC 382

RESULT 63
ABX12452
ID ABX12452 standard; DNA; 552 BP.
XX
AC ABX12452;
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #7.
XX
KW Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
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```
PD 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Disclosure; Page 73; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX (CBV-4) strain VD2921 associated polynucleotide
XX
XX Sequence 552 BP; 131 A; 143 C; 140 G; 138 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 8; Length 552;
XX Best Local Similarity 100.0%; Pred. No. 2.9;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCCCTGAATGGGCTAATC 19
XX 365 CCCCTGAATGGGCTAATC 383
XX
XX RESULT 64
XX ABX12457
XX ID ABX12457 standard; DNA; 554 BP.
XX
XX AC ABX12457;
XX
XX 10-MAY-2003 (first entry)
XX
XX Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #12.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Disclosure; Page 73; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX (CBV-4) strain VD2921 associated polynucleotide
XX
XX Sequence 552 BP; 131 A; 143 C; 140 G; 138 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 8; Length 552;
XX Best Local Similarity 100.0%; Pred. No. 2.9;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCCCTGAATGGGCTAATC 19
XX 365 CCCCTGAATGGGCTAATC 383
XX
XX RESULT 64
XX ABX12457
XX ID ABX12457 standard; DNA; 554 BP.
XX
XX AC ABX12457;
XX
XX 10-MAY-2003 (first entry)
XX
XX Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #12.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Disclosure; Page 73; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX (CBV-4) strain VD2921 associated polynucleotide
XX
XX Sequence 554 BP; 130 A; 149 C; 142 G; 133 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 8; Length 554;
XX Best Local Similarity 100.0%; Pred. No. 2.9;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCCCTGAATGGGCTAATC 19
XX 362 CCCCTGAATGGGCTAATC 380
XX
XX RESULT 65
XX ABX12449
XX ID ABX12449 standard; DNA; 556 BP.
XX
XX AC ABX12449;
XX
XX 10-MAY-2003 (first entry)
XX
XX Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #4.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Disclosure; Page 72-73; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
```

CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide

XX SQ Sequence 556 BP; 125 A; 153 C; 143 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 556;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCTGAATGCGGCTAATC 19

DB 366 CCCCTGAATGCGGCTAATC 384

RESULT 66

ABX12450

ID ABX12450 standard; DNA; 556 BP.

XX AC ABX12450;

XX DT 10-MAY-2003 (first entry)

XX DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #5.

XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.

XX OS Coxsackievirus.

XX PN WO2002103060-A2.

XX PD 27-DEC-2002.

XX PF 19-JUN-2002; 2002WO-IB003278.

XX PR 20-JUN-2001; 2001SE-00002198.

XX PA (INNO-) INNOVENTUS PROJECT AB.

XX PI Tuvemo HT, Frisk GE, Yin H;

XX DR WPI; 2003-278229/27.

XX PT Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.

XX PS Disclosure; Page 73; 79pp; English.

XX CC The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX (CBV-4) strain VD2921 associated polynucleotide

XX SQ Sequence 556 BP; 127 A; 147 C; 145 G; 137 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 556;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCTGAATGCGGCTAATC 19

DB 365 CCCCTGAATGCGGCTAATC 383

RESULT 67

ABX12456

ID ABX12456 standard; DNA; 559 BP.

XX AC ABX12456;

XX DT 10-MAY-2003 (first entry)

XX DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #11.

XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.

XX OS Coxsackievirus.

XX PN WO2002103060-A2.

XX PD 27-DEC-2002.

XX PF 19-JUN-2002; 2002WO-IB003278.

XX PR 20-JUN-2001; 2001SE-00002198.

XX PA (INNO-) INNOVENTUS PROJECT AB.

XX PI Tuvemo HT, Frisk GE, Yin H;

XX DR WPI; 2003-278229/27.

XX PT Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.

XX PS Disclosure; Page 74-75; 79pp; English.

XX CC The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX (CBV-4) strain VD2921 associated polynucleotide.

XX SQ Sequence 559 BP; 134 A; 150 C; 140 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 559;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCTGAATGCGGCTAATC 19

DB 362 CCCCTGAATGCGGCTAATC 380

RESULT 68

ABX12447

ID ABX12447 standard; DNA; 560 BP.

XX AC ABX12447;

XX DT 10-MAY-2003 (first entry)

XX DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #2.

XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;

KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
FN WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetic enterovirus B virus-4 strain VD2921.
XX
XX Disclosure; Page 72; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetic enterovirus B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetic enterovirus RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetic enterovirus B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX
SQ Sequence 560 BP; 135 A; 143 C; 144 G; 138 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
Db 361 CCCCTGAATGGGCTAATC 379

RESULT 69
ABX12454
ID ABX12454 standard; DNA; 562 BP.
XX
XX AC ABX12454;
XX
XX DT 10-MAY-2003 (first entry)
XX
XX DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #9.
XX
XX KW Cocksackie virus strain VD2921; diabetic enterovirus B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
XX OS Cocksackievirus.
XX
XX FN WO2002103060-A2.
XX
XX PD 27-DEC-2002.
XX
XX PF 19-JUN-2002; 2002WO-IB003278.
XX
XX PR 20-JUN-2001; 2001SE-00002198.

XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetic enterovirus B virus-4 strain VD2921.
XX
XX Disclosure; Page 74; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetic enterovirus B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetic enterovirus RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetic enterovirus B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX
SQ Sequence 562 BP; 134 A; 148 C; 140 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 562;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
Db 365 CCCCTGAATGGGCTAATC 383

RESULT 70
ABX12455
ID ABX12455 standard; DNA; 567 BP.
XX
XX AC ABX12455;
XX
XX DT 10-MAY-2003 (first entry)
XX
XX DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #10.
XX
XX KW Cocksackie virus strain VD2921; diabetic enterovirus B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
XX OS Cocksackievirus.
XX
XX FN WO2002103060-A2.
XX
XX PD 27-DEC-2002.
XX
XX PF 19-JUN-2002; 2002WO-IB003278.
XX
XX PR 20-JUN-2001; 2001SE-00002198.
XX
XX PA (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetic enterovirus B virus-4 strain VD2921.
XX
XX Disclosure; Page 74; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for

CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
 CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
 CC P3C and P3D nucleic acids). The methods and primers are used for the
 CC detection of CBV-4 strain VD2921 which is associated with diabetes
 CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
 CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
 CC cells, can improve prognosis by allowing treatment e.g. with antiviral
 CC drugs, to prevent further loss of beta cells and severe long term
 CC consequences of diabetes including blindness, renal failure and leg
 CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
 CC (CBV-4) strain VD2921 associated polynucleotide
 XX
 SQ Sequence 567 BP; 140 A; 147 C; 141 G; 139 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 567;
 Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19

Db 366 CCCCTGAATGCGGCTAATC 384

RESULT 71

AAQ58715

ID AAQ58715 standard; DNA; 628 BP.

XX AC AAQ58715;

XX AC AAQ58715;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 29-SEP-1994 (first entry)

XX DE Poliovirus type 1 5'-UTR with C to G substn. at position 610.

XX KW Platelet-Derived Growth Factor; heterodimer; PDGF-AB;

XX KW recombinant protein production; PDGF-A chain; PDGF-B chain;

XX KW bicistronic vector system; ss.

XX OS Human poliovirus 1 Mahoney.

XX PH Key Location/Qualifiers

FT 5'UTR 1..628

FT mutation /tag= a

FT /tag= b

FT /note= "wild-type C has been substituted by G"

XX WO9405786-A1.

XX PD 17-MAR-1994.

XX PF 26-AUG-1993; 93WO-EP002295.

XX PR 27-AUG-1992; 92DE-04228457.

XX PA (BEIE) BEIERSDORF AG.

XX PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.

XX PI Eichner W, Achterberg V, Doerschner A, Meyer-Ingold W, Mielke H;

XX PI Dirks W, Wirth M, Hauser H;

XX WPI; 1994-101191/12.

XX Heterodimer platelet-derived-growth factor (PDGF) prodn. - using a

XX PT polycistronic vector system in mammalian host cells for equimolar prodn

XX PT of A- and B-chains.

XX PS Claim 5; Page 41; 64pp; German.

XX A PDGF-AB heterodimer is recombinantly produced using a bicistronic

XX expression unit in which a sequence responsible for internal translation

XX start (designated "IRES") is located between cistrons coding for the PDGF

CC -B and PDGF-A chains. The preferred IRES sequence for inclusion in the
 CC bicistronic construct is the 5'-UTR from Poliovirus type 1 Mahoney strain
 CC of sequence AAQ58715. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 628;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19

Db 451 CCCCTGAATGCGGCTAATC 469

RESULT 72

AAQ58726

ID AAQ58726 standard; DNA; 628 BP.

XX AC AAQ58726;

XX AC AAQ58726;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 29-SEP-1994 (first entry)

XX DE Poliovirus type 1 5'-UTR with C to G substn. at position 610.

XX KW Multicistronic expression unit; recombinant protein production;

XX KW internal translation start; initiation; 5'-untranslated region; ss.

XX OS Human poliovirus 1 Mahoney.

XX PH Key Location/Qualifiers

FT 5'UTR 1..628

FT mutation /tag= a

FT /tag= b

FT /note= "wild-type C has been substituted by G"

XX WO9405785-A1.

XX PD 17-MAR-1994.

XX PF 26-AUG-1993; 93WO-EP002294.

XX PR 27-AUG-1992; 92DE-04228458.

XX PA (BEIE) BEIERSDORF AG.

XX PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.

XX PI Dirks W, Wirth M, Hauser H, Eichner W, Achterberg V;

XX PI Doerschner A, Meyer-Ingold W, Mielke H;

XX WPI; 1994-101190/12.

XX New multicistronic expression units - for producing equimolar amts. of

XX polypeptide(s) in mammalian cells as hosts.

XX PS Claim 6; Page 50; 109pp; German.

XX Heterodimeric proteins can be recombinantly produced using a

XX multicistronic (esp. bicistronic) expression unit in which a sequence

XX responsible for internal translation start (designated "IRES") is located

XX between cistrons coding for the different subunits. The preferred IRES

XX sequence is the 5'-UTR from Poliovirus type 1 Mahoney strain of sequence

XX AAQ58726. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-

XX AUG-2003 to correct OS field.)

XX SQ Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 628;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
 Db 451 CCCCTGAATGGCGCTAATC 469

RESULT 73
 ADP74707
 ID ADP74707 standard; DNA; 639 BP.
 XX AC ADP74707;
 XX DT 26-AUG-2004 (first entry)
 XX DE Novel bicistronic retroviral vector related poliovirus IRES sequence.
 XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
 KW severe combined immune deficiency syndrome; protein expression;
 KW antisense; ds; gene.
 XX OS Unidentified.
 XX FN EP1428886-A1.
 XX PD 16-JUN-2004.
 XX PF 09-DEC-2002; 2002EP-00027555.
 XX PR 09-DEC-2002; 2002EP-00027555.
 XX PA (CELL-) CELTECH GMBH BIOTECHNOLOGIE.
 XX FI Heberlein C, Gindullis F, Hannemann J, Strathmann G;
 XX DR WPI; 2004-452367/43.
 XX PT Bicistronic retroviral vector, useful in gene therapy, particularly of
 PT graft versus host disease, contains components of both murine embryonic
 PT stem cell and myeloproliferative sarcoma viruses.
 XX PS Disclosure: Page 70; 91pp; German.
 XX CC The present invention relates to a new bicistronic retroviral vector.
 CC These are used for (over)expression of proteins, suppressing expression
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
 CC suppress a dominant-negative phenotype, also infectious viral particles
 CC that contain the vectors, in gene therapy, particularly for control of
 CC guest versus host disease, especially where haematopoietic cells are
 CC transduced with the vector or where T cells are transduced, for adoptive
 CC immunotherapy, but also for treating severe combined immune deficiency
 CC syndrome and for expression cloning of genes. The present sequence is a
 CC vector sequence fragment shown in the exemplification of the invention.
 XX SQ Sequence 639 BP; 146 A; 171 C; 164 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
 Db 455 CCCCTGAATGGCGCTAATC 473

RESULT 74
 AAC85153
 ID AAC85153 standard; RNA; 646 BP.
 XX AC AAC85153;
 XX DT 08-MAY-2001 (first entry)
 XX

DE Echo virus (ECV12) 5' non-translated region (NTR) sequence.
 XX KW Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
 KW Cocksackievirus B3; CVB3; NTR; non-translated region; echo virus; ds.
 XX OS Echo virus.

XX FH Location/Qualifiers
 FT stem_loop 2..87
 FT /*tag= a
 FT /note= "Domain I"
 FT 103..180
 FT /*tag= b
 FT /note= "Domain II"
 FT 183..232
 FT /*tag= c
 FT /note= "Domain III"
 FT 240..443
 FT /*tag= d
 FT /note= "Domain IV"
 FT 451..559
 FT /*tag= e
 FT /note= "Domain V"
 FT 586..622
 FT /*tag= f
 FT /note= "Domain VI"
 FT 623..643
 FT /*tag= g
 FT /note= "Domain VII"

WO200104136-A1.
 18-JAN-2001.
 08-JUL-2000; 2000WO-US018681.
 09-JUL-1999; 99US-0143104P.
 (UYNE-) UNIV NEBRASKA.
 Romero JR, Bradrick SS, Dunn JJ;
 WPI; 2001-138310/14.

Recombinant enterovirus genome for use as vector or vaccine, modified by
 replacing a part or all of its 5' non-translated region by 5' NTR of
 enterovirus genome that encodes virus modified in tropism or virulence.
 Disclosure: Fig 2; 49pp; English.

The invention provides an enterovirus genome (I) for use as a vector or
 vaccine, modified to produce a virus (VI) having a restricted or altered
 species or tissue tropism, compared to an equivalent unmodified virus, or
 modified to produce an attenuated virus (V2), by replacing a part or all
 of the 5' non-translated region (5'NTR) of (I) with a 5'NTR of an
 enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
 vector in targeting genes of interest to specific cells or tissues. (I)
 is also useful for diagnostic purposes, e.g. to identify virulent, versus
 nonvirulent strains of an enterovirus. The present sequence represents
 the 5' NTR (non-translated region) sequence of echo virus (ECV12)

SQ Sequence 646 BP; 145 A; 176 C; 163 G; 0 T; 162 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 646;
 Best Local Similarity 78.9%; Pred. No. 2.9;
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
 Db 454 CCCCTGAATGGCGCTAATC 472

RESULT 75

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AAC85173
ID AAC85173 standard; DNA; 654 BP.
XX
AC AAC85173;
XX
DT 08-MAY-2001 (first entry)
XX
DE Cxsackievirus B3 (CVB3)/AS 5' non-translated region (NTR) sequence.
XX
KW Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
KW Cxsackievirus B3; CVB3; NTR; non-translated region; ds.
OS Cxsackievirus.
XX
FN WO200104136-A1.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-US018681.
XX
PR 09-JUL-1999; 99US-0143104P.
XX
PA (UYNE-) UNIV NEBRASKA.
PI Romero JR, Bradrick SS, Dunn JJ;
XX
DR WPI; 2001-138310/14.
XX
PT Recombinant enterovirus genome for use as vector or vaccine, modified by
PT replacing a part or all of its 5' non-translated region by 5'NTR of
PT enterovirus genome that encodes virus modified in tropism or virulence.
XX
PS Example 2; Page 24; 49pp; English.
XX
CC The invention provides an enterovirus genome (I) for use as a vector or
CC vaccine, modified to produce a virus (VI) having a restricted or altered
CC species or tissue tropism, compared to an equivalent unmodified virus, or
CC modified to produce an attenuated virus (V2), by replacing a part or all
CC of the 5' non-translated region (5'NTR) of (I) with a 5'NTR of an
CC enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
CC vector in targeting genes of interest to specific cells or tissues. (I)
CC is also useful for diagnostic purposes, e.g. to identify virulent, versus
CC nonvirulent strains of an enterovirus. The present sequence represents
CC the 5' NTR (non-translated region) of the cardiovirulent enterovirus
CC Cxsackievirus B3 (CVB3)/AS strain
XX
SQ Sequence 654 BP; 166 A; 161 C; 159 G; 168 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 654;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGGCTAATC 19
Db 367 CCCCTGAATGGGCTAATC 385

RESULT 76
AAC85174
ID AAC85174 standard; DNA; 660 BP.
XX
AC AAC85174;
XX
DT 08-MAY-2001 (first entry)
XX
DE Cxsackievirus B3 (CVB3)/CO 5' non-translated region (NTR) sequence.
XX
KW Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
KW Cxsackievirus B3; CVB3; NTR; non-translated region; ds.
OS Cxsackievirus.
XX
FN WO200104136-A1.

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XX 18-JAN-2001.
XX
PD 08-JUL-2000; 2000WO-US018681.
XX
PF 09-JUL-1999; 99US-0143104P.
XX
PR (UYNE-) UNIV NEBRASKA.
XX
PI Romero JR, Bradrick SS, Dunn JJ;
XX
DR WPI; 2001-138310/14.
XX
PT Recombinant enterovirus genome for use as vector or vaccine, modified by
PT replacing a part or all of its 5' non-translated region by 5'NTR of
PT enterovirus genome that encodes virus modified in tropism or virulence.
XX
PS Example 2; Page 25; 49pp; English.
XX
CC The invention provides an enterovirus genome (I) for use as a vector or
CC vaccine, modified to produce a virus (VI) having a restricted or altered
CC species or tissue tropism, compared to an equivalent unmodified virus, or
CC modified to produce an attenuated virus (V2), by replacing a part or all
CC of the 5' non-translated region (5'NTR) of (I) with a 5'NTR of an
CC enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
CC vector in targeting genes of interest to specific cells or tissues. (I)
CC is also useful for diagnostic purposes, e.g. to identify virulent, versus
CC nonvirulent strains of an enterovirus. The present sequence represents
CC the 5' NTR (non-translated region) of a non-cardiovirulent enterovirus
CC Cxsackievirus B3 (CVB3)/CO strain
XX
SQ Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGGCTAATC 19
Db 373 CCCCTGAATGGGCTAATC 391

RESULT 77
AEB56828
ID AEB56828 standard; DNA; 660 BP.
XX
AC AEB56828;
XX
DT 22-SEP-2005 (first entry)
XX
DE Cxsackie virus B5 polynucleotide sequence SEQ ID NO:67.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Human cxsackievirus B5.
XX
PN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PF 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
DR WPI; 2005-512251/52.
DR GENBANK; AF169665.
XX
XX

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PT Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
PS Disclosure; SEQ ID NO 67; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a coxsackie virus B5 polynucleotide sequence,
CC which is given in the exemplification of the present invention. Note: the
CC present sequence is designated as SEQ ID NO:67 in the Sequence Listing.
CC but corresponds with the sequence given in figure 2 designated SEQ ID
CC NO:14 in the description of the drawings.
XX
XX
SQ Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 660;
Best Local Similarity 100.0%; Pred. NO. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 373 CCCCTGAATCGGCTAATC 391

RESULT 78
ADU77356
ID ADU77356 standard; DNA; 682 BP.
XX
AC ADU77356;
XX
DT 10-FEB-2005 (first entry)
XX
DE Prima7 virus 5' UTR region DNA.
XX
XX Enteroviral genus related disease; Prima7-related disease; gene therapy;
XX ds.
XX
XX Prima7 virus.
XX
XX EP1479761-A1.
XX
XX 24-NOV-2004.
XX
XX 21-MAY-2003; 2003EP-00076529.
XX
XX 21-MAY-2003; 2003EP-00076529.
XX
XX (PRIM-) PRIMAGEN HOLDING BV.
XX
XX Maas HCGI, Van Den Broek PJM, Mang R;
XX
XX WPI; 2004-823915/82.
XX
XX New isolated or recombinant virus, useful for detecting a molecule
XX capable of specifically binding the virus in a sample, and as a vaccine
XX or medicament for treating or preventing Prima7-related disease.
XX
XX Example; SEQ ID NO 39; 51pp; English.
XX
XX The present invention provides a new isolated or recombinant virus called
XX Prima7 (which belong to enteroviral species) comprising a nucleic acid

CC sequence or its functional part, derivative or analogue of the said
CC virus. The invention is useful for detecting and/or identifying a Prima7
CC enterovirus in a sample and for diagnosing an enteroviral genus related
CC disease. The vaccine or medicament prepared from the Prima7 virus is
CC useful for preventing and/or treating a Prima7-related disease. The
CC invention is also useful in gene therapy. The present sequence is Prima7
CC virus 5' UTR region DNA.
XX
SQ Sequence 682 BP; 176 A; 157 C; 159 G; 190 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 13; Length 682;
Best Local Similarity 100.0%; Pred. NO. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 390 CCCCTGAATCGGCTAATC 408

RESULT 79
AEA00424
ID AEA00424 standard; DNA; 709 BP.
XX
AC AEA00424;
XX
DT 28-JUL-2005 (first entry)
XX
DE Enterovirus 71 5' untranslated region internal ribosome entry site DNA.
XX
XX vector; neurological disease; ds; gene therapy;
XX internal ribosome entry site; cystic fibrosis; cns-gen.;
XX respiratory-gen.; factor VIII deficiency; hemostatic; genetic disorder;
XX factor IX deficiency; Duchenne dystrophy; muscular-gen.;
XX Becker's disease; cancer; cytostatic; neoplasm;
XX acquired immune deficiency syndrome; anti-hiv; infectious disease;
XX antimicrobial.
XX
XX Human enterovirus 71; strain TW/2086/98.
XX
XX US2005112095-A1.
XX
XX 26-MAY-2005.
XX
XX 08-JUL-2003; 2003US-00614283.
XX
XX 09-JUL-2002; 2002US-0394269P.
XX
XX (HSUT/) HSU T.
XX (WUT/) WU T.
XX (LEEJ/) LEE J.
XX
XX Hsu T, Wu T, Lee J;
XX
XX WPI; 2005-371616/38.
XX
XX New nucleic acid vector for the expression of at least two cistrons
XX comprising a nucleotide sequence comprising an internal ribosome entry
XX site (IRES) e.g. enterovirus 71 (EV71), useful for treating a patient
XX having e.g. AIDS.
XX
XX Example 2; SEQ ID NO 1; 23pp; English.
XX
XX The present invention relates to a nucleic acid vector for the expression
XX of at least two cistrons. The vector comprises a promoter operably linked
XX to a nucleotide sequence comprising at least two cistrons and at least
XX one nucleotide sequence comprising an internal ribosome entry site (IRES)
XX selected from Human enterovirus 71 (EV71), Hepatitis C virus (HCV), or
XX Encephalomyocarditis virus (EMCV). The invention also provides a method
XX for screening of anti-viral compounds using the IRES. The invention is
XX useful for the genetic treatment of patients with cystic fibrosis,
XX hemophilia A or B, Duchenne or Becker type myopathy, cancer, AIDS and
XX other bacterial or infectious diseases due to a pathogenic organism and
XX in gene therapy. The present sequence is the enterovirus 71 5'

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CC untranslated region (UTR) IRES DNA.
SQ Sequence 709 BP; 165 A; 185 C; 172 G; 187 T; 0 U; 0 Other;

Query Match      100.0%; Score 19; DB 14; Length 709;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 420 CCCCTGAATGCGGCTAATC 438

RESULT 80
ADW37919
ID ADW37919 standard; cDNA; 743 BP.
AC ADW37919;
XX
XX
XX
XX 24-MAR-2005 (first entry)
XX
XX Poliovirus type 1 strain mahoney internal ribosomal entry site cDNA.
XX
XX SARS-coronavirus virus-like particle; SARS-Cov-VLP;
XX cellular immune response; humoral immune response; vaccine;
XX immunogenicity; cytotoxic T-lymphocyte; internal ribosomal entry site;
XX IRES; ss.
XX
XX Human poliovirus 1.
XX
XX US2005002953-A1.
XX
XX 06-JAN-2005.
XX
XX 04-MAY-2004; 2004US-00839729.
XX
XX 06-MAY-2003; 2003US-0468703P.
XX
XX (HERO/) HEROLD J.
XX
XX Herold J;
XX
XX WPI; 2005-065191/07.
XX
XX New system comprising one or more recombinant vectors that expresses the
XX SARS-Cov E-protein, SARS-Cov M-protein, and SARS-Cov S-protein, useful
XX for making SARS-coronavirus virus-like particles.
XX
XX Example 2; SEQ ID NO 21; 111pp; English.
XX
XX The present invention provides a system for making SARS-coronavirus virus
XX -like particles (SARS-Cov-VLPs) comprising one or more recombinant
XX vectors that expresses the SARS-Cov E (small membrane)-protein, SARS-Cov
XX M (membrane)-protein and SARS-Cov S (spike)-protein. The invention is
XX useful for inducing cellular and/or humoral immune response. The
XX invention is also useful to reduce the symptoms of SARS-Cov infections
XX and in vaccine preparations. The present sequence is Poliovirus type 1
XX strain mahoney internal ribosomal entry site (IRES) cDNA. This cDNA
XX sequence is used in the preparation of plasmid for the expression of SARS
XX -Cov M, E and S proteins.
XX
XX Sequence 743 BP; 175 A; 185 C; 181 G; 202 T; 0 U; 0 Other;

Query Match      100.0%; Score 19; DB 14; Length 743;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 448 CCCCTGAATGCGGCTAATC 466

RESULT 81
AAC85152
ID AAC85152 standard; RNA; 745 BP.
XX
XX AAC85152;
XX
XX 08-MAY-2001 (first entry)
XX
XX Coxsackievirus B3 (CVB3) 5' non-translated region (NTR) sequence.
XX
XX Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
XX Coxsackievirus B3; CVB3; NTR; non-translated region; ds.
XX
XX Coxsackievirus.
XX
XX Key Location/Qualifiers
XX stem_loop 2..87
XX /*tag= d
XX /note= "Domain I"
XX stem_loop 10..34
XX /*tag= a
XX /note= "stemloop B"
XX stem_loop 35..45
XX /*tag= b
XX /note= "stemloop C"
XX stem_loop 57..70
XX /*tag= c
XX /note= "stemloop D"
XX stem_loop 105..181
XX /*tag= e
XX /note= "Domain II"
XX stem_loop 184..233
XX /*tag= f
XX /note= "Domain III"
XX stem_loop 241..444
XX /*tag= g
XX /note= "Domain IV"
XX stem_loop 452..560
XX /*tag= h
XX /note= "Domain V"
XX stem_loop 587..623
XX /*tag= i
XX /note= "Domain VI"
XX stem_loop 624..644
XX /*tag= j
XX /note= "Domain VII"
XX
XX WO200104136-A1.
XX
XX 18-JAN-2001.
XX
XX 08-JUL-2000; 2000WO-US018681.
XX
XX 09-JUL-1999; 99US-0143104P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Romero JR, Bradrick SS, Dunn JJ;
XX WPI; 2001-138310/14.
XX
XX Recombinant enterovirus genome for use as vector or vaccine, modified by
XX replacing a part or all of its 5'non-translated region by 5'NTR of
XX enterovirus genome that encodes virus modified in tropism or virulence.
XX
XX Disclosure; Fig 1; 49pp; English.
XX
XX The invention provides an enterovirus genome (I) for use as a vector or
XX vaccine, modified to produce a virus (V1) having a restricted or altered
XX species or tissue tropism, compared to an equivalent unmodified virus, or
XX modified to produce an attenuated virus (V2), by replacing a part or all
XX of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an
XX enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
XX vector in targeting genes of interest to specific cells or tissues. (I)

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CC is also useful for diagnostic purposes, e.g. to identify virulent, versus
 CC nonvirulent strains of an enterovirus. The present sequence represents
 CC the enterovirus Cxsackievirus B3 (CVB3) 5' NTR (non-translated region)
 CC sequence

XX
 XX
 SQ Sequence 745 BP; 184 A; 192 C; 181 G; 1 T; 187 U; 0 Other;
 Query Match 100.0%; Score 19; DB 4; Length 745;
 Best Local Similarity 78.9%; Pred. No. 3;
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
 |||||:|||||:|||||:
 Db 455 CCCUGAAGCGGCUAUC 473

RESULT 82
 ACC48197
 ID ACC48197 standard; cDNA; 745 BP.
 XX
 AC ACC48197;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Poliovirus internal ribosome entry site-containing mRNA 5' UTR.
 XX
 KW Internal ribosome entry site; IRES; translation; ss.
 XX
 OS Poliovirus.

XX Key Location/Qualifiers
 XX 5'UTR 1..742
 FT /*tag= a

XX
 XX WO2003020927-A2.
 XX
 XX 13-MAR-2003.
 XX
 XX 03-SEP-2002; 2002WO-EP009843.
 XX
 XX 04-SEP-2001; 2001DE-01043237.
 XX
 XX (ICON-) ICON GENETICS INC.
 XX
 XX Atabekov J, Dorokhov Y, Skulachev M, Ivanov P, Ivanov P, Gleba Y;
 XX WPI; 2003-313089/30.
 XX
 XX Creating nucleic acid sequence for carrying out translation by internal
 XX ribosome entry site element and expressing nucleotide sequence of
 XX interest in eukaryotic cell, by creating a nucleic acid having adenine-
 XX rich block.
 XX
 XX Disclosure; Fig 3; 48pp; English.

XX
 XX The present sequence is that of a known internal ribosome entry site
 XX (IRES) element contained in the 5' untranslated region of poliovirus
 XX mRNA. The invention provides a method of creating an artificial IRES
 XX element having an adenine-rich (40-100 mol%) nucleic acid block of at
 XX least 25 nucleotides and capable of causing cap-independent translation
 XX of a downstream nucleotide sequence of interest in eukaryotic cells, such
 XX as plant, animal or yeast cells (claimed). A method of identifying
 XX nucleic acid elements having IRES activity involving genome database
 XX searches is also provided. The methods allow the creation or
 XX identification of IRES elements that are universal with cross-kingdom and
 XX tailor-made activity

XX Sequence 745 BP; 163 A; 202 C; 193 G; 187 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 8; Length 745;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
 |||||:|||||:|||||:
 Db 454 CCCCTGAATGGCGCTAATC 472

RESULT 83
 ADP82873
 ID ADP82873 standard; DNA; 810 BP.
 XX
 AC ADP82873;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human coxsackievirus B1 complete genomic DNA.
 XX
 KW hMPV detection; ds.
 XX
 OS Human coxsackievirus B1.
 XX
 PN WO2004057021-A2.
 XX
 PD 08-JUL-2004.
 XX
 PF 19-DEC-2003; 2003WO-CA001994.
 XX
 PR 19-DEC-2002; 2002CA-02411264.
 PR 24-JAN-2003; 2003CA-02418004.
 XX
 PA (UYLA-) UNIV LAVAL.

XX Boivin G;
 XX WPI; 2004-500307/47.
 XX
 XX Detecting and/or quantifying human, metapneumovirus (hMPV) in a sample
 XX comprises contacting the at least one probe and/or primer with the sample
 XX to allow annealing of the probe and/or primer with the nucleic acid
 XX sequence.
 XX
 XX Claim 32; SEQ ID NO 137; 158pp; English.

XX The invention relates to a novel method for detecting and/or quantifying
 XX Human metapneumovirus (hMPV) in a sample comprising providing at least
 XX one probe or primer specific for a nucleic acid sequence of hMPV,
 XX contacting the one probe and/or primer with the sample to allow annealing
 XX of the probe and/or primer with the nucleic acid sequence and detecting
 XX and/or quantifying the nucleic acid sequence using the annealed probe
 XX and/or primer. The method of the invention may be useful for detecting
 XX and/or quantifying Human metapneumovirus (hMPV) in a sample. The current
 XX sequence is that of the Human coxsackievirus B1 complete genomic DNA of
 XX the invention.

SQ Sequence 810 BP; 243 A; 180 C; 190 G; 197 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 12; Length 810;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
 |||||:|||||:|||||:
 Db 4 CCCCTGAATGGCGCTAATC 22

RESULT 84
 ADU47469
 ID ADU47469 standard; cDNA; 1560 BP.

XX
 AC ADU47469;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Enterovirus type 71 (EV71) cDNA.
 XX

KW Detection; enterovirus type 71; EV71; ss.
 XX Enterovirus.
 OS
 XX Key Location/Qualifiers
 FH primer_bind 72..87
 FT /tag= a
 FT /note= "f1 primer"
 FT 167..187
 FT /tag= b
 FT /note= "f2 primer"
 FT 248..266
 FT /tag= c
 FT /note= "f3 primer"
 FT 423..439
 FT /tag= d
 FT /note= "f5 primer"
 FT 448..474
 FT /tag= e
 FT /bound_moiety= "p1 probe"
 FT 514..546
 FT /tag= f
 FT /bound_moiety= "p2 probe"
 FT 547..574
 FT /tag= g
 FT /bound_moiety= "p3 probe"
 FT 583..602
 FT /tag= h
 FT /note= "r2 primer"
 FT 627..645
 FT /tag= i
 FT /note= "r1 primer"
 FT 1179..1198
 FT /tag= j
 FT /note= "f7 primer"
 FT 1344..1373
 FT /tag= k
 FT /bound_moiety= "16-1 probe"
 FT 1390..1419
 FT /tag= l
 FT /bound_moiety= "71-2/16-2 probe"
 FT 1454..1481
 FT /tag= m
 FT /bound_moiety= "71-3 probe"
 FT 1485..1504
 FT /tag= n
 FT /note= "r3 primer"
 XX
 XX US6818397-B1.
 XX
 XX 16-NOV-2004.
 XX
 XX 28-NOV-2000; 2000US-00724678.
 XX
 XX 28-NOV-2000; 2000US-00724678.
 XX
 XX (CHIP-) CHIP BIOTECHNOLOGY INC.
 XX
 XX Lee K, Bair C, Tseng Y, Wang Y, Wang S;
 XX WPI; 2004-793563/78.
 XX GENBANK; U22521.
 XX
 XX New kit comprising a pair of oligonucleotide primers for nucleic acid
 PT amplification, useful in detecting and differentiating an enterovirus in
 PT a sample.
 XX
 XX Disclosure; SEQ ID NO 16; 14pp; English.
 XX
 XX The invention provides a method and a kit for detecting and
 CC differentiating an enterovirus type 71 (EV71) in a sample. The method
 CC involves contacting nucleic acids in the sample with a pair of primers to
 CC form an amplification product; contacting the amplification product with
 CC

CC at least one synthetic nucleotide sequence fixed on a solid substrate and
 CC detecting hybridisation. The present sequence is the enterovirus type 71
 CC (EV71) cDNA.
 XX
 SQ Sequence 1560 BP; 421 A; 401 C; 346 G; 392 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 13; Length 1560;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 |||||
 DB 456 CCCCTGAATGCGGCTAATC 474
 RESULT 85
 ABK14791
 ID ABK14791 standard; DNA; 2076 BP.
 XX
 AC ABK14791;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Platelet-derived growth factor expression cassette insert used in pBC701.
 XX
 KW Platelet-derived growth factor; PDGF; transgenic; milk; gene;
 KW wound healing; diabetic foot ulcer; decubitus ulcer; ophthalmic disease;
 KW venous stasis ulcer; periodontal regeneration; bone formation;
 KW prosthetic vascular graft; pBC701; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200198520-A1.
 XX
 PD 27-DEC-2001.
 XX
 PF 19-JUN-2001; 2001WO-US041044.
 XX
 PR 19-JUN-2000; 2000US-0212406P.
 XX
 PA (GENZ) GENZYME TRANSGENICS CORP.
 XX
 PI Echelard Y, Meade H, Eichner W, Sommermeyer K;
 XX
 DR WPI; 2002-083329/11.
 XX
 PT Production of platelet derived growth factor (PDGF) comprises expression
 PT in the milk of a non-human transgenic animal.
 XX
 PS Example 1; Fig 1; 59pp; English.
 XX
 CC The invention relates to the production of platelet-derived growth factor
 CC (PDGF) comprising a transgenic mammal whose somatic and germ cells
 CC comprise a nucleic acid sequence (I) encoding PDGF, operably linked to a
 CC promoter directing expression into mammalian gland epithelial cells, and
 CC obtaining the milk from the transgenic mammal where at least 30% of the
 CC PDGF in the milk is as a dimer. Also described is a method of producing a
 CC transgenic mammal capable of expressing an active PDGF molecule in milk.
 CC Pharmaceutical compositions can be obtained from this milk and can be
 CC used to stimulate or enhance the wound healing process, in particular
 CC diabetic foot ulcers, decubitus ulcers and venous stasis ulcers.
 CC Transgenic PDGF (II) can also be used in the treatment of periodontal
 CC regeneration, stimulation of bone formation, ophthalmic diseases or
 CC healing of prosthetic vascular grafts. (III) can also be used for non-
 CC medical applications, e.g., as a supplement for cell culture media or as
 CC a component of diagnostic kits. The present sequence represents the
 CC platelet-derived growth factor expression cassette insert used in pBC701
 CC vector of the invention
 XX
 SQ Sequence 2076 BP; 441 A; 612 C; 607 G; 416 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 6; Length 2076;
 Best Local Similarity 100.0%; Pred. No. 3.4;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGCGGCTAATC 19
Db 1203 CCCCTGAATGCGGCTAATC 1221

RESULT 86
AAH20890
ID AAH20890 standard; DNA; 4148 BP.
XX
AC AAH20890;
XX
DT 11-SEP-2003 (revised)
DT 24-AUG-2001 (first entry)
XX
DE Vector containing HIV gp41 DNA SEQ ID 1.
XX
DE Transmembrane anchor; gene therapy; endoplasmic reticulum; gp41;
KW antiviral; HIV replication inhibitor; T lymphocyte; viral infection;
KW hematopoietic stem cell; ds.
XX
OS Human immunodeficiency virus 1.
XX
FH Key Location/Qualifiers
FT CDS 1438..1773
FT /*tag= a
XX
PN WO200137881-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-EP011733.
XX
PR 25-NOV-1999; 99DE-01057838.
XX
PA (PETT-) PETTE INST HEINRICH.
XX
PI Von Laer M;
XX
DR WPI; 2001-367622/38.
DR P-PSDB; AAB86198.
XX
PT New nucleic acid encoding membrane-anchored gp41 fusion protein, useful
PT for gene therapy of human immunodeficiency virus (HIV) infection,
PT prevents entry of virus into cells.
XX
PS Claim 11; Page 28-30; 39pp; German.
XX
CC This invention describes a novel nucleic acid (I) comprising elements
CC that encode a signal peptide (SP) that provides transfer of expressed
CC polypeptide into the endoplasmic reticulum, a fragment (PI) of HIV gp41
CC protein, containing a segment from a heptad repeat region, a
CC transmembrane anchor (MSD) of a type I membrane protein and a flexible
CC linker (hinge) linking PI and MSD, therefore the formula of (I) is SP-PI-
CC hinge-MSD. The products of the invention have antiviral activity and act
CC as HIV replication inhibitors. Vectors containing (I), also T lymphocytes
CC or hematopoietic stem cells transfected in vitro with (I), are used in
CC gene therapy of HIV infection. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 4148 BP; 880 A; 1177 C; 1103 G; 988 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 5; Length 4148;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGCGGCTAATC 19
Db 2245 CCCCTGAATGCGGCTAATC 2263

RESULT 87
```

```
AD007652
ID AD007652 standard; DNA; 5252 BP.
AC AD007652;
XX
DT 15-JUL-2004 (first entry)
XX
DE Tricistronic expression cassette containing murine coding sequences.
XX
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene.
XX
OS Mus sp.
OS Synthetic.
OS Unidentified.
XX
PN WO2004035799-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011252.
XX
PR 11-OCT-2002; 2002DE-01048141.
XX
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI Waehler R; Schnieders F;
XX
DR WPI; 2004-357221/33.
XX
PT Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
PS Disclosure; Fig 18; 129pp; German.
XX
CC The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumors, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a tricistronic expression cassette used in the
CC exemplification of the invention.
XX
SQ Sequence 5252 BP; 1347 A; 1386 C; 1300 G; 1219 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 5252;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGCGGCTAATC 19
Db 2739 CCCCTGAATGCGGCTAATC 2757

RESULT 88
ADP74699
ID ADP74699 standard; DNA; 7185 BP.
AC ADP74699;
XX
XX 26-AUG-2004 (first entry)
DT
DE Novel bicistronic retroviral vector related vector #1.
XX
KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
KW severe combined immune deficiency syndrome; protein expression;
KW antisense; ds; gene.
XX
OS Synthetic.
OS Unidentified.
XX
```

FH Key Location/Qualifiers
 FT LTR 424..994
 FT /tag= a
 FT /standard_name= "5'-LTR"
 FT 5'UTR 995..1487
 FT /tag= b
 FT CDS 1488..2615
 FT /tag= c
 FT /product= "HSV-TK"
 FT misc_RNA 2626..3250
 FT /tag= d
 FT /standard_name= "IRES"
 FT CDS 3298..4098
 FT /tag= e
 FT /product= "neo"
 FT LTR 4345..4931
 FT /tag= f
 FT /standard_name= "3'-LTR"
 XX
 PN EP1428886-A1.
 XX
 XX 16-JUN-2004.
 XX
 XX 09-DEC-2002; 2002EP-00027555.
 XX
 XX 09-DEC-2002; 2002EP-00027555.
 XX
 XX (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;
 XX WPI; 2004-452367/43.
 XX
 XX Bicistronic retroviral vector, useful in gene therapy, particularly of
 PT graft versus host disease, contains components of both murine embryonic
 PT stem cell and myeloproliferative sarcoma viruses.
 XX
 XX Disclosure; Page 58-59; 91pp; German.
 XX
 XX The present invention relates to a new bicistronic retroviral vector.
 CC These are used for (over)expression of proteins, suppressing expression
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
 CC suppress a dominant-negative phenotype, also infectious viral particles
 CC that contain the vectors, in gene therapy, particularly for control of
 CC guest versus host disease, especially where haematopoietic cells are
 CC transduced with the vector or where T cells are transduced, for adoptive
 CC immunotherapy, but also for treating severe combined immune deficiency
 CC syndrome and for expression cloning of genes. The present sequence is a
 CC vector sequence shown in the exemplification of the invention.
 XX
 XX Sequence 7185 BP; 1579 A; 2013 C; 1943 G; 1650 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 19; DB 12; Length 7185;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 Db 3074 CCCCTGAATGCGGCTAATC 3092
 RESULT 89
 ADP74701
 ID ADP74701 standard; DNA; 7185 BP.
 XX
 AC ADP74701;
 XX
 XX 26-AUG-2004 (first entry)
 DT
 DE Novel bicistronic retroviral vector related vector #3.
 XX
 XX immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
 KW severe combined immune deficiency syndrome; protein expression;

KW antisense; ds; gene.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT LTR 424..994
 FT /tag= a
 FT /standard_name= "5'-LTR"
 FT 5'UTR 995..1487
 FT /tag= b
 FT CDS 1488..2615
 FT /tag= c
 FT /product= "HSV-TK splice variant"
 FT misc_RNA 2626..3250
 FT /tag= d
 FT /standard_name= "IRES"
 FT CDS 3298..4098
 FT /tag= e
 FT /product= "neo"
 FT LTR 4345..4931
 FT /tag= f
 FT /standard_name= "3'-LTR"
 XX
 XX EP1428886-A1.
 XX
 XX 16-JUN-2004.
 XX
 XX 09-DEC-2002; 2002EP-00027555.
 XX
 XX 09-DEC-2002; 2002EP-00027555.
 XX
 XX (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;
 XX WPI; 2004-452367/43.
 XX
 XX Bicistronic retroviral vector, useful in gene therapy, particularly of
 PT graft versus host disease, contains components of both murine embryonic
 PT stem cell and myeloproliferative sarcoma viruses.
 XX
 XX Disclosure; Page 63-65; 91pp; German.
 XX
 XX The present invention relates to a new bicistronic retroviral vector.
 CC These are used for (over)expression of proteins, suppressing expression
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
 CC suppress a dominant-negative phenotype, also infectious viral particles
 CC that contain the vectors, in gene therapy, particularly for control of
 CC guest versus host disease, especially where haematopoietic cells are
 CC transduced with the vector or where T cells are transduced, for adoptive
 CC immunotherapy, but also for treating severe combined immune deficiency
 CC syndrome and for expression cloning of genes. The present sequence is a
 CC vector sequence shown in the exemplification of the invention.
 XX
 XX Sequence 7185 BP; 1581 A; 2013 C; 1942 G; 1649 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 19; DB 12; Length 7185;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATGCGGCTAATC 19
 Db 3074 CCCCTGAATGCGGCTAATC 3092
 RESULT 90
 ADP74714
 ID ADP74714 standard; DNA; 7235 BP.
 XX
 AC ADP74714;
 XX
 XX 26-AUG-2004 (first entry)
 DT

XX DE Novel bicistronic retroviral vector related vector #6.
 XX AC immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
 KW severe combined immune deficiency syndrome; protein expression;
 KW antisense; ds; gene.
 XX OS Synthetic.
 OS Unidentified.
 XX FH Key Location/Qualifiers
 FT LTR 424..994
 FT /*tag= a
 FT /standard_name= "5'-LTR"
 FT 5'UTR 995..1537
 FT /*tag= b
 FT CDS 1538..2665
 FT /*tag= c
 FT /product= "HSV-TK splice variant"
 FT misc_RNA 2676..3300
 FT /*tag= d
 FT /standard_name= "IRES"
 FT CDS 3348..4148
 FT /*tag= e
 FT /product= "neo"
 FT LTR 4395..4981
 FT /*tag= f
 FT /standard_name= "3'-LTR"
 XX EPI428886-A1.
 XX PN 16-JUN-2004.
 XX PD 09-DEC-2002; 2002EP-00027555.
 XX PF 09-DEC-2002; 2002EP-00027555.
 XX PR (CELL-) CELTECH GMBH BIOTECHNOLOGIE.
 XX PA Heberlein C, Gindullis F, Hannemann J, Strathmann G;
 XX PI WPI; 2004-452367/43.
 XX DR Bicistronic retroviral vector, useful in gene therapy, particularly of
 XX PT graft versus host disease, contains components of both murine embryonic
 XX stem cell and myeloproliferative sarcoma viruses.
 XX PS Disclosure; Page 75-77; 91pp; German.
 XX CC The present invention relates to a new bicistronic retroviral vector.
 XX CC These are used for (over)expression of proteins, suppressing expression
 XX CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
 XX CC suppress a dominant-negative phenotype, also infectious viral particles
 XX CC that contain the vectors, in gene therapy, particularly for control of
 XX CC guest versus host disease, especially where haematopoietic cells are
 XX CC transduced with the vector or where T cells are transduced, for adoptive
 XX CC immunotherapy, but also for treating severe combined immune deficiency
 XX CC syndrome and for expression cloning of genes. The present sequence is a
 XX CC vector sequence shown in the exemplification of the invention.
 XX SQ Sequence 7235 BP; 1594 A; 2025 C; 1950 G; 1666 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 7235;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATCGGCTAATC 19
 Db 3124 CCCCTGAATCGGCTAATC 3142
 |||||

RESULT 91
 ADP74715

ID ADP74715 standard; DNA; 7235 BP.
 XX AC ADP74715;
 XX DT 26-AUG-2004 (first entry)
 XX DE Novel bicistronic retroviral vector related vector #7.
 XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
 KW severe combined immune deficiency syndrome; protein expression;
 KW antisense; ds; gene.
 XX OS Synthetic.
 OS Unidentified.
 XX FH Key Location/Qualifiers
 FT LTR 424..994
 FT /*tag= a
 FT /standard_name= "5'-LTR"
 FT 5'UTR 995..1537
 FT /*tag= b
 FT CDS 1538..2665
 FT /*tag= c
 FT /product= "HSV-TK splice variant"
 FT misc_RNA 2676..3300
 FT /*tag= d
 FT /standard_name= "IRES"
 FT CDS 3348..4148
 FT /*tag= e
 FT /product= "neo"
 FT LTR 4395..4981
 FT /*tag= f
 FT /standard_name= "3'-LTR"
 XX EPI428886-A1.
 XX PN 16-JUN-2004.
 XX PD 09-DEC-2002; 2002EP-00027555.
 XX PF 09-DEC-2002; 2002EP-00027555.
 XX PR (CELL-) CELTECH GMBH BIOTECHNOLOGIE.
 XX PA Heberlein C, Gindullis F, Hannemann J, Strathmann G;
 XX PI WPI; 2004-452367/43.
 XX DR Bicistronic retroviral vector, useful in gene therapy, particularly of
 XX PT graft versus host disease, contains components of both murine embryonic
 XX stem cell and myeloproliferative sarcoma viruses.
 XX PS Disclosure; Page 78-79; 91pp; German.
 XX CC The present invention relates to a new bicistronic retroviral vector.
 XX CC These are used for (over)expression of proteins, suppressing expression
 XX CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
 XX CC suppress a dominant-negative phenotype, also infectious viral particles
 XX CC that contain the vectors, in gene therapy, particularly for control of
 XX CC guest versus host disease, especially where haematopoietic cells are
 XX CC transduced with the vector or where T cells are transduced, for adoptive
 XX CC immunotherapy, but also for treating severe combined immune deficiency
 XX CC syndrome and for expression cloning of genes. The present sequence is a
 XX CC vector sequence shown in the exemplification of the invention.
 XX SQ Sequence 7235 BP; 1595 A; 2025 C; 1949 G; 1666 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 7235;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATCGGCTAATC 19
 |||||

Db 3124 CCCCTGAATCGGCTAATC 3142

RESULT 92

ID ADP74700

ADP74700 standard; DNA; 7235 BP.

XX AC ADP74700;

XX DT 26-AUG-2004 (first entry)

XX DE Novel bicistronic retroviral vector related vector #2.

XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;

XX KW severe combined immune deficiency syndrome; protein expression;

XX KW antisense; ds; gene.

XX OS Synthetic.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT LTR 424..994

XX FT /*tag= a

XX FT /standard_name= "5'-LTR"

XX FT 5'UTR 995..1537

XX FT /*tag= b

XX FT CDS 1538..2665

XX FT /*tag= c

XX FT /product= "HSV-TK"

XX FT misc_RNA 2676..3300

XX FT /*tag= d

XX FT /standard_name= "IRES"

XX FT CDS 3348..4148

XX FT /*tag= e

XX FT /product= "neo"

XX FT LTR 4395..4981

XX FT /*tag= f

XX FT /standard_name= "3'-LTR"

XX PN EP1428886-A1.

XX PD 16-JUN-2004.

XX PF 09-DEC-2002; 2002EP-00027555.

XX PR 09-DEC-2002; 2002EP-00027555.

XX PA (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.

XX PI Heberlein C, Gindullis F, Hannemann J, Strathmann G;

XX DR WPI; 2004-452367/43.

XX KW Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.

XX PS Disclosure; Page 60-62; 91pp; German.

XX CC The present invention relates to a new bicistronic retroviral vector. These are used for (over)expression of proteins, suppressing expression of (non-)viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where hematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence shown in the exemplification of the invention.

XX SQ Sequence 7235 BP; 1592 A; 2025 C; 1951 G; 1667 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 7235;

Best Local Similarity 100.0%; Pred. No. 4;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19

DB 3124 CCCCTGAATCGGCTAATC 3142

RESULT 93

ID ADP74713

ADP74713 standard; DNA; 7235 BP.

XX AC ADP74713;

XX DT 26-AUG-2004 (first entry)

XX DE Novel bicistronic retroviral vector related vector #5.

XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;

XX KW severe combined immune deficiency syndrome; protein expression;

XX KW antisense; ds; gene.

XX OS Synthetic.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT LTR 424..994

XX FT /*tag= a

XX FT /standard_name= "5'-LTR"

XX FT 5'UTR 995..1537

XX FT /*tag= b

XX FT CDS 1538..2665

XX FT /*tag= c

XX FT /product= "HSV-TK"

XX FT misc_RNA 2676..3300

XX FT /*tag= d

XX FT /standard_name= "IRES"

XX FT CDS 3348..4148

XX FT /*tag= e

XX FT /product= "neo"

XX FT LTR 4395..4981

XX FT /*tag= f

XX FT /standard_name= "3'-LTR"

XX PN EP1428886-A1.

XX PD 16-JUN-2004.

XX PF 09-DEC-2002; 2002EP-00027555.

XX PR 09-DEC-2002; 2002EP-00027555.

XX PA (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.

XX PI Heberlein C, Gindullis F, Hannemann J, Strathmann G;

XX DR WPI; 2004-452367/43.

XX KW Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.

XX PS Disclosure; Page 72-74; 91pp; German.

XX CC The present invention relates to a new bicistronic retroviral vector. These are used for (over)expression of proteins, suppressing expression of (non-)viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where hematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a

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CC vector sequence shown in the exemplification of the invention.
XX
SQ Sequence 7235 BP; 1593 A; 2025 C; 1950 G; 1667 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 7235;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 3124 CCCCTGAATCGGCTAATC 3142

RESULT 94
ABX12440
ID ABX12440 standard; DNA; 7392 BP.
XX
AC ABX12440;
XX
DT 10-MAY-2003 (first entry)
XX
DE Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome.
XX
KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Coxsackievirus.
XX
XX Key Location/Qualifiers
FH misc_feature 1..87
FT /tag= a
FT /note= "Specifically claimed in claim 16"
FT misc_feature 88..512
FT /tag= b
FT /note= "Specifically claimed in claim 19"
FT misc_feature 513..742
FT /tag= c
FT /note= "Specifically claimed in claim 22"
FT misc_feature 742
FT /tag= d
FT /note= "Specifically claimed in claim 25"
FT CDS 743..7303
FT /tag= f
FT /product= "Polyprotein"
FT misc_feature 743..952
FT /tag= e
FT /note= "Specifically claimed in claim 26"
FT misc_feature 953..1726
FT /tag= g
FT /note= "Specifically claimed in claim 29"
FT misc_feature 1727..2441
FT /tag= h
FT /note= "Specifically claimed in claim 32"
FT misc_feature 2442..3296
FT /tag= i
FT /note= "Specifically claimed in claim 35"
FT misc_feature 3297..3737
FT /tag= j
FT /note= "Specifically claimed in claim 38"
FT misc_feature 3738..4033
FT /tag= k
FT /note= "Specifically claimed in claim 41"
FT misc_feature 4034..5029
FT /tag= l
FT /note= "Specifically claimed in claim 44"
XX
PN WO2002103060-A2.
XX
PD 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
PF

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XX 20-JUN-2001; 2001SE-00002198.
XX
FA (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX P-PSDB; ABG75961.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Example 5; Page 64-66; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents the genome of diabetogenic
XX coxsackie B virus 4 (CBV-4) strain VD2921
XX
SQ Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 7392;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 455 CCCCTGAATCGGCTAATC 473

RESULT 95
AAQ11816
ID AAQ11816 standard; RNA; 7399 BP.
XX
AC AAQ11816;
XX
XX 25-MAR-2003 (revised)
DT 05-AUG-1991 (first entry)
XX
XX RNA encoding enteroviral polypeptide.
XX
XX Enteroviruses; monoclonal antibodies; myocarditis; myositis; meningitis;
XX encephalitis; pancreatitis; post viral fatigue syndrome; ss.
XX
XX Enterovirus sp.
XX
XX Key Location/Qualifiers
FH CDS 742..7299
FT /tag= a
FT /product= "enteroviral polypeptide"
XX
XX DE3939200-A.
XX
XX 29-MAY-1991.
XX
XX 27-NOV-1989; 89DE-03939200.
XX
XX 27-NOV-1989; 89DE-03939200.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Kandolf R;
XX
XX WPI; 1991-165150/23.
XX

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DR P-PSDB; AAR12141.
 XX New enteroviral polypeptide for raising group specific antibodies - for
 PT detecting any type of enterovirus in blood or serum, also new DNA
 PT encoding it.
 XX
 XX Claim 7; Page 17-21; 26pp; German.
 XX
 CC This RNA encodes an enteroviral polypeptide which is used to raise poly-
 CC or monoclonal antibodies (Abs). These are useful in assays for detecting
 CC enterovirus specific antigens, as an indication of enteroviral disease.
 CC All 70 serotypes of the enteroviral family can be detected. Diseases such
 CC as myocarditis, myositis, meningitis, encephalitis and pancreatitis can
 CC be diagnosed using the Abs. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 0 T; 1740 U; 0 Other;
 SQ

Query Match 100.0%; Score 19; DB 2; Length 7399;
 Best Local Similarity 78.9%; Pred. No. 4;
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 454 CCCUGAUGCGGCUAUC 472

QY 1 CCCCTGAATGCGGCTAATC 19
 ||||:||||:||||:|
 Db 454 CCCUGAUGCGGCUAUC 472

RESULT 96
 ABV76134
 ID ABV76134 standard; DNA; 7399 BP.
 XX
 XX ABV76134;
 XX
 DT 07-MAR-2003 (first entry)
 DE Coxsackievirus capsid protein VP1 nucleic acid.
 XX
 KW Gene therapy; vector; hepatitis B virus; cardiovascular disease; heart;
 KW cardiant; vasotropic; antiarrhythmic; antiarteriosclerotic;
 KW capsid protein; gene; ss.
 XX
 OS Coxsackievirus.
 XX
 PN WO200287594-A1.
 XX
 PD 07-NOV-2002.
 XX
 PF 30-APR-2002; 2002WO-US013644.
 XX
 PR 30-APR-2001; 2001US-0287423P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Chien KR, Hoshijima M;
 XX
 DR WPI; 2003-111844/10.
 XX
 XX Novel non-viral vector comprises vesicular membrane with hepatitis B
 PT envelope protein with cardiac targeting sequence, and nucleotide sequence
 PT for gene therapy useful for treating, e.g., heart failure, arrhythmia and
 PT atherosclerosis.
 XX
 PS Disclosure; Page 27-31; 53pp; English.
 XX
 CC The present sequence is that of a coxsackie virus B3 capsid protein VP1
 CC nucleic acid. The invention provides a non-viral vesicle vector for the
 CC delivery of nucleic acid to various cardiac cell types. The vesicle
 CC vector contains the hepatitis B virus envelope protein in which at least
 CC part of the liver targeting sequence is deleted and replaced with a
 CC specific cardiac cell targeting sequence. For example, the coxsackie
 CC virus B3, VP1 sequence can be used to target the vector to
 CC cardiomyocytes. The vesicle vector can be delivered intravenously or
 CC intra-arterially rather than by more invasive methods such as direct
 CC cardiac injection. It can be used to deliver gene products to replace or

CC enhance expression of proteins for treatment of heart failure,
 CC arrhythmia, reperfusion injury, atherosclerosis, to promote angiogenesis,
 CC etc. The vesicles are highly stable and can be produced in large
 CC quantities, making them ideal for gene therapy
 XX
 SQ Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 1740 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 10; Length 7399;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 454 CCCCTGAATGCGGCTAATC 472

QY 1 CCCCTGAATGCGGCTAATC 19
 ||||:||||:||||:|
 Db 454 CCCCTGAATGCGGCTAATC 472

RESULT 97
 AAZ98719
 ID AAZ98719 standard; cDNA; 7400 BP.
 XX
 XX AAZ98719;
 AC
 DT 20-JUN-2000 (first entry)
 DE Swine vesicular disease virus (SVDV) N3 mutant strain gene sequence.
 XX
 KW Swine vesicular disease virus; SVDV; swine vesicular disease;
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
 KW differentiation; vaccine; prevent; ss.
 XX
 OS Swine vesicular disease virus.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 2693..2710
 FT /*tag= a
 FT /note= "Nucleotides in this position replace the wild-
 FT type nucleotide sequence of strain Taiwan Yu-Li (see
 XX AAZ98717)"
 XX
 PN EP982403-A1.
 XX
 PD 01-MAR-2000.
 XX
 PF 14-AUG-1998; 98EP-00306486.
 XX
 PR 14-AUG-1998; 98EP-00306486.
 XX
 PA (BIOT-) DEV CENT BIOTECHNOLOGY.
 XX
 PI Hwang CL, Lo C, Yang Y, Jeng K, Chang EL;
 XX
 DR WPI; 2000-258616/23.
 XX
 PT Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
 PT to prevent swine vesicular disease.
 XX
 PS Claim 4; Page; 66pp; English.
 XX
 CC This sequence represents the full length Swine vesicular disease virus
 CC (SVDV) gene sequence from the SVDV strain N3. SVDV is the causative agent
 CC of swine vesicular disease, which is very similar to foot and mouth
 CC disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA
 CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
 CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
 CC prophylaxis of swine vesicular disease. The invention also includes a
 CC method for differentiating the mutant SVDV nucleotide sequences from the
 CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
 CC virus through the use of polymerase chain reaction. Note: This sequence
 CC is not present in the specification, but has been derived from the wild-
 CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
 CC 34-38 of the specification
 XX
 SQ Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 3; Length 7400;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 |||||
 Db 454 CCCCTGAATCGGCTAATC 472

RESULT 98

AAZ98717
 ID AAZ98717 standard; cDNA; 7400 BP.

AC AAZ98717;

XX 20-JUN-2000 (first entry)

DT Swine vesicular disease virus (SVDV) gene sequence.

DE Swine vesicular disease virus; SVDV; swine vesicular disease;
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
 KW differentiation; vaccine; prevent; ss.

XX Swine vesicular disease virus.

XX EP982403-A1.

XX 01-MAR-2000.

XX 14-AUG-1998; 98EP-00306486.

XX 14-AUG-1998; 98EP-00306486.

XX (BIOT-) DEV CENT BIOTECHNOLOGY.

XX Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;

XX WPI; 2000-258616/23.

XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
 to prevent swine vesicular disease.

PS Claim 1; Page 34-38; 66pp; English.

XX This sequence represents the full length Swine vesicular disease virus
 (SVDV) gene sequence from the SVDV strain Taiwan Yu-Li. SVDV is the
 causative agent of swine vesicular disease, which is very similar to foot
 and mouth disease. The invention relates to the wild-type Taiwan Yu-Li
 strain cDNA sequence, and the gene sequences of the mutant SVDV strains
 N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a
 vaccine for the prophylaxis of swine vesicular disease. The invention
 also includes a method for differentiating the mutant SVDV nucleotide
 sequences from the wild type strain of SVDV, coxsackievirus and foot-and-
 mouth disease virus through the use of polymerase chain reaction

XX Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 3; Length 7400;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 |||||
 Db 454 CCCCTGAATCGGCTAATC 472

RESULT 99

AAZ98718

ID AAZ98718 standard; cDNA; 7400 BP.

XX AAZ98718;

XX

DT 20-JUN-2000 (first entry)
 XX Swine vesicular disease virus (SVDV) H21 mutant strain gene sequence.
 DE Swine vesicular disease virus; SVDV; swine vesicular disease;
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
 KW differentiation; vaccine; prevent; ss.
 XX Swine vesicular disease virus.

XX Key Location/Qualifiers
 FH misc_feature /tag= a
 FT 2705..2710
 FT /note= "Nucleotides in this position replace the wild-
 FT type nucleotide sequence of strain Taiwan Yu-Li AAZ98717"

XX EP982403-A1.

XX 01-MAR-2000.

XX 14-AUG-1998; 98EP-00306486.

XX 14-AUG-1998; 98EP-00306486.

XX (BIOT-) DEV CENT BIOTECHNOLOGY.

XX Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;

XX WPI; 2000-258616/23.

XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
 to prevent swine vesicular disease.

PS Claim 3; Page; 66pp; English.

XX This sequence represents the full length Swine vesicular disease virus
 (SVDV) gene sequence from the SVDV strain H21. SVDV is the causative
 agent of swine vesicular disease, which is very similar to foot and mouth
 disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA
 sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
 SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
 prophylaxis of swine vesicular disease. The invention also includes a
 method for differentiating the mutant SVDV nucleotide sequences from the
 wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
 virus through the use of polymerase chain reaction. Note: This sequence
 is not present in the specification, but has been derived from the wild-
 CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
 CC 34-38 of the specification

SQ Sequence 7400 BP; 2082 A; 1785 C; 1863 G; 1670 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 3; Length 7400;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 |||||
 Db 454 CCCCTGAATCGGCTAATC 472

RESULT 100

AAZ29863

ID AAZ29863 standard; cDNA; 7400 BP.

XX AAZ29863;

XX

XX 30-AUG-2000 (first entry)

XX Swine vesicular disease virus (SVDV) nucleotide sequence.

XX Swine vesicular disease virus; SVDV; vesicular disease; vaccine; ss.

XX Swine vesicular disease virus.

XX
PN CN1244583-A.
XX
PD 16-FEB-2000.
XX
PF 12-AUG-1998; 98CN-00117165.
XX
PR 12-AUG-1998; 98CN-00117165.
XX
PA (BIOL-) BIOLOGICAL TECHNOLOGY DEV CENT.
XX
PA Huang Q, Luo Z, Yang Y;
XX
PI WPI; 2000-388169/34.
XX
DR Native swine vascular disease virus gene and its variant - useful as
XX
PT vaccines.
XX
PS Claim 1; Page 1-5; 54pp; Chinese.
XX
CC The present invention describes a native swine vascular disease virus
CC (SVDV) gene and its variant. Also described are: (1) an expression
CC plasmid containing the gene; (2) preparation of the gene and its variant;
CC and (3) a vaccine comprising the gene or its variant. The new gene is
CC useful for the treatment of vesicular disease. The present sequence
CC represents a specifically claimed SVDV nucleotide sequence from the
CC present invention
XX
XX Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCTGAATCGGCTAATC 19
|||||
DB 454 CCCCTGAATCGGCTAATC 472
Search completed: March 9, 2006, 00:29:57
Job time : 213.369 secs

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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:09:45 ; Search time 802.058 Seconds
(without alignments)
1346.567 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19

Sequence: 1 cccctgaatcggttaac 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : GenEmbl.*

1: gb_ba:**

2: gb_in:**

3: gb_env:**

4: gb_on:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pr:**

9: gb_ro:**

10: gb_sts:**

11: gb_sy:**

12: gb_un:**

13: gb_vi:**

14: gb_vtg:**

15: gb_pl:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	27	6 AR595531 ✓	Sequence
2	19	100.0	30	6 AX348200 ✓	Sequence
3	19	100.0	30	6 AX348202 ✓	Sequence
4	19	100.0	30	6 AX348204 ✓	Sequence
5	19	100.0	39	6 AX711149	Sequence
6	19	100.0	100	13 POLIBRA	D00260 Human polio
7	19	100.0	100	13 POLISAK	D00257 Human polio
8	19	100.0	100	13 POLISAL	D00254 Human polio
9	19	100.0	100	13 POLISA	D00261 Human polio
10	19	100.0	100	13 POLISA2	D00255 Human polio
11	19	100.0	100	13 POLIBRA	D00263 Human polio
12	19	100.0	100	13 POL3FIN	D00258 Human polio
13	19	100.0	100	13 POL3VDB	D00259 Human polio
14	19	100.0	100	13 POL3YUN	D00262 Human polio
15	19	100.0	109	13 DQ029090	DQ029090 Human ech
16	19	100.0	109	13 DQ029091	DQ029091 Human ech
17	19	100.0	109	13 DQ029092	DQ029092 Human ech
18	19	100.0	109	13 DQ029094	DQ029094 Human ech

19	19	100.0	109	13	DQ029095	DQ029095 Human ech
20	19	100.0	109	13	DQ029096	DQ029096 Human ech
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23	19	100.0	120	13	AF380624	AF380624 Human pol
24	19	100.0	122	13	AF380623	AF380623 Human pol
25	19	100.0	128	13	AF783777	AF783777 Human pol
26	19	100.0	145	13	HEN312090	HEN312090 Human ech
27	19	100.0	145	13	HEN312091	HEN312091 Human ech
28	19	100.0	147	13	AF314006	AF314006 Enterovir
29	19	100.0	147	13	AF316322	AF316322 Enterovir
30	19	100.0	153	13	AF314004	AF314004 Enterovir
31	19	100.0	154	13	AF314003	AF314003 Enterovir
32	19	100.0	154	13	AF314005	AF314005 Enterovir
33	19	100.0	154	13	AF314007	AF314007 Enterovir
34	19	100.0	154	13	AF314008	AF314008 Enterovir
35	19	100.0	154	13	AY027864	AY027864 Enterovir
36	19	100.0	154	13	AY027865	AY027865 Enterovir
37	19	100.0	154	13	AY027866	AY027866 Enterovir
c	38	19	100.0	171	13 HCO295181	HCO295181 Human ech
c	39	19	100.0	172	13 HEN312088	HEN312088 Human ech
c	40	19	100.0	177	13 ESP295207	ESP295207 Echovirus
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91	19	100.0	185	13	AF521488	AF521488 Human ech

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117	19	100.0	185	13	AF521516	Human	ech	AF521516	Human	ech	190	19	100.0	188	13	AY342857	Human	ech
118	19	100.0	185	13	AF5													

238	19	100.0	188	13	AY342908	Human	ech	311	19	100.0	188	13	AY342983	Human	ech
239	19	100.0	188	13	AY342909	Human	ech	312	19	100.0	188	13	AY342984	Human	ech
240	19	100.0	188	13	AY342910	Human	ech	313	19	100.0	188	13	AY342985	Human	ech
241	19	100.0	188	13	AY342911	Human	ech	314	19	100.0	188	13	AY342986	Human	ech
242	19	100.0	188	13	AY342912	Human	ech	315	19	100.0	188	13	AY342987	Human	ech
243	19	100.0	188	13	AY342913	Human	ech	316	19	100.0	188	13	AY342988	Human	ech
244	19	100.0	188	13	AY342914	Human	ech	317	19	100.0	188	13	AY342989	Human	ech
245	19	100.0	188	13	AY342915	Human	ech	318	19	100.0	188	13	AY342990	Human	ech
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257	19	100.0	188	13	AY342928	Human	ech	330	19	100.0	188	13	AY343002	Human	ech
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386	19	100.0	236	13	AJ783784	AJ783784 Human pol
387	19	100.0	264	13	AJ783779	AJ783779 Human pol
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400	19	100.0	266	13	AY271460	AY271460 Human ent
401	19	100.0	266	13	AY271461	AY271461 Human ent
402	19	100.0	266	13	AY271462	AY271462 Human ent
403	19	100.0	266	13	AY271463	AY271463 Human ent
404	19	100.0	266	13	AY271464	AY271464 Human ent
405	19	100.0	266	13	AY271465	AY271465 Human ent
406	19	100.0	266	13	AY271466	AY271466 Human ent
407	19	100.0	266	13	AY271467	AY271467 Human ent
408	19	100.0	266	13	AY271469	AY271469 Human ent
409	19	100.0	266	13	AY271470	AY271470 Human ent
410	19	100.0	266	13	AY271471	AY271471 Human ent
411	19	100.0	266	13	AY271473	AY271473 Human ent
412	19	100.0	266	13	AY271475	AY271475 Human ent
413	19	100.0	266	13	AY271476	AY271476 Human ent
414	19	100.0	266	13	AY271477	AY271477 Human ent
415	19	100.0	266	13	AY271478	AY271478 Human ent
416	19	100.0	266	13	AY271479	AY271479 Human ent
417	19	100.0	267	13	AY271472	AY271472 Human ent
418	19	100.0	267	13	AY271474	AY271474 Human ent
419	19	100.0	269	13	AY935539	AY935539 Human ent
420	19	100.0	269	13	AY935540	AY935540 Human ent
421	19	100.0	269	13	AY935542	AY935542 Human ent
422	19	100.0	269	13	AY935543	AY935543 Human ent
423	19	100.0	275	13	HCO417545	HCO417545 Human ent
424	19	100.0	275	13	HCO417547	HCO417547 Human ent
425	19	100.0	275	13	HCO417549	HCO417549 Human ent
426	19	100.0	278	13	HCO417546	HCO417546 Human ent
427	19	100.0	278	13	HCO417548	HCO417548 Human ent
428	19	100.0	296	13	AJ783735	AJ783735 Human pol
429	19	100.0	296	13	CVU30919	CVU30919 Coxsackiev
430	19	100.0	296	13	CVU30923	CVU30923 Coxsackiev
431	19	100.0	296	13	CVU30924	CVU30924 Coxsackiev
432	19	100.0	296	13	CVU30929	CVU30929 Coxsackiev
433	19	100.0	297	13	CVU30915	CVU30915 Coxsackiev
434	19	100.0	297	13	CVU30916	CVU30916 Coxsackiev
435	19	100.0	297	13	CVU30917	CVU30917 Coxsackiev
436	19	100.0	297	13	CVU30918	CVU30918 Coxsackiev
437	19	100.0	297	13	CVU30920	CVU30920 Coxsackiev
438	19	100.0	297	13	CVU30921	CVU30921 Coxsackiev
439	19	100.0	297	13	CVU30925	CVU30925 Coxsackiev
440	19	100.0	297	13	CVU30927	CVU30927 Coxsackiev
441	19	100.0	297	13	CVU30928	CVU30928 Coxsackiev
442	19	100.0	297	13	E1U11706	E1U11706 Echovirus 1
443	19	100.0	297	13	E2U11707	E2U11707 Echovirus 2
444	19	100.0	297	13	E4U11708	E4U11708 Echovirus 4
445	19	100.0	297	13	E9U11710	E9U11710 Echovirus 9
446	19	100.0	298	13	CBU31213	CBU31213 Coxsackiev
447	19	100.0	298	13	CVU30922	CVU30922 Coxsackiev
448	19	100.0	298	13	CVU30926	CVU30926 Coxsackiev
449	19	100.0	299	13	CBU31212	CBU31212 Coxsackiev
450	19	100.0	300	13	AJ783781	AJ783781 Human pol
451	19	100.0	302	13	AJ783775	AJ783775 Human pol
452	19	100.0	309	13	AJ783770	AJ783770 Human pol
453	19	100.0	314	13	ECV7345	ECV7345 Echovirus
454	19	100.0	315	13	AJ783774	AJ783774 Human pol
455	19	100.0	316	13	ECV7335	ECV7335 Echovirus
456	19	100.0	316	13	ECV7336	ECV7336 Echovirus

457	19	100.0	316	13	ECV7337	AJ007337 Echovirus
458	19	100.0	316	13	ECV7338	AJ007338 Echovirus
459	19	100.0	316	13	ECV7339	AJ007339 Echovirus
460	19	100.0	316	13	ECV7341	AJ007341 Echovirus
461	19	100.0	316	13	ECV7342	AJ007342 Echovirus
462	19	100.0	316	13	ECV7343	AJ007343 Echovirus
463	19	100.0	316	13	ECV7344	AJ007344 Echovirus
464	19	100.0	317	13	ECV7340	AJ007340 Echovirus
465	19	100.0	317	13	ECV7346	AJ007346 Echovirus
466	19	100.0	319	13	HEC579630	AJ579630 Human ech
467	19	100.0	319	13	HEC579631	AJ579631 Human ech
468	19	100.0	319	13	HEC579632	AJ579632 Human ech
469	19	100.0	319	13	HEC579633	AJ579633 Human ech
470	19	100.0	319	13	HEC579634	AJ579634 Human ech
471	19	100.0	319	13	HEC579635	AJ579635 Human ech
472	19	100.0	319	13	HEC579636	AJ579636 Human ech
473	19	100.0	319	13	HEC579637	AJ579637 Human ech
474	19	100.0	319	13	HEC579638	AJ579638 Human ech
475	19	100.0	319	13	HEC579639	AJ579639 Human ech
476	19	100.0	319	13	HEC579640	AJ579640 Human ech
477	19	100.0	330	13	AF542452	AF542452 Human rhl
478	19	100.0	338	6	CQ964036	CQ964036 Sequence
479	19	100.0	339	6	CQ964030	CQ964030 Sequence
480	19	100.0	340	6	CQ964029	CQ964029 Sequence
481	19	100.0	340	6	CQ964031	CQ964031 Sequence
482	19	100.0	340	6	CQ964032	CQ964032 Sequence
483	19	100.0	340	6	CQ964033	CQ964033 Sequence
484	19	100.0	340	6	CQ964034	CQ964034 Sequence
485	19	100.0	340	6	CQ964035	CQ964035 Sequence
486	19	100.0	345	13	EU37767	U37767 Echovirus 9
487	19	100.0	346	13	AF412341	AF412341 Human cox
488	19	100.0	346	13	AF412342	AF412342 Human cox
489	19	100.0	346	13	AF412343	AF412343 Human cox
490	19	100.0	346	13	AF412344	AF412344 Human cox
491	19	100.0	346	13	AF412345	AF412345 Human cox
492	19	100.0	346	13	AF412346	AF412346 Human cox
493	19	100.0	346	13	AF412348	AF412348 Human cox
494	19	100.0	346	13	AF412349	AF412349 Human cox
495	19	100.0	346	13	AF412357	AF412357 Human cox
496	19	100.0	346	13	AF412358	AF412358 Human cox
497	19	100.0	346	13	AF412359	AF412359 Human ech
498	19	100.0	346	13	AF412360	AF412360 Human ech
499	19	100.0	346	13	AF412361	AF412361 Human ech
500	19	100.0	346	13	AF412362	AF412362 Human ech

ALIGNMENTS

RESULT 1	AR595531	AR595531	Sequence 9 from patent US 6818397.	27 bp	DNA	linear	PAT 15-DEC-2004
LOCUS	AR595531	Sequence 9 from patent US 6818397.					
DEFINITION	AR595531	Sequence 9 from patent US 6818397.					
ACCESSION	AR595531	Sequence 9 from patent US 6818397.					
VERSION	AR595531.1	GI:56646343					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 27)						
AUTHORS	Lee, K.-H., Bair, C.-H., Teeng, Y.-Y., Wang, Y.-W. and Wang, S.-H.						
TITLE	Methods for detecting and differentiating enteroviruses and the primers and probes therefor						
JOURNAL	Patent: US 6818397-A 9 16-NOV-2004;						
FEATURES	Dr. Chip Biotechnology Incorporation; Taichung; TWX;						
source	Location/Qualifiers						
ORIGIN	1..27						
Query Match	100.0%;	Score 19;	DB 6;	Length 27;			

Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
|||||
Db 9 CCCCTGAATGGGCTAATC 27

RESULT 2
AX348200
LOCUS AX348200 linear DNA PAT 06-FEB-2002
DEFINITION Sequence 70 from Patent WO0202811.
ACCESSION AX348200
VERSION AX348200.1 GI:18614300
KEYWORDS
SOURCE Human poliovirus 2
ORGANISM Human poliovirus 2

REFERENCE
AUTHORS Renaud, P., Guillot, E., Mabilat, C., Vachon, C., Lacroix, B.,
Vernet, G., Armand, M.A. and Laffaire, P.
TITLE Method for controlling the microbiological quality of an aqueous
medium and kit therefor
JOURNAL Patent: WO 0202811-A 70 10-JAN-2002;
BIO MERIEUX (FR)

FEATURES
source
Location/Qualifiers
1..30
/organism="Human poliovirus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:12083"

ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
|||||
Db 7 CCCCTGAATGGGCTAATC 25

RESULT 3
AX348202
LOCUS AX348202 linear DNA PAT 06-FEB-2002
DEFINITION Sequence 72 from Patent WO0202811.
ACCESSION AX348202
VERSION AX348202.1 GI:18614302
KEYWORDS
SOURCE Human coxsackievirus A21

REFERENCE
AUTHORS Renaud, P., Guillot, E., Mabilat, C., Vachon, C., Lacroix, B.,
Vernet, G., Armand, M.A. and Laffaire, P.
TITLE Method for controlling the microbiological quality of an aqueous
medium and kit therefor
JOURNAL Patent: WO 0202811-A 72 10-JAN-2002;
BIO MERIEUX (FR)

FEATURES
source
Location/Qualifiers
1..30
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/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
|||||

Db 6 CCCCTGAATGGGCTAATC 24

RESULT 4
AX348204

LOCUS AX348204 linear DNA PAT 06-FEB-2002
DEFINITION Sequence 74 from Patent WO0202811.
ACCESSION AX348204
VERSION AX348204.1 GI:18614304
KEYWORDS
SOURCE Human echovirus 12

ORGANISM Human echovirus 12
REFERENCE
AUTHORS Renaud, P., Guillot, E., Mabilat, C., Vachon, C., Lacroix, B.,
Vernet, G., Armand, M.A. and Laffaire, P.

TITLE Method for controlling the microbiological quality of an aqueous
medium and kit therefor
JOURNAL Patent: WO 0202811-A 74 10-JAN-2002;
BIO MERIEUX (FR)

FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:35293"

ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
|||||
Db 11 CCCCTGAATGGGCTAATC 29

RESULT 5
AX711149

LOCUS AX711149 39 bp RNA PAT 11-APR-2003
DEFINITION Sequence 449 from Patent EP1288296.
ACCESSION AX711149
VERSION AX711149.1 GI:29787530
KEYWORDS
SOURCE unidentified

ORGANISM unidentified
REFERENCE
AUTHORS Draper, K.G., McSwiggen, J.A., Holecsek, J.J., Dudycz, L.W.,
Macejak, D.G. and Mamone, J.A.

TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 449 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
source
Location/Qualifiers
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/mol_type="unassigned RNA"
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/note="P3 Picornovirus"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
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Db 13 CCCCTGAATGGGCTAATC 31

RESULT 6
POL1BRA

LOCUS POL1BRA 100 bp RNA linear VRL 21-MAY-2003

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DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/8-3827/Brazil/81.
ACCESSION D00260
VERSION D00260.1 GI:222344
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
source
Location/Qualifiers
1..100
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/mol_type="genomic RNA"
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/db_xref="taxon:12080"
/note="451 bp downstream of the 5' end of virion RNA."
<1..>100
5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 7
POLIHK
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/15/HK/81.
ACCESSION D00257
VERSION D00257.1 GI:222345
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
source
Location/Qualifiers
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/organism="Human poliovirus 1"
/mol_type="genomic RNA"
/isolate="wild-type isolate PI/15/HK/81"
/db_xref="taxon:12080"
/note="451 bp downstream of the 5' end of virion RNA."
<1..>100
5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 7
POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/2171/USA/77.
ACCESSION D00261
VERSION D00261.1 GI:222347
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
source
Location/Qualifiers
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/isolate="wild-type isolate PI/2171/USA/77"
/db_xref="taxon:12080"
5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 9
POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/2171/USA/77.
ACCESSION D00261
VERSION D00261.1 GI:222347
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
source
Location/Qualifiers
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/mol_type="genomic RNA"
/isolate="wild-type isolate PI/2171/USA/77"
/db_xref="taxon:12080"
5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

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Db 7 CCCCTGAATCGGCTAATC 25
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POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, vaccine strains
Sabin 1, Cox, CHAT.
ACCESSION D00254
VERSION D00254.1 GI:222346
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
source
Location/Qualifiers
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/mol_type="genomic RNA"
/strain="vaccine strains Sabin 1, Cox, CHAT"
/db_xref="taxon:12080"
/note="451 bp downstream of the 5' end of virion RNA."
<1..>100
5'UTR
variation
36
/note="g in Sabin 1; a in Cox and CHAT"
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 9
POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/2171/USA/77.
ACCESSION D00261
VERSION D00261.1 GI:222347
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
source
Location/Qualifiers
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/mol_type="genomic RNA"
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5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 9
POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/2171/USA/77.
ACCESSION D00261
VERSION D00261.1 GI:222347
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
source
Location/Qualifiers
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/mol_type="genomic RNA"
/isolate="wild-type isolate PI/2171/USA/77"
/db_xref="taxon:12080"
5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

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/note="451 bp downstream of the 5' end of virion RNA."
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5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 7 CCCCTGAATGCGGCTAATC 25

RESULT 10
POL2SA2
LOCUS Human poliovirus 2 RNA, 5'UTR, partial sequence, vaccine strain
DEFINITION Sabin 2.
ACCESSION D00255
VERSION D00255.1 GI:222350
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 2
ORGANISM Human poliovirus 2
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor, P.D. and Dunn, G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].

FEATURES
Location/Qualifiers
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/mol_type="genomic RNA"
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/db_xref="taxon:12083"
/note="451 bp downstream of the 5' end of virion RNA."
<1. >100

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 7 CCCCTGAATGCGGCTAATC 25

RESULT 11
POL3BRA
LOCUS Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolate
DEFINITION P3/3054/Brazil/81.
ACCESSION D00263
VERSION D00263.1 GI:222351
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor, P.D. and Dunn, G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
```

```
wild-type isolates of serotype 1, 3 were determined in [1].
Location/Qualifiers
1..100
/mol_type="genomic RNA"
/isolate="wild-type isolate P3/3054/Brazil/81"
/db_xref="taxon:12086"
/note="451 bp downstream of the 5' end of virion RNA."
<1. >100

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 7 CCCCTGAATGCGGCTAATC 25

RESULT 12
POL3FIN
LOCUS Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolates
DEFINITION P3/Fin/60212/85, P3/Fin/25725/85.
ACCESSION D00258
VERSION D00258.1 GI:222352
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor, P.D. and Dunn, G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].

FEATURES
Location/Qualifiers
1..100
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/isolate="wild-type isolates P3/Fin/60212/85,
P3/Fin/25725/85"
/db_xref="taxon:12086"
/note="451 bp downstream of the 5' end of virion RNA."
<1. >100

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 7 CCCCTGAATGCGGCTAATC 25

RESULT 13
POL3VDB
LOCUS Human poliovirus 3 RNA, 5'UTR, partial sequence, vaccine strain
DEFINITION USOL-D-BAC.
ACCESSION D00259
VERSION D00259.1 GI:222354
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
        replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
        polioviruses which include vaccine strains of serotype 1, 2, 3 and
        wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
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        Location/Qualifiers
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            /mol_type="genomic RNA"
            /strain="vaccine strain USOL-D-BAC"
            /db_xref="taxon:12086"
            /note="451 bp downstream of the 5' end of virion RNA."
            <1..>100
    5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 14
POL3YUN
LOCUS Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolate
        P3/Yunan/2/84.
DEFINITION
ACCESSION D00262
VERSION D00262.1 GI:222355
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
        replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
        polioviruses which include vaccine strains of serotype 1, 2, 3 and
        wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
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        Location/Qualifiers
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            /mol_type="genomic RNA"
            /isolate="wild-type isolate P3/Yunan/2/84"
            /db_xref="taxon:12086"
            /note="451 bp downstream of the 5' end of virion RNA."
            <1..>100
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ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 15
DQ029090
LOCUS Human echovirus 11 strain MON-ES9 5' UTR.
DEFINITION
ACCESSION DQ029090

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VERSION DQ029090.1 GI:66473298
KEYWORDS Human echovirus 11
SOURCE Human echovirus 11
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 109)
AUTHORS Gharbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
        N'Saibia,S. and Aouni,M.
TITLE Nucleotide sequences of the IRES domains IV and V of natural
        isolates ECHO virus type 11 with different replicative capacities
        phenotypes
JOURNAL Unpublished (2005)
REFERENCE 2 (bases 1 to 109)
AUTHORS Gharbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
        N'Saibia,S. and Aouni,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
        Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
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        Location/Qualifiers
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            /organism="Human echovirus 11"
            /viroion
            /mol_type="genomic RNA"
            /strain="MON-ES9"
            /db_xref="taxon:12078"
            /country="Tunisia"
            <1..>109
            /note="domain V of IRES (internal ribosome entry site)"
    5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 4 CCCCTGAATCGGCTAATC 22

RESULT 16
DQ029091
LOCUS Human echovirus 11 strain MON-ES36 5' UTR.
DEFINITION
ACCESSION DQ029091
VERSION DQ029091.1 GI:66473299
KEYWORDS Human echovirus 11
SOURCE Human echovirus 11
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 109)
AUTHORS Gharbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
        N'Saibia,S. and Aouni,M.
TITLE Nucleotide sequences of the IRES domains IV and V of natural
        isolates ECHO virus type 11 with different replicative capacities
        phenotypes
JOURNAL Unpublished (2005)
REFERENCE 2 (bases 1 to 109)
AUTHORS Gharbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
        N'Saibia,S. and Aouni,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
        Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
    source
        Location/Qualifiers
            1..109
            /organism="Human echovirus 11"
            /viroion
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            /strain="MON-ES36"
            /db_xref="taxon:12078"
            /country="Tunisia"
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    5'UTR

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ORIGIN
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Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22

RESULT 17
DQ029092
LOCUS Human echovirus 11 strain STE-5793 5' UTR. linear VRL 29-MAY-2005
DEFINITION Human echovirus 11 strain STE-5793 5' UTR.
ACCESSION DQ029092
VERSION DQ029092.1 GI:66473300
KEYWORDS
SOURCE Human echovirus 11
ORGANISM Human echovirus 11
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
TITLE Nucleotide sequences of the IRES domains IV and V of natural
isolates ECHO virus type 11 with different replicative capacities
phenotypes
JOURNAL Unpublished (2005)
REFERENCE 2 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
source
Location/Qualifiers
1..109
/organism="Human echovirus 11"
/virion
/mol_type="genomic RNA"
/strain="STE-5793"
/db_xref="taxon:12078"
/country="France"
<1..>109
/Note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22

RESULT 18
DQ029094
LOCUS Human echovirus 11 strain STE-11730 5' UTR. linear VRL 29-MAY-2005
DEFINITION Human echovirus 11 strain STE-11730 5' UTR.
ACCESSION DQ029094
VERSION DQ029094.1 GI:66473302
KEYWORDS
SOURCE Human echovirus 11
ORGANISM Human echovirus 11
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
TITLE Nucleotide sequences of the IRES domains IV and V of natural
isolates ECHO virus type 11 with different replicative capacities
phenotypes
JOURNAL Unpublished (2005)
REFERENCE 2 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
source
Location/Qualifiers
1..109
/organism="Human echovirus 2"
/virion
/mol_type="genomic RNA"
/strain="MON-ECV2"
/db_xref="taxon:35294"
/country="Tunisia"
<1..>109
/Note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22
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phenotypes
Unpublished (2005)
2 (bases 1 to 109)
Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
Direct Submission
Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
Location/Qualifiers
1..109
/organism="Human echovirus 11"
/virion
/mol_type="genomic RNA"
/strain="STE-11730"
/db_xref="taxon:12078"
/country="France"
<1..>109
/Note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22

RESULT 19
DQ029095
LOCUS Human echovirus 2 strain MON-ECV2 5' UTR. linear VRL 29-MAY-2005
DEFINITION Human echovirus 2 strain MON-ECV2 5' UTR.
ACCESSION DQ029095
VERSION DQ029095.1 GI:66473303
KEYWORDS
SOURCE Human echovirus 2
ORGANISM Human echovirus 2
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
TITLE Nucleotide sequences of the IRES domains IV and V of natural
isolates ECHO virus type 11 with different replicative capacities
phenotypes
JOURNAL Unpublished (2005)
REFERENCE 2 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
source
Location/Qualifiers
1..109
/organism="Human echovirus 2"
/virion
/mol_type="genomic RNA"
/strain="MON-ECV2"
/db_xref="taxon:35294"
/country="Tunisia"
<1..>109
/Note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22
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RESULT 20
DQ029096
LOCUS      DQ029096                109 bp      RNA      linear      VRL 29-MAY-2005
DEFINITION Human echovirus 12 strain Travis prototype 5' UTR.
ACCESSION  DQ029096
VERSION     DQ029096.1 GI:66473304
KEYWORDS
SOURCE      Human echovirus 12
ORGANISM    Human echovirus 12
REFERENCE   1 (bases 1 to 109)
AUTHORS     Charbi J., Elhjar, R., Ben M'Hadheb, M., Jaidane, H., Bouslama, L.,
            N'Saibia, S. and Aouni, M.
TITLE       Nucleotide sequences of the IRES domains IV and V of natural
            isolates ECHO virus type 11 with different replicative capacities
            phenotypes
JOURNAL     Unpublished (2005)
REFERENCE   2 (bases 1 to 109)
AUTHORS     Charbi, J., Elhjar, R., Ben M'Hadheb, M., Jaidane, H., Bouslama, L.,
            N'Saibia, S. and Aouni, M.
TITLE       Direct Submission
JOURNAL     Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
            Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES   Location/Qualifiers
            source
            1..109
            /organism="Human echovirus 12"
            /viral
            /mol_type="genomic RNA"
            /strain="Travis prototype"
            /db_xref="taxon:35293"
            <1..>109
            /note="domain V of IRES (internal ribosome entry site)"

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      4 CCCCTGAATCGGCTAATC 22

RESULT 21
AF380621
LOCUS      AF380621                120 bp ss-RNA linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 1 5' untranslated region, partial sequence.
ACCESSION  AF380621
VERSION     AF380621.1 GI:14290213
KEYWORDS
SOURCE      Human poliovirus 1
ORGANISM    Human poliovirus 1
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Direct Submission
JOURNAL     Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
            College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
FEATURES   Location/Qualifiers
            source
            1..120
            /organism="Human poliovirus 1"
            /viral
            /mol_type="genomic RNA"
            /specific_host="Homo sapiens"
            /db_xref="taxon:12080"

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      9 CCCCTGAATCGGCTAATC 27

RESULT 22
AF380622
LOCUS      AF380622                120 bp ss-RNA linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 1 5' untranslated region, partial sequence.
ACCESSION  AF380622
VERSION     AF380622.1 GI:14290214
KEYWORDS
SOURCE      Human poliovirus 1
ORGANISM    Human poliovirus 1
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Direct Submission
JOURNAL     Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
            College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
FEATURES   Location/Qualifiers
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            1..120
            /organism="Human poliovirus 1"
            /viral
            /mol_type="genomic RNA"
            /specific_host="Homo sapiens"
            /db_xref="taxon:12080"
            /note="wild type isolate from 1999"

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      9 CCCCTGAATCGGCTAATC 27

RESULT 23
AF380624
LOCUS      AF380624                120 bp ss-RNA linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 3 5' untranslated region, partial sequence.
ACCESSION  AF380624
VERSION     AF380624.1 GI:14290216
KEYWORDS
SOURCE      Human poliovirus 3
ORGANISM    Human poliovirus 3
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Direct Submission

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5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      9 CCCCTGAATCGGCTAATC 27

RESULT 22
AF380622
LOCUS      AF380622                120 bp ss-RNA linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 1 5' untranslated region, partial sequence.
ACCESSION  AF380622
VERSION     AF380622.1 GI:14290214
KEYWORDS
SOURCE      Human poliovirus 1
ORGANISM    Human poliovirus 1
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Direct Submission
JOURNAL     Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
            College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
FEATURES   Location/Qualifiers
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            /viral
            /mol_type="genomic RNA"
            /specific_host="Homo sapiens"
            /db_xref="taxon:12080"
            /note="wild type isolate from 1999"

5'UTR
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Query Match      100.0%; Score 19; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      9 CCCCTGAATCGGCTAATC 27

RESULT 23
AF380624
LOCUS      AF380624                120 bp ss-RNA linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 3 5' untranslated region, partial sequence.
ACCESSION  AF380624
VERSION     AF380624.1 GI:14290216
KEYWORDS
SOURCE      Human poliovirus 3
ORGANISM    Human poliovirus 3
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu, A., Neale, M.L. and Fox, J.D.
TITLE       Direct Submission

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JOURNAL	Submitted (14-MAY-2001) Medical Microbiology, University of Wales, College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
FEATURES	Location/Qualifiers
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	/specific_host="Homo sapiens"
	/db_xref="taxon:12086"
	/notes="wild type isolate from 1999"
	<1. .>120
5'UTR	
ORIGIN	
Query Match	100.0%; Score 19; DB 13; Length 120;
Best Local Similarity	100.0%; Pred. No. 9.5;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCCCTGAATCGGCTAATC 19
Db	9 CCCCTGAATCGGCTAATC 27
RESULT 24	
AF380623	122 bp ss-RNA linear VRL 05-JUN-2001
LOCUS	Human poliovirus 2 5' untranslated region, partial sequence.
DEFINITION	AF380623
ACCESSION	AF380623
VERSION	AF380623.1 GI:14290215
KEYWORDS	
SOURCE	Human poliovirus 2
ORGANISM	Human poliovirus 2
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS	Picornaviridae; Enterovirus.
TITLE	1 (bases 1 to 122)
	Mengistu,A., Neale,M.L. and Fox,J.D.
	Detection and Typing of Enteroviruses by Analysis of the 2C Gene
Sequence	
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 122)
AUTHORS	Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE	Direct Submission
JOURNAL	Submitted (14-MAY-2001) Medical Microbiology, University of Wales, College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
FEATURES	Location/Qualifiers
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	/organism="Human poliovirus 2"
	/viroion
	/mol_type="genomic RNA"
	/specific_host="Homo sapiens"
	/db_xref="taxon:12083"
	/notes="wild type isolate from 1999"
	<1. .>122
5'UTR	
ORIGIN	
Query Match	100.0%; Score 19; DB 13; Length 122;
Best Local Similarity	100.0%; Pred. No. 9.5;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCCCTGAATCGGCTAATC 19
Db	10 CCCCTGAATCGGCTAATC 28
RESULT 25	
AJ783777	128 bp RNA linear VRL 12-AUG-2005
LOCUS	Human poliovirus 1, partial 5'UTR, genomic RNA, isolate P20.
DEFINITION	AJ783777
ACCESSION	AJ783777
VERSION	AJ783777.1 GI:72534022
KEYWORDS	
SOURCE	Human poliovirus 1
ORGANISM	Human poliovirus 1
	Viruses; ssRNA positive-strand viruses, no DNA stage;

Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 7 CCCCTGAATGCGGCTAATC 25
|||||

RESULT 27
HEN312091 HEN312091 145 bp RNA linear VRL 02-JUL-2003
LOCUS Human coxsackievirus B2 partial 5'UTR, strain /ro/Roma98.
DEFINITION
ACCESSION AJ312091
VERSION AJ312091.1 GI:16555709
KEYWORDS
SOURCE Human coxsackievirus B2
ORGANISM Human coxsackievirus B2
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1
AUTHORS Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and Fadda, G.
TITLE Molecular identification and typing of enteroviruses isolated from clinical specimens
J. Clin. Microbiol. 40 (12), 4554-4560 (2002)

JOURNAL
PUBMED 12454151
AUTHORS Muscillo, M.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy

FEATURES
source Location/Qualifiers
1..145
/organism="Human coxsackievirus B2"
/viral
/mol_type="genomic RNA"
/strain="/ro/Roma98"
/isolate="IT98-5102"
/db_xref="taxon:82639"
/lab_host="vero cell culture"
/note="throat swab from child with aseptic meningitis, identified by immunofluorescence assay"
<1..>145

5'UTR
ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 145;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 6 CCCCTGAATGCGGCTAATC 24
|||||

RESULT 28
AF314006 AF314006 147 bp mRNA linear VRL 31-JUL-2002
LOCUS Enterovirus 5506/SIN/001309 5' UTR, partial sequence.
DEFINITION
ACCESSION AF314006
VERSION AF314006.1 GI:12667229
KEYWORDS
SOURCE Enterovirus 5506/SIN/001309
ORGANISM Enterovirus 5506/SIN/001309
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)

12149336
2 (bases 1 to 107)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
FEATURES
source Location/Qualifiers
1..147
/organism="Enterovirus 5506/SIN/001309"
/mol_type="mRNA"
/strain="5506/SIN/001309"
/db_xref="taxon:150715"
<1..>147

5'UTR
ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 8 CCCCTGAATGCGGCTAATC 26
|||||

RESULT 29
AF316322 AF316322 147 bp mRNA linear VRL 31-JUL-2002
LOCUS Enterovirus 71 isolate 5855/sin/000009 5'UTR, partial sequence.
DEFINITION
ACCESSION AF316322
VERSION AF316322.1 GI:12744302
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)

JOURNAL
PUBMED 12149336
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-2000) Department of Microbiology, National University of Singapore, 5, Science Drive 2, Singapore 117597, Singapore

FEATURES
source Location/Qualifiers
1..147
/organism="Human enterovirus 71"
/mol_type="mRNA"
/isolate="5855/sin/000009"
/db_xref="taxon:39054"
/note="Human enterovirus 71 derived from isolates collected from human mouth swab, saliva, lung, heart, brain, rectal swab, tonsils, spleen, foot swab, throat swab, intestine, and oral mucosa."
<1..>147

5'UTR
ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 8 CCCCTGAATGCGGCTAATC 26
|||||

RESULT 30
AF314004

LOCUS AF314004 153 bp mRNA linear VRL 31-JUL-2002
 DEFINITION Enterovirus 5589/SIN/001809 5' UTR, partial sequence.
 ACCESSION AF314004
 VERSION AF314004.2 GI:131111667
 KEYWORDS
 SOURCE
 ORGANISM Enterovirus 5589/SIN/001809
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
 REFERENCE 1 (bases 1 to 153)
 AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
 TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
 J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
 JOURNAL PUBLISHED 12149336
 REFERENCE 2 (bases 1 to 153)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REFERENCE 3 (bases 1 to 153)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REMARK Sequence update by submitter
 COMMENT On Feb 23, 2001 this sequence version replaced gi:12667227.
 FEATURES
 Location/Qualifiers
 source 1..153
 /organism="Enterovirus 5589/SIN/001809"
 /mol_type="mRNA"
 /strain="5589/SIN/001809"
 /db_xref="taxon:150718"
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 Query Match 100.0%; Score 19; DB 13; Length 153;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATCGCGCTAATC 19
 |||||
 Db 8 CCCCTGAATCGCGCTAATC 26
 |||||
 RESULT 31
 AF314003
 LOCUS AF314003 154 bp mRNA linear VRL 31-JUL-2002
 DEFINITION Enterovirus 5627/SIN/002009 5' UTR, partial sequence.
 ACCESSION AF314003
 VERSION AF314003.2 GI:131111666
 KEYWORDS
 SOURCE Enterovirus 5627/SIN/002009
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
 REFERENCE 1 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
 TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
 J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
 JOURNAL PUBLISHED 12149336
 REFERENCE 2 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REFERENCE 3 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REMARK Sequence update by submitter
 COMMENT On Feb 23, 2001 this sequence version replaced gi:12667228.
 FEATURES
 Location/Qualifiers
 source 1..154
 /organism="Enterovirus 5627/SIN/002009"
 /mol_type="mRNA"
 /strain="5627/SIN/002009"
 /db_xref="taxon:150720"
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 ORIGIN
 Query Match 100.0%; Score 19; DB 13; Length 154;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATCGCGCTAATC 19
 |||||
 Db 8 CCCCTGAATCGCGCTAATC 26
 |||||
 RESULT 32
 AF314005
 LOCUS AF314005 154 bp mRNA linear VRL 31-JUL-2002
 DEFINITION Enterovirus 5656/SIN/002209 5' UTR, partial sequence.
 ACCESSION AF314005
 VERSION AF314005.2 GI:131111668
 KEYWORDS
 SOURCE Enterovirus 5656/SIN/002209
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
 REFERENCE 1 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
 TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
 J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
 JOURNAL PUBLISHED 12149336
 REFERENCE 2 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REFERENCE 3 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REMARK Sequence update by submitter
 COMMENT On Feb 23, 2001 this sequence version replaced gi:12667228.
 FEATURES
 Location/Qualifiers
 source 1..154
 /organism="Enterovirus 5656/SIN/002209"
 /mol_type="mRNA"
 /strain="5656/SIN/002209"
 /db_xref="taxon:150720"
 <1..>154
 5'UTR
 ORIGIN
 Query Match 100.0%; Score 19; DB 13; Length 154;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATCGCGCTAATC 19
 |||||
 Db 8 CCCCTGAATCGCGCTAATC 26
 |||||
 RESULT 33
 AF314005
 LOCUS AF314005 154 bp mRNA linear VRL 31-JUL-2002
 DEFINITION Enterovirus 5656/SIN/002209 5' UTR, partial sequence.
 ACCESSION AF314005
 VERSION AF314005.2 GI:131111668
 KEYWORDS
 SOURCE Enterovirus 5656/SIN/002209
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
 REFERENCE 1 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
 TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
 J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
 JOURNAL PUBLISHED 12149336
 REFERENCE 2 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REFERENCE 3 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REMARK Sequence update by submitter
 COMMENT On Feb 23, 2001 this sequence version replaced gi:12667228.
 FEATURES
 Location/Qualifiers
 source 1..154
 /organism="Enterovirus 5656/SIN/002209"
 /mol_type="mRNA"
 /strain="5656/SIN/002209"
 /db_xref="taxon:150720"
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 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATCGCGCTAATC 19
 |||||
 Db 8 CCCCTGAATCGCGCTAATC 26
 |||||
 RESULT 33

TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REMARK Sequence update by submitter
 COMMENT On Feb 23, 2001 this sequence version replaced gi:12667226.
 FEATURES
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 /organism="Enterovirus 5627/SIN/002009"
 /mol_type="mRNA"
 /strain="5627/SIN/002009"
 /db_xref="taxon:150719"
 <1..>154
 5'UTR
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 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATCGCGCTAATC 19
 |||||
 Db 8 CCCCTGAATCGCGCTAATC 26
 |||||
 RESULT 32
 AF314005
 LOCUS AF314005 154 bp mRNA linear VRL 31-JUL-2002
 DEFINITION Enterovirus 5656/SIN/002209 5' UTR, partial sequence.
 ACCESSION AF314005
 VERSION AF314005.2 GI:131111668
 KEYWORDS
 SOURCE Enterovirus 5656/SIN/002209
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
 REFERENCE 1 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
 TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
 J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
 JOURNAL PUBLISHED 12149336
 REFERENCE 2 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REFERENCE 3 (bases 1 to 154)
 AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
 REMARK Sequence update by submitter
 COMMENT On Feb 23, 2001 this sequence version replaced gi:12667228.
 FEATURES
 Location/Qualifiers
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 /organism="Enterovirus 5656/SIN/002209"
 /mol_type="mRNA"
 /strain="5656/SIN/002209"
 /db_xref="taxon:150720"
 <1..>154
 5'UTR
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 Query Match 100.0%; Score 19; DB 13; Length 154;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCCTGAATCGCGCTAATC 19
 |||||
 Db 8 CCCCTGAATCGCGCTAATC 26
 |||||
 RESULT 33

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AF314007
LOCUS AF314007 154 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 5536/SIN/001409 5' UTR, partial sequence.
ACCESSION AF314007
VERSION AF314007.2 GI:13111669
KEYWORDS
SOURCE
ORGANISM Enterovirus 5536/SIN/001409
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 154)
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
        from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
        Reverse Transcription-PCR with Universal Enterovirus and
        EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
REFERENCE 2 (bases 1 to 154)
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of
        Singapore, 5 Science Drive 2, Singapore 117597, Singapore
REFERENCE 3 (bases 1 to 154)
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of
        Singapore, 5 Science Drive 2, Singapore 117597, Singapore
REMARK Sequence update by submitter
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667230.
FEATURES
        source
            1..154
                /organism="Enterovirus 5536/SIN/001409"
                /mol_type="mRNA"
                /strain="5536/SIN/001409"
                /db_xref="taxon:150716"
                <1..>154

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGCTAATC 19
    |||||
Db 8 CCCCTGAATGCGCTAATC 26

RESULT 34
AF314008
LOCUS AF314008 154 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 5546/SIN/000009 5' UTR, partial sequence.
ACCESSION AF314008
VERSION AF314008.1 GI:12667231
KEYWORDS
SOURCE
ORGANISM Enterovirus 5546/SIN/000009
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 154)
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
        from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
        Reverse Transcription-PCR with Universal Enterovirus and
        EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
REFERENCE 2 (bases 1 to 154)
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of
        Singapore, 5 Science Drive 2, Singapore 117597, Singapore
FEATURES
        Location/Qualifiers
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1..154
/organism="Enterovirus 5546/SIN/000009"
/mol_type="mRNA"
/strain="5546/SIN/000009"
/db_xref="taxon:150717"
<1..>154

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGCTAATC 19
    |||||
Db 8 CCCCTGAATGCGCTAATC 26

RESULT 35
AY027864
LOCUS AY027864 154 bp RNA linear VRL 31-JUL-2002
DEFINITION Enterovirus TS/SIN/001002 5'UTR, partial sequence.
ACCESSION AY027864
VERSION AY027864.1 GI:13591397
KEYWORDS
SOURCE
ORGANISM Enterovirus TS/SIN/001002
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 154)
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
        from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
        Reverse Transcription-PCR with Universal Enterovirus and
        EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
REFERENCE 2 (bases 1 to 154)
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2001) Microbiology, National University of
        Singapore, 5 Science Drive 2, Singapore 117597, Singapore
FEATURES
        Location/Qualifiers
            1..154
                /organism="Enterovirus TS/SIN/001002"
                /mol_type="genomic RNA"
                /strain="TS/SIN/001002"
                /db_xref="taxon:155431"
                /note="isolated from throat swab"
                <1..>154

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGCTAATC 19
    |||||
Db 8 CCCCTGAATGCGCTAATC 26

RESULT 36
AY027865
LOCUS AY027865 154 bp RNA linear VRL 10-APR-2001
DEFINITION Enterovirus TF/SIN/000704 5'UTR, partial sequence.
ACCESSION AY027865
VERSION AY027865.1 GI:13591398
KEYWORDS
SOURCE
ORGANISM Enterovirus TF/SIN/000704
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 154)
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
```

```

TITLE      Enterovirus strains from an outbreak of Hand, Foot and Mouth
            disease in Singapore (2000)
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 154)
AUTHORS    Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE      Direct Submission
JOURNAL    Submitted (22-FEB-2001) Microbiology, National University of
            Singapore, 5 Science Drive 2, Singapore 117597, Singapore
FEATURES   Location/Qualifiers
            source
            1..154
            /organism="Enterovirus TF/SIN/000704"
            /mol_type="genomic RNA"
            /strain="TF/SIN/000704"
            /db_xref="taxon:155429"
            /note="Isolated from tissue fluid"
            <1..>154

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 8 CCCCTGAATGCGGCTAATC 26

RESULT 37
AY027866      154 bp RNA linear VRL 10-APR-2001
LOCUS      Enterovirus 5571/SIN/001809 5'UTR, partial sequence.
DEFINITION
ACCESSION    AY027866
VERSION      AY027866.1 GI:13591399
KEYWORDS
SOURCE
ORGANISM      Enterovirus 5571/SIN/001809
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 154)
AUTHORS      Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE      Enterovirus strains from an outbreak of Hand, Foot and Mouth
            disease in Singapore (2000)
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 154)
AUTHORS      Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE      Direct Submission
JOURNAL    Submitted (22-FEB-2001) Microbiology, National University of
            Singapore, 5 Science Drive 2, Singapore 117597, Singapore
FEATURES   Location/Qualifiers
            source
            1..154
            /organism="Enterovirus 5571/SIN/001809"
            /mol_type="genomic RNA"
            /strain="5571/SIN/001809"
            /db_xref="taxon:155430"
            /note="Isolated from stool sample"
            <1..>154

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 8 CCCCTGAATGCGGCTAATC 26

RESULT 38
HCO295181/c      171 bp RNA linear VRL 15-MAY-2001
LOCUS      Human coxsackievirus B5 genomic RNA for partial 5'UTR, isolate
            IT999-21.
DEFINITION
ACCESSION    HCO295181
            AJ295181

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VERSION      AJ295181.1 GI:14139958
KEYWORDS
SOURCE      Human coxsackievirus B5
ORGANISM    Human coxsackievirus B5
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1
AUTHORS      Muscillo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,
            Zaniratti, S., Cattani, P., Manzara, S., Fadda, G., Comparcola, D. and
            Ticca, P.
TITLE      A phylogenetic analysis of the two echovirus 30 isolated in Rome
            (Italy) in 1997 from an outbreak of aseptic meningitis associated
            with swimming pools
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 171)
AUTHORS      Muscillo, M.
TITLE      Direct Submission
JOURNAL    Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
            Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
            00161, Italy
FEATURES   Location/Qualifiers
            source
            1..171
            /organism="Human coxsackievirus B5"
            /mol_type="genomic RNA"
            /strain="F/Roma99"
            /isolate="ITA99-21"
            /specific_host="Homo sapiens"
            /db_xref="taxon:12074"
            /note="sporadic case of aseptic meningitis; BGM cell
            culture of stools from a four years old child"
            <1..>171

5'UTR
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 155 CCCCTGAATGCGGCTAATC 137

RESULT 39
HEN312088      172 bp RNA linear VRL 02-JUL-2003
LOCUS      Human enterovirus 71 partial 5'UTR, strain /di/Roma98.
DEFINITION
ACCESSION    AJ312088
VERSION      AJ312088.1 GI:16555706
KEYWORDS
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1
AUTHORS      Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and
            Fadda, G.
TITLE      Molecular identification and typing of enteroviruses isolated from
            clinical specimens
JOURNAL    J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
PUBMED      12454151
REFERENCE  2 (bases 1 to 172)
AUTHORS      Muscillo, M.
TITLE      Direct Submission
JOURNAL    Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
            Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
            00161, Italy
FEATURES   Location/Qualifiers
            source
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            /mol_type="genomic RNA"
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/db xref="taxon:39054"
/lab host="vero cell cultures"
/note="throat swab from child with aseptic meningitis,
identified by immunofluorescence assay"
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5'UTR
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Best Local Similarity 100.0%; Pred. No. 9.5; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 CCCCTGAATCGGCTAATC 19
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Db 6 CCCCTGAATCGGCTAATC 24
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RESULT 40
ESP295207/c
LOCUS ESP295207 177 bp RNA linear VRL 15-MAY-2001
DEFINITION Echovirus sp. genomic RNA for partial 5'UTR, isolate ATCC VR-322.
ACCESSION AJ295207
VERSION AJ295207.1 GI:14140008
KEYWORDS
SOURCE
ORGANISM Echovirus sp.
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1
REFERENCE
AUTHORS Muscillo,M., La Rosa,G., Marianelli,C., Capobianchi,M.R.,
Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and
Ticca,P.
TITLE A phylogenetic analysis of the two echovirus 30 isolated in Rome
(Italy) in 1997 from an outbreak of aseptic meningitis associated
with swimming pools
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 177)
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
00161, Italy
FEATURES
source
Location/Qualifiers
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/virion
/mol_type="genomic RNA"
/strain="Bastiani"
/isolate="ATCC VR-322"
/db_xref="taxon:145390"
/note="isolated from fecal specimen of 10-year-old boy
with symptoms of headache, stiff neck, fever"
<1..>177

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 9.5; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 CCCCTGAATCGGCTAATC 19
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Db 172 CCCCTGAATCGGCTAATC 154
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RESULT 41
AF521491
LOCUS AF521491 184 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 13 isolate BE00-82 5' UTR, partial sequence.
ACCESSION AF521491
VERSION AF521491.1 GI:31790833
KEYWORDS
SOURCE Human echovirus 13
ORGANISM Human echovirus 13
Viruses; ssRNA positive-strand viruses, no DNA stage;

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Picornaviridae; Enterovirus.
1 (bases 1 to 184)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
REFERENCE
PUBMED 2 (bases 1 to 184)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source
Location/Qualifiers
1..184
/organism="Human echovirus 13"
/virion
/mol_type="genomic RNA"
/isolate="BE00-82"
/isolation source="patient 82 - zipcode Belgium 8560"
/db_xref="taxon:47501"
<1..>184

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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
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Db 14 CCCCTGAATCGGCTAATC 32
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RESULT 42
AF521433
LOCUS AF521433 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-14 5' UTR, partial sequence.
ACCESSION AF521433
VERSION AF521433.1 GI:31790775
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
REFERENCE
PUBMED 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source
Location/Qualifiers
1..185
/organism="Human echovirus 30"
/virion
/mol_type="genomic RNA"
/isolate="BE00-14"
/isolation source="patient 14 - zipcode Belgium 9310"
/db_xref="taxon:41846"
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5'UTR

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RESULT	44
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LOCUS	185 bp RNA linear VRL 17-JUN-2003
DEFINITION	Human coxsackievirus B5 isolate BE00-1 5' UTR, partial sequence.
ACCESSION	AF521435
VERSION	AF521435.1 GI:31790777
KEYWORDS	
SOURCE	Human coxsackievirus B5
ORGANISM	Human coxsackievirus B5
	Viruses; ssRNA positive-strand viruses, no DNA stage;
	Picornaviridae; Enterovirus.
REFERENCE	1 (bases 1 to 185)
AUTHORS	Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K., Lindberg,A.M. and Van Ranst,M.
TITLE	Molecular typing and epidemiology of enteroviruses identified from

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FEATURES
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   /location/Qualifiers
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   /isolation_source="patient 2 - zipcode Belgium 3001"
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Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Qy 1 CCCCTGAATCGGCTAATC 19
Db 14 CCCCTGAATCGGCTAATC 32

RESULT 46
AF521437
LOCUS AF521437 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-3 5' UTR, partial sequence.
ACCESSION AF521437
VERSION AF521437.1 GI:31790779
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE
2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 14 CCCCTGAATCGGCTAATC 32

RESULT 47
AF521438
LOCUS AF521438 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-4 5' UTR, partial sequence.
ACCESSION AF521438
VERSION AF521438.1 GI:31790780
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE
2 (bases 1 to 185)

Qy 1 CCCCTGAATCGGCTAATC 19
Db 14 CCCCTGAATCGGCTAATC 32

RESULT 48
AF521439
LOCUS AF521439 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-5 5' UTR, partial sequence.
ACCESSION AF521439
VERSION AF521439.1 GI:31790781
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE
2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
KEYWORDS
SOURCE Location/Qualifiers
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/organism="Human echovirus 6"
/mol_type="genomic RNA"
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 CCCCTGAATCGGCTAATC 32

RESULT 49
AF521439
LOCUS AF521439 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-5 5' UTR, partial sequence.
ACCESSION AF521439
VERSION AF521439.1 GI:31790781
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE
2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
KEYWORDS
SOURCE Location/Qualifiers
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Qy 1 CCCCTGAATCGGCTAATC 19
Db 14 CCCCTGAATCGGCTAATC 32

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RESULT 49
AF521440
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human echovirus 30
Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
1. .185
/organism="Human echovirus 30"
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/mol_type="genomic RNA"
/isolate="BE00-6"
/isolation_source="patient 6 - zipcode Belgium 9400"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 14 CCCCTGAATGCGGCTAATC 32

RESULT 50
AF521441
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human echovirus 6
Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
1. .185
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/isolate="BE00-7"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
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DB 14 CCCCTGAATGCGGCTAATC 32

RESULT 51
AF521442
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human echovirus 6
Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
1. .185
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/isolate="BE00-8"
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Query Match 100.0%; Score 19; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
|||
DB 14 CCCCTGAATGCGGCTAATC 32

RESULT 52
AF521443
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human echovirus 6 isolate BE00-10 5' UTR, partial sequence.
185 bp RNA linear VRL 17-JUN-2003

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for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||
DB 14 CCCCTGAATGCGGCTAATC 32

RESULT 51
AF521442
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human echovirus 6 isolate BE00-8 5' UTR, partial sequence.
185 bp RNA linear VRL 17-JUN-2003
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
1. .185
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/isolation_source="patient 8 - zipcode Belgium 3290"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
|||
DB 14 CCCCTGAATGCGGCTAATC 32

RESULT 52
AF521443
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human echovirus 6 isolate BE00-10 5' UTR, partial sequence.
185 bp RNA linear VRL 17-JUN-2003

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ACCESSION AF521443
VERSION AF521443.1 GI:31790785
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source
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/virion
/mol_type="genomic RNA"
/isolate="BE00-10"
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5'UTR
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 53
AF521444
LOCUS Human echovirus 30 isolate BE00-11 5' UTR, partial sequence.
DEFINITION Human echovirus 30 isolate BE00-11 5' UTR, partial sequence.
ACCESSION AF521444
VERSION AF521444.1 GI:31790786
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source
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/virion
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/db_xref="taxon:12062"
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5'UTR
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
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Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 54
AF521445
LOCUS Human echovirus 30 isolate BE00-12 5' UTR, partial sequence.
DEFINITION Human echovirus 30 isolate BE00-12 5' UTR, partial sequence.
ACCESSION AF521445
VERSION AF521445.1 GI:31790787
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 55
AF521446
LOCUS Human echovirus 16 isolate BE00-13 5' UTR, partial sequence.
DEFINITION Human echovirus 16 isolate BE00-13 5' UTR, partial sequence.
ACCESSION AF521446
VERSION AF521446.1 GI:31790788
KEYWORDS
SOURCE Human echovirus 16
ORGANISM Human echovirus 16

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```

Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen,I., Lemey,P., Van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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/virion
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 56
LOCUS
AF521447
DEFINITION
Human echovirus 30 isolate BE00-30 5' UTR, partial sequence.
ACCESSION
AF521447.1 GI:31790789
VERSION
AF521447.1
KEYWORDS
Human echovirus 30
SOURCE
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen,I., Lemey,P., Van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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/db_xref="taxon:41846"

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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 57
LOCUS
AF521448
DEFINITION
Human coxsackievirus B5 isolate BE00-31 5' UTR, partial sequence.
ACCESSION
AF521448
VERSION
AF521448.1 GI:31790790
KEYWORDS
Human coxsackievirus B5
SOURCE
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
1..185
/organism="Human coxsackievirus B5"
/virion
/mol type="genomic RNA"
/isolate="BE00-31"
/isolation_source="patient 31 - zipcode Belgium 9320"
/db_xref="taxon:12074"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 58
LOCUS
AF521449
DEFINITION
Human echovirus 30 isolate BE00-32 5' UTR, partial sequence.
ACCESSION
AF521449
VERSION
AF521449.1 GI:31790791
KEYWORDS
Human echovirus 30
SOURCE
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.

```

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES Location/Qualifiers

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1..185

/organism="Human echovirus 30"

/virion

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/isolate="BE00-32"

/isolation_source="patient 32 - zipcode Belgium 1703"

/db_xref="taxon:41846"

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Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 14 CCCCTGAATCGGCTAATC 32

RESULT 59

AF521450

LOCUS

AF521450 Human echovirus 30 isolate BE00-33 5' UTR, partial sequence. VRL 17-JUN-2003

DEFINITION

AF521450

ACCESSION

VERSION

AF521450.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES Location/Qualifiers

source

1..185

/organism="Human echovirus 30"

/virion

/mol_type="genomic RNA"

/isolate="BE00-33"

/isolation_source="patient 33 - zipcode Belgium 1745"

/db_xref="taxon:41846"

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ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 14 CCCCTGAATCGGCTAATC 32

RESULT 60

AF521451

LOCUS

AF521451 Human echovirus 30 isolate BE00-34 5' UTR, partial sequence. VRL 17-JUN-2003

DEFINITION

AF521451

ACCESSION

VERSION

AF521451.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES Location/Qualifiers

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1..185

/organism="Human echovirus 30"

/virion

/mol_type="genomic RNA"

/isolate="BE00-34"

/isolation_source="patient 34 - zipcode Belgium 1770"

/db_xref="taxon:41846"

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Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 14 CCCCTGAATCGGCTAATC 32

RESULT 61

AF521452

LOCUS

AF521452 Human echovirus 6 isolate BE00-35 5' UTR, partial sequence. VRL 17-JUN-2003

DEFINITION

AF521452

ACCESSION

VERSION

AF521452.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

```

REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
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                /viral
                /mol_type="genomic RNA"
                /isolate="BE00-35"
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                /db_xref="taxon:12062"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 62
AF521453
LOCUS Human echovirus 6 isolate BE00-36 5' UTR, linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-36 5' UTR, partial sequence.
ACCESSION AF521453
VERSION AF521453.1 GI:31790795
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
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                /viral
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 14 CCCCTGAATGCGGCTAATC 32

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RESULT 63
AF521455
LOCUS Human echovirus 6 isolate BE00-39 5' UTR, linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-39 5' UTR, partial sequence.
ACCESSION AF521455
VERSION AF521455.1 GI:31790797
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
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Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 64
AF521456
LOCUS Human echovirus 6 isolate BE00-41 5' UTR, linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-41 5' UTR, partial sequence.
ACCESSION AF521456
VERSION AF521456.1 GI:31790798
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological

```

Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

FEATURES

source
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5'UTR

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19

Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 65

AF521457

LOCUS AF521457 185 bp RNA linear VRL 17-JUN-2003

DEFINITION Human echovirus 6 isolate BE00-42 5' UTR, partial sequence.

ACCESSION AF521457

VERSION AF521457.1 GI:31790799

KEYWORDS

SOURCE Human echovirus 6

ORGANISM

Human echovirus 6

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,

Lindberg, M.A. and Van Ranst, M.

Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,

Lindberg, M.A. and Van Ranst, M.

Direct Submission

TITLE

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

Location/Qualifiers

FEATURES

source

1. .185
/organism="Human echovirus 6"
/virology
/mol_type="genomic RNA"
/isolate="BE00-42"
/isolation_source="patient 42 - zipcode Belgium 3593"
/db_xref="taxon:12062"
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ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19

Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 66

AF521458

LOCUS AF521458 185 bp RNA linear VRL 17-JUN-2003

DEFINITION

Human echovirus 30 isolate BE00-43 5' UTR, partial sequence.

AF521458

VERSION AF521458.1 GI:31790800

KEYWORDS

SOURCE

Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,

Lindberg, M.A. and Van Ranst, M.

Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,

Lindberg, M.A. and Van Ranst, M.

AUTHORS

TITLE

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

Location/Qualifiers

FEATURES

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1. .185
/organism="Human echovirus 30"
/virology
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5'UTR

ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19

Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 67

AF521459

LOCUS

AF521459 185 bp RNA linear VRL 17-JUN-2003

DEFINITION Human echovirus 6 isolate BE00-44 5' UTR, partial sequence.

ACCESSION AF521459

VERSION AF521459.1 GI:31790801

KEYWORDS

SOURCE

Human echovirus 6

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,

Lindberg, M.A. and Van Ranst, M.

Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,

Lindberg, M.A. and Van Ranst, M.

AUTHORS

TITLE

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

Location/Qualifiers

FEATURES

source

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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 68
AF521460 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human coxsackievirus B5 isolate BE00-47 5' UTR, partial sequence.
DEFINITION AF521460
ACCESSION AF521460.1 GI:31790802
VERSION
KEYWORDS
SOURCE
ORGANISM
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 69
AF521461 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-48 5' UTR, partial sequence.
DEFINITION AF521461
ACCESSION AF521461.1 GI:31790803
VERSION
KEYWORDS
SOURCE
ORGANISM
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/isolation_sources="patient 49 - zipcode Belgium 3202"

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5'UTR
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 14 CCCCTGAATCGGCTAATC 32

RESULT 71
AF521463 LOCUS      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION      Human echovirus 6 isolate BE00-50 5' UTR, partial sequence.
ACCESSION      AF521463
VERSION      AF521463.1 GI:31790805
KEYWORDS
SOURCE      Human echovirus 6
ORGANISM      Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE      1 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
AUTHORS      Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
DIRECT SUBMISSION
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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RESULT 73
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DEFINITION      Human echovirus 6 isolate BE00-52 5' UTR, partial sequence.
ACCESSION      AF521465
VERSION      AF521465.1 GI:31790807
KEYWORDS
SOURCE      Human echovirus 6
ORGANISM      Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE      1 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
AUTHORS      Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
DIRECT SUBMISSION
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATCGGCTAATC 32

RESULT 72
AF521464 LOCUS      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION      Human echovirus 13 isolate BE00-51 5' UTR, partial sequence.
ACCESSION      AF521464
VERSION      AF521464.1 GI:31790806
KEYWORDS
SOURCE      Human echovirus 13
ORGANISM      Human echovirus 13
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE      1 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,

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TITLE
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE      2 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
DIRECT SUBMISSION
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATCGGCTAATC 32

RESULT 73
AF521465 LOCUS      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION      Human echovirus 6 isolate BE00-52 5' UTR, partial sequence.
ACCESSION      AF521465
VERSION      AF521465.1 GI:31790807
KEYWORDS
SOURCE      Human echovirus 6
ORGANISM      Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE      1 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE      2 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
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DIRECT SUBMISSION
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 74
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LOCUS Human coxsackievirus B5 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-55 5' UTR, partial sequence.
ACCESSION AF521467
VERSION AF521467.1 GI:31790809
KEYWORDS
SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
JOURNAL
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 75
AF521469
LOCUS Human echovirus 6 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-24 5' UTR, partial sequence.
ACCESSION AF521469
VERSION AF521469.1 GI:31790811
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
JOURNAL
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 76
AF521471
LOCUS Human coxsackievirus B5 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-25 5' UTR, partial sequence.
ACCESSION AF521471
VERSION AF521471.1 GI:31790813
KEYWORDS
SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
JOURNAL
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATCGGCTAATC 32
RESULT 77
AF521473 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human coxsackievirus B5 isolate BE00-29 5' UTR, partial sequence.
DEFINITION
AF521473
ACCESSION
AF521473.1 GI:31790815
KEYWORDS
SOURCE
ORGANISM Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATCGGCTAATC 32
RESULT 78
AF521474 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-16 5' UTR, partial sequence.
DEFINITION
AF521474
ACCESSION
AF521474.1 GI:31790816
KEYWORDS
SOURCE
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATCGGCTAATC 32
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AF521475 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-17 5' UTR, partial sequence.
DEFINITION
AF521475
ACCESSION
AF521475.1 GI:31790817
KEYWORDS
SOURCE
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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RESULT 80
AF521476
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATCGGCTAATC 32
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LOCUS AF521476 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-18 5' UTR, partial sequence.
ACCESSION AF521476
VERSION AF521476.1 GI:31790818
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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AF521477
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DEFINITION Human echovirus 30 isolate BE00-19 5' UTR, partial sequence.
ACCESSION AF521477
VERSION AF521477.1 GI:31790819
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db
RESULT 82
AF521478
LOCUS AF521478 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-20 5' UTR, partial sequence.
ACCESSION AF521478
VERSION AF521478.1 GI:31790820
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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LOCUS AF521480 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-27 5' UTR, partial sequence.
ACCESSION AF521480
VERSION AF521480.1 GI:31790822
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Db
RESULT 82
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LOCUS AF521478 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-20 5' UTR, partial sequence.
ACCESSION AF521478
VERSION AF521478.1 GI:31790820
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
KEYWORDS Location/Qualifiers
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/isolation_source="patient 20 - zipcode Belgium 3294"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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14 CCCCTGAATGGCGCTAATC 32
Db
RESULT 83
AF521480
LOCUS AF521480 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-27 5' UTR, partial sequence.
ACCESSION AF521480
VERSION AF521480.1 GI:31790822
KEYWORDS

SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

J. Med. Virol. 70 (3), 420-429 (2003)
J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

FEATURES
source Location/Qualifiers
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/virion
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/isolation_source="patient 27 - zipcode Belgium 9840"
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Best Local Similarity 100.0%; Pred. No. 9.5;
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Db 14 CCCCTGAATCGGCTAATC 32

RESULT 84
LOCUS AF521481 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 16 isolate BE00-72 5' UTR, partial sequence.
ACCESSION AF521481
VERSION AF521481.1 GI:31790823
KEYWORDS
SOURCE Human echovirus 16
ORGANISM Human echovirus 16
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

J. Med. Virol. 70 (3), 420-429 (2003)
J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

FEATURES
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 14 CCCCTGAATCGGCTAATC 32

RESULT 85
LOCUS AF521482 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 13 isolate BE00-73 5' UTR, partial sequence.
ACCESSION AF521482
VERSION AF521482.1 GI:31790824
KEYWORDS
SOURCE Human echovirus 13
ORGANISM Human echovirus 13
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

J. Med. Virol. 70 (3), 420-429 (2003)
J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

FEATURES
source Location/Qualifiers
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Db 14 CCCCTGAATCGGCTAATC 32

RESULT 86
LOCUS AF521483 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-74 5' UTR, partial sequence.
ACCESSION AF521483
VERSION AF521483.1 GI:31790825
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
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ORIGIN
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QY 1 CCCCTGAATGCGGCTAATC 19
|||||
DB 14 CCCCTGAATGCGGCTAATC 32
RESULT 87
AF521484
LOCUS Human echovirus 16 isolate BE00-75 5' UTR, linear VRL 17-JUN-2003
DEFINITION Human echovirus 16 isolate BE00-75 5' UTR, partial sequence.
ACCESSION AF521484
VERSION AF521484.1 GI:31790826
KEYWORDS
SOURCE Human echovirus 16
ORGANISM Human echovirus 16
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source Location/Qualifiers
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/organism="Human echovirus 16"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCTGAATGCGGCTAATC 19
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DB 14 CCCCTGAATGCGGCTAATC 32
RESULT 88
AF521485
LOCUS Human echovirus 30 isolate BE00-76 5' UTR, linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-76 5' UTR, partial sequence.
ACCESSION AF521485
VERSION AF521485.1 GI:31790827
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source Location/Qualifiers
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ORIGIN
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCTGAATGCGGCTAATC 19
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DB 14 CCCCTGAATGCGGCTAATC 32
RESULT 89
AF521486
LOCUS Human echovirus 30 isolate BE00-77 5' UTR, linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-77 5' UTR, partial sequence.
ACCESSION AF521486
VERSION AF521486.1 GI:31790828
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

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J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 14 CCCCTGAATCGGCTAATC 32

RESULT 90
AF521487
LOCUS
DEFINITION Human echovirus 13 isolate BE00-78 5' UTR, partial sequence.
ACCESSION AF521487
VERSION AF521487.1 GI:31790829
KEYWORDS
SOURCE
ORGANISM Human echovirus 13
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
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Db 14 CCCCTGAATCGGCTAATC 32

J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Db 14 CCCCTGAATCGGCTAATC 32

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14 CCCCTGAATCGGCTAATC 32

RESULT 91
AF521488
LOCUS
DEFINITION Human echovirus 16 isolate BE00-79 5' UTR, partial sequence.
ACCESSION AF521488
VERSION AF521488.1 GI:31790830
KEYWORDS
SOURCE
ORGANISM Human echovirus 16
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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/mol type="genomic RNA"
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Db 14 CCCCTGAATCGGCTAATC 32

RESULT 92
AF521490
LOCUS
DEFINITION Human echovirus 6 isolate BE00-81 5' UTR, partial sequence.
ACCESSION AF521490
VERSION AF521490.1 GI:31790832
KEYWORDS
SOURCE
ORGANISM Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 14 CCCCTGAATCGGCTAATC 32

RESULT 92
AF521490
LOCUS
DEFINITION Human echovirus 6 isolate BE00-81 5' UTR, partial sequence.
ACCESSION AF521490
VERSION AF521490.1 GI:31790832
KEYWORDS
SOURCE
ORGANISM Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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/organism="Human echovirus 6"
/mol type="genomic RNA"
/isolate="BE00-81"
/isolation source="patient 81 - zipcode Belgium 3012"
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 14 CCCCTGAATCGGCTAATC 32

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TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES

source
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ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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14 CCCCTGAATGCGGCTAATC 32
Db

RESULT 93
AF521492

LOCUS Human echovirus 30 isolate BE00-83 5' UTR, partial sequence.
DEFINITION Human echovirus 30 isolate BE00-83 5' UTR, partial sequence.
ACCESSION AF521492
VERSION AF521492.1 GI:31790834

KEYWORDS

SOURCE

ORGANISM Human echovirus 30

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

JOURNAL
PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers

source

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/organism="Human echovirus 30"

/viralion

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCTGAATGCGGCTAATC 19
14 CCCCTGAATGCGGCTAATC 32
Db

RESULT 94

AF521493

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human coxsackievirus B5

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

Direct Submission

TITLE Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers

source

1. .185

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/viralion

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/db_xref="taxon:12074"

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Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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14 CCCCTGAATGCGGCTAATC 32

Db

RESULT 95

AF521494

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human coxsackievirus B5

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

Direct Submission

TITLE Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers

source

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5'UTR
ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19

14 CCCCTGAATGCGGCTAATC 32

Db

RESULT 95

AF521494

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human coxsackievirus B5

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

Direct Submission

TITLE Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human coxsackievirus B5

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

Direct Submission

TITLE Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers

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VERSION AF521498.1 GI:31790840
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Picornaviridae; Enterovirus.

REFERENCE
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)

JOURNAL
PUBMED 12767006
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

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Viruses; ssRNA positive-strand viruses, no DNA stage;
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1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)

JOURNAL
PUBMED 12767006
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

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GenCore version 5.1.7
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C 134	14.8	77.9	7605	7	US-10-437-963-9963	Sequence 9963, Ap	C 207	14.2	74.7	577	4	US-09-925-065A-442742	Sequence 442742, A
C 135	14.8	77.9	7708	7	US-10-437-963-53032	Sequence 53032, A	C 208	14.2	74.7	583	3	US-09-764-877-2972	Sequence 2972, Ap
C 136	14.8	77.9	8279	7	US-10-437-963-14820	Sequence 14820, A	C 209	14.2	74.7	583	6	US-10-242-515-2972	Sequence 2972, Ap
C 137	14.8	77.9	9057	5	US-10-114-170-194	Sequence 194, App	C 210	14.2	74.7	586	7	US-10-021-323-16484	Sequence 16484, A
C 138	14.8	77.9	9807	7	US-10-437-963-48751	Sequence 48751, A	C 211	14.2	74.7	587	4	US-09-925-065A-740537	Sequence 740537, A
C 139	14.8	77.9	9972	6	US-10-085-959-167	Sequence 167, App	212	14.2	74.7	592	4	US-09-925-065A-123839	Sequence 123839, A
C 140	14.8	77.9	9974	6	US-10-238-075-379	Sequence 379, App	C 213	14.2	74.7	592	7	US-10-437-963-54393	Sequence 54393, A
C 141	14.8	77.9	10549	7	US-10-437-963-99620	Sequence 99620, A	C 214	14.2	74.7	597	7	US-10-021-323-5517	Sequence 5517, Ap
C 142	14.8	77.9	11647	7	US-10-437-963-53268	Sequence 53268, A	C 215	14.2	74.7	608	8	US-10-653-047-1622	Sequence 1622, Ap
C 143	14.8	77.9	16929	7	US-10-437-963-43835	Sequence 43835, A	C 216	14.2	74.7	609	4	US-09-925-065A-361614	Sequence 361614, A
C 144	14.8	77.9	25235	6	US-10-164-230-2	Sequence 2, Appl	C 217	14.2	74.7	609	4	US-09-925-065A-361614	Sequence 361614, A
C 145	14.8	77.9	37672	6	US-10-004-113-49	Sequence 49, Appl	C 218	14.2	74.7	618	7	US-10-663-561-17	Sequence 17, Appl
C 146	14.8	77.9	55050	7	US-10-467-752-4	Sequence 4, Appl	C 219	14.2	74.7	628	7	US-10-424-599-14673	Sequence 14673, A
C 147	14.8	77.9	93483	6	US-10-034-650-49	Sequence 49, Appl	C 220	14.2	74.7	648	4	US-09-925-065A-390368	Sequence 390368, A
C 148	14.8	77.9	114280	8	US-10-719-993-6808	Sequence 6808, Ap	C 221	14.2	74.7	649	4	US-09-925-065A-530535	Sequence 530535, A
C 149	14.8	77.9	137935	8	US-10-741-600-17667	Sequence 17667, A	C 222	14.2	74.7	665	4	US-09-925-065A-93414	Sequence 93414, A
C 150	14.8	77.9	160921	5	US-10-087-192-1672	Sequence 1672, Ap	C 223	14.2	74.7	669	4	US-09-925-065A-778189	Sequence 778189, A
C 151	14.8	77.9	161334	5	US-10-087-192-730	Sequence 730, App	C 224	14.2	74.7	683	5	US-10-027-632-141009	Sequence 141009, A
C 152	14.8	77.9	263852	8	US-10-812-232-6	Sequence 6, Appl	C 225	14.2	74.7	683	6	US-10-027-632-141009	Sequence 141009, A
C 153	14.8	77.9	713059	5	US-10-027-632-174581	Sequence 174581, A	C 226	14.2	74.7	721	8	US-10-425-115-126748	Sequence 126748, A
C 154	14.8	77.9	713059	6	US-10-027-632-174581	Sequence 174581, A	C 227	14.2	74.7	771	4	US-09-925-065A-68422	Sequence 68422, A
C 155	14.4	75.8	145	3	US-09-736-457-1724	Sequence 1724, Ap	C 228	14.2	74.7	771	4	US-09-925-065A-68423	Sequence 68423, A
C 156	14.4	75.8	145	3	US-09-902-941-1724	Sequence 1724, Ap	C 229	14.2	74.7	796	5	US-10-027-632-1515	Sequence 1515, Ap
C 157	14.4	75.8	145	3	US-09-849-626-1724	Sequence 1724, Ap	C 230	14.2	74.7	796	5	US-10-027-632-1515	Sequence 1515, Ap
C 158	14.4	75.8	145	5	US-10-017-754-1724	Sequence 1724, Ap	C 231	14.2	74.7	796	6	US-10-027-632-1515	Sequence 1515, Ap
C 159	14.4	75.8	145	6	US-10-113-872-1724	Sequence 1724, Ap	C 232	14.2	74.7	796	6	US-10-027-632-1515	Sequence 1515, Ap
C 160	14.4	75.8	145	6	US-10-283-017-1724	Sequence 1724, Ap	C 233	14.2	74.7	817	5	US-10-066-543-88	Sequence 88, Appl
C 161	14.4	75.8	243	8	US-10-425-115-126798	Sequence 126798, A	C 234	14.2	74.7	864	8	US-10-425-115-165688	Sequence 165688, A
C 162	14.4	75.8	265	7	US-10-437-963-65910	Sequence 65910, A	C 235	14.2	74.7	866	10	US-11-097-143-15347	Sequence 15347, A
C 163	14.4	75.8	360	8	US-10-425-115-114899	Sequence 114899, A	C 236	14.2	74.7	875	7	US-10-424-599-111894	Sequence 111894, A
C 164	14.4	75.8	364	7	US-10-424-599-94676	Sequence 94676, A	C 237	14.2	74.7	926	9	US-10-450-763-29760	Sequence 29760, A
C 165	14.4	75.8	459	4	US-09-925-065A-259192	Sequence 259192, A	C 238	14.2	74.7	939	9	US-10-282-122A-22841	Sequence 22841, A
C 166	14.4	75.8	482	6	US-10-388-934-541	Sequence 541, App	C 239	14.2	74.7	1095	3	US-09-738-626-1791	Sequence 61, Appl
C 167	14.4	75.8	585	4	US-09-925-065A-692313	Sequence 692313, A	C 240	14.2	74.7	1095	3	US-10-029-180-61	Sequence 61, Appl
C 168	14.4	75.8	715	8	US-10-425-115-178047	Sequence 178047, A	C 241	14.2	74.7	1095	9	US-10-952-045-61	Sequence 61, Appl
C 169	14.4	75.8	810	7	US-10-282-122A-12875	Sequence 12875, A	C 242	14.2	74.7	1099	7	US-10-282-122A-10642	Sequence 10642, A

243	14.2	74.7	1104	5	US-10-011-445-38	Sequence 38, Appl	316	14.2	74.7	12908	6	US-10-270-846-1	Sequence 1, Appl
244	14.2	74.7	1135	5	US-10-282-122A-10392	Sequence 1092, A	317	14.2	74.7	16181	8	US-10-723-860-1452	Sequence 1452, Ap
245	14.2	74.7	1221	6	US-10-156-761-6592	Sequence 6592, Ap	318	14.2	74.7	166181	8	US-10-723-860-3281	Sequence 3281, Ap
246	14.2	74.7	1232	7	US-10-424-599-124847	Sequence 124847, A	319	14.2	74.7	201332	7	US-10-322-281-459	Sequence 459, App
247	14.2	74.7	1297	4	US-09-925-065A-31739	Sequence 31739, A	320	14.2	74.7	519599	9	US-10-737-082-73	Sequence 73, Appl
248	14.2	74.7	1297	4	US-09-925-065A-31740	Sequence 31740, A	321	14.2	74.7	519599	9	US-10-765-790-73	Sequence 73, Appl
249	14.2	74.7	1297	5	US-10-027-633-254358	Sequence 254358, A	322	14.2	74.7	78452	8	US-10-719-933-6822	Sequence 6822, Ap
250	14.2	74.7	1297	6	US-10-027-633-254358	Sequence 254358, A	323	14.2	74.7	1601042	5	US-10-027-632-59064	Sequence 59064, A
251	14.2	74.7	1346	4	US-09-925-065A-86422	Sequence 86422, A	324	14.2	74.7	1601042	6	US-10-027-632-59064	Sequence 59064, A
252	14.2	74.7	1346	4	US-09-925-065A-86422	Sequence 86422, A	325	14.2	74.7	2731748	7	US-10-297-465A-1	Sequence 1, Appl
253	14.2	74.7	1400	9	US-10-956-157-5885	Sequence 5885, Ap	326	14.2	74.7	3309400	3	US-09-738-626-1	Sequence 1, Appl
254	14.2	74.7	1477	7	US-10-767-701-13331	Sequence 13331, A	327	14.2	74.7	9025608	6	US-10-156-761-1	Sequence 1, Appl
255	14.2	74.7	1503	3	US-09-974-300-1681	Sequence 1681, Ap	328	14	73.7	14	9	US-10-760-048-3	Sequence 3, Appl
256	14.2	74.7	1612	10	US-11-097-143-3351	Sequence 5351, Ap	329	14	73.7	25	7	US-10-719-956-300284	Sequence 300284, A
257	14.2	74.7	1665	8	US-10-780-002-44	Sequence 44, Appl	330	14	73.7	430	7	US-10-424-599-56607	Sequence 56607, A
258	14.2	74.7	1755	10	US-11-097-143-28781	Sequence 28781, A	331	14	73.7	430	7	US-10-424-599-56607	Sequence 56607, A
259	14.2	74.7	1985	6	US-10-341-961A-241	Sequence 241, App	332	14	73.7	440	7	US-10-424-599-15745	Sequence 15745, A
260	14.2	74.7	2063	5	US-10-011-445-39	Sequence 39, Appl	333	14	73.7	502	7	US-10-424-599-140730	Sequence 140730, A
261	14.2	74.7	2136	3	US-09-938-842A-803	Sequence 803, App	334	14	73.7	591	3	US-09-917-800A-117	Sequence 117, App
262	14.2	74.7	2136	3	US-09-938-842A-803	Sequence 803, App	335	14	73.7	966	7	US-10-282-122A-41793	Sequence 41793, A
263	14.2	74.7	2136	3	US-09-938-842A-803	Sequence 803, App	336	14	73.7	1356	7	US-10-282-122A-31041	Sequence 31041, A
264	14.2	74.7	2217	10	US-11-069-633-13	Sequence 13, Appl	337	14	73.7	1473	3	US-09-815-242-4616	Sequence 4616, Ap
265	14.2	74.7	2255	8	US-09-925-065A-699467	Sequence 699467, A	338	14	73.7	1515	3	US-09-815-242-8594	Sequence 8594, Ap
266	14.2	74.7	2445	7	US-10-425-115-37954	Sequence 37954, A	339	14	73.7	1536	7	US-10-282-122A-8244	Sequence 8244, Ap
267	14.2	74.7	2445	7	US-10-425-115-857	Sequence 857, App	340	14	73.7	1660	9	US-10-764-420-539	Sequence 539, App
268	14.2	74.7	2535	7	US-10-424-599-42490	Sequence 42490, A	341	14	73.7	2465	10	US-11-057-143-24463	Sequence 24463, A
269	14.2	74.7	2592	3	US-09-822-846-444	Sequence 444, App	342	14	73.7	11823	2	US-08-781-986A-136	Sequence 136, App
270	14.2	74.7	2668	10	US-11-097-143-34972	Sequence 34972, A	343	14	73.7	92076	7	US-10-329-624-136	Sequence 136, App
271	14.2	74.7	2907	6	US-10-745-237-317	Sequence 317, App	344	14	73.7	276	7	US-10-322-281-465	Sequence 465, App
272	14.2	74.7	2944	10	US-11-097-143-15346	Sequence 15346, A	345	13.8	72.6	25	7	US-10-719-956-360997	Sequence 360997, A
273	14.2	74.7	3036	7	US-10-425-114-33141	Sequence 33141, A	346	13.8	72.6	25	7	US-10-719-956-360997	Sequence 360997, A
274	14.2	74.7	3080	10	US-11-097-143-4339	Sequence 4339, Ap	347	13.8	72.6	25	8	US-10-719-900-11080	Sequence 11080, A
275	14.2	74.7	3084	10	US-11-097-143-5329	Sequence 5329, Ap	348	13.8	72.6	25	8	US-10-719-900-326601	Sequence 326601, A
276	14.2	74.7	3090	7	US-10-149-310-139	Sequence 139, App	349	13.8	72.6	25	9	US-10-956-157-289056	Sequence 289056, A
277	14.2	74.7	3111	8	US-10-437-963-47196	Sequence 47196, A	350	13.8	72.6	129	6	US-10-392-808-19	Sequence 19, Appl
278	14.2	74.7	3140	8	US-10-425-115-22365	Sequence 22365, A	351	13.8	72.6	142	8	US-10-425-115-56593	Sequence 56593, A
279	14.2	74.7	3165	6	US-10-108-260A-1501	Sequence 1501, Ap	352	13.8	72.6	201	8	US-10-719-993-40233	Sequence 40233, A
280	14.2	74.7	3344	6	US-10-172-118-636	Sequence 636, App	353	13.8	72.6	254	3	US-09-923-876-225	Sequence 225, App
281	14.2	74.7	3344	9	US-10-831-704-73	Sequence 73, Appl	354	13.8	72.6	254	3	US-09-923-876-225	Sequence 225, App
282	14.2	74.7	3344	9	US-10-831-704-73	Sequence 73, Appl	355	13.8	72.6	254	3	US-09-923-876-225	Sequence 225, App
283	14.2	74.7	3344	9	US-10-956-157-650	Sequence 650, App	356	13.8	72.6	270	7	US-10-437-963-43091	Sequence 43091, A
284	14.2	74.7	3505	9	US-10-765-700-63	Sequence 63, Appl	357	13.8	72.6	296	9	US-10-779-543-921	Sequence 921, App
285	14.2	74.7	3810	10	US-11-097-143-3350	Sequence 3350, Ap	358	13.8	72.6	298	3	US-09-294-093B-4990	Sequence 4990, Ap
286	14.2	74.7	3814	10	US-11-097-143-28780	Sequence 28780, A	359	13.8	72.6	303	7	US-10-242-535A-20448	Sequence 20448, A
287	14.2	74.7	4281	10	US-11-097-143-1100	Sequence 1100, Ap	360	13.8	72.6	303	7	US-10-085-783A-20448	Sequence 20448, A
288	14.2	74.7	4519	7	US-10-467-685-33	Sequence 33, Appl	361	13.8	72.6	329	8	US-10-425-115-70161	Sequence 70161, A
289	14.2	74.7	4557	7	US-10-437-963-10388	Sequence 10388, A	362	13.8	72.6	430	3	US-09-764-891-6469	Sequence 6469, Ap
290	14.2	74.7	4667	8	US-10-618-941-52	Sequence 52, Appl	363	13.8	72.6	430	6	US-10-081-414-248	Sequence 248, App
291	14.2	74.7	4771	10	US-11-097-143-8512	Sequence 8512, Ap	364	13.8	72.6	432	3	US-09-783-590-2730	Sequence 2730, App
292	14.2	74.7	5165	8	US-10-425-115-108158	Sequence 108158, A	365	13.8	72.6	442	8	US-10-674-124A-10837	Sequence 10837, A
293	14.2	74.7	5549	6	US-10-354-358-23	Sequence 23, Appl	366	13.8	72.6	462	3	US-09-918-995-831	Sequence 831, App
294	14.2	74.7	5549	9	US-10-490-592-1	Sequence 1, Appl	367	13.8	72.6	462	8	US-10-425-115-70325	Sequence 70325, A
295	14.2	74.7	5677	9	US-10-499-065A-384	Sequence 384, App	368	13.8	72.6	463	3	US-09-786-692-2606	Sequence 2606, Ap
296	14.2	74.7	5687	10	US-11-097-143-1099	Sequence 1099, Ap	369	13.8	72.6	463	5	US-10-040-862-2606	Sequence 2606, Ap
297	14.2	74.7	7005	9	US-10-745-237-85	Sequence 85, Appl	370	13.8	72.6	463	6	US-10-057-475B-2606	Sequence 2606, Ap
298	14.2	74.7	7005	9	US-11-097-143-20273	Sequence 20273, A	371	13.8	72.6	463	6	US-10-154-884B-2606	Sequence 2606, Ap
299	14.2	74.7	8201	6	US-10-240-485-63	Sequence 63, Appl	372	13.8	72.6	463	8	US-10-764-324-2606	Sequence 2606, Ap
300	14.2	74.7	13075	10	US-11-097-143-20272	Sequence 20272, A	373	13.8	72.6	467	8	US-10-674-124A-6772	Sequence 6772, Ap
301	14.2	74.7	16929	3	US-09-984-429-725	Sequence 725, App	374	13.8	72.6	469	3	US-09-918-995-7115	Sequence 7115, Ap
302	14.2	74.7	19802	10	US-11-097-143-16666	Sequence 16666, A	375	13.8	72.6	471	7	US-10-242-535A-43397	Sequence 43397, A
303	14.2	74.7	22111	7	US-10-212-993-11	Sequence 11, Appl	376	13.8	72.6	471	7	US-10-085-783A-43397	Sequence 43397, A
304	14.2	74.7	26933	7	US-10-322-281-541	Sequence 541, App	377	13.8	72.6	493	7	US-10-424-599-113911	Sequence 113911, A
305	14.2	74.7	33993	7	US-10-322-281-238	Sequence 238, App	378	13.8	72.6	500	4	US-09-925-065A-487214	Sequence 487214, A
306	14.2	74.7	4413	8	US-10-741-600-17915	Sequence 17915, A	379	13.8	72.6	508	4	US-09-925-065A-213946	Sequence 213946, A
307	14.2	74.7	4413	8	US-10-719-993-6790	Sequence 6790, Ap	380	13.8	72.6	519	3	US-09-974-300-1460	Sequence 1460, Ap
308	14.2	74.7	69770	6	US-10-292-798-1323	Sequence 1323, Ap	381	13.8	72.6	535	7	US-10-437-963-2381	Sequence 2381, Ap
309	14.2	74.7	96598	3	US-09-997-722-167	Sequence 167, App	382	13.8	72.6	542	8	US-09-925-065A-494214	Sequence 494214, A
310	14.2	74.7	119057	5	US-10-270-875-1	Sequence 1, Appl	383	13.8	72.6	545	8	US-10-425-115-121776	Sequence 121776, A
311	14.2	74.7	129908	5	US-10-270-875-1	Sequence 1, Appl	384	13.8	72.6	547	4	US-09-925-065A-251345	Sequence 251345, A
312	14.2	74.7	129908	5	US-10-270-875-1	Sequence 1, Appl	385	13.8	72.6	548	4	US-09-925-065A-19336	Sequence 19336, A
313	14.2	74.7	129908	5	US-10-270-786-1	Sequence 1, Appl	386	13.8	72.6	548	4	US-09-925-065A-19336	Sequence 19336, A
314	14.2	74.7	129908	5	US-10-270-710-1	Sequence 1, Appl	387	13.8	72.6	548	4	US-09-925-065A-19337	Sequence 19337, A
315	14.2	74.7	129908	5	US-10-270-859-1	Sequence 1, Appl	388	13.8	72.6	548	4	US-09-925-065A-19938	Sequence 19938, A

C 389	13.8	72.6	550	4	US-09-925-065A-374022	Sequence 374022,	462	13.8	72.6	1034	9	US-10-450-763-6388	Sequence 6388, Ap
C 390	13.8	72.6	558	5	US-10-106-698-1875	Sequence 1875, Ap	C 463	13.8	72.6	1053	9	US-10-450-763-28412	Sequence 28412, A
C 391	13.8	72.6	558	5	US-10-487-901-166	Sequence 166, App	C 464	13.8	72.6	1099	7	US-10-282-122A-40036	Sequence 40036, A
C 392	13.8	72.6	560	5	US-10-027-632-142053	Sequence 142053,	C 465	13.8	72.6	1102	3	US-09-974-300-2671	Sequence 2671, Ap
C 393	13.8	72.6	560	6	US-10-027-632-142053	Sequence 142053,	C 466	13.8	72.6	1103	7	US-10-282-122A-37102	Sequence 37102, A
C 394	13.8	72.6	564	4	US-09-925-065A-157232	Sequence 157232,	C 467	13.8	72.6	1155	7	US-10-425-114-14768	Sequence 14768, A
C 395	13.8	72.6	569	4	US-09-925-065A-434002	Sequence 434002,	C 468	13.8	72.6	1218	7	US-10-282-122A-10923	Sequence 10923, A
C 396	13.8	72.6	573	4	US-09-925-065A-274574	Sequence 274574,	C 469	13.8	72.6	1218	7	US-10-282-122A-19434	Sequence 19434, A
C 397	13.8	72.6	576	4	US-09-925-065A-163903	Sequence 163903,	C 470	13.8	72.6	1218	7	US-10-424-599-49257	Sequence 49257, A
C 398	13.8	72.6	581	4	US-09-925-065A-440004	Sequence 440004,	C 471	13.8	72.6	1249	4	US-09-925-065A-715166	Sequence 715166,
C 399	13.8	72.6	581	4	US-09-925-065A-440004	Sequence 440004,	C 472	13.8	72.6	1302	2	US-08-945-038-5	Sequence 5, Appli
C 400	13.8	72.6	581	4	US-09-925-065A-440005	Sequence 440005,	C 473	13.8	72.6	1302	7	US-10-335-977-3738	Sequence 3738, Ap
C 401	13.8	72.6	583	7	US-10-430-201-303	Sequence 303, App	C 474	13.8	72.6	1314	7	US-10-335-977-3738	Sequence 3739, Ap
C 402	13.8	72.6	583	7	US-10-430-201-304	Sequence 304, App	C 475	13.8	72.6	1326	7	US-10-282-122A-23449	Sequence 23449, A
C 403	13.8	72.6	591	4	US-09-925-065A-530517	Sequence 530517,	C 476	13.8	72.6	1335	5	US-10-270-333-80	Sequence 80, Appl
C 404	13.8	72.6	595	7	US-10-767-701-3936	Sequence 3936, Ap	C 477	13.8	72.6	1356	5	US-10-745-237-187	Sequence 187, App
C 405	13.8	72.6	599	9	US-10-972-079-34027	Sequence 34027, A	C 478	13.8	72.6	1356	9	US-10-745-237-187	Sequence 16259, A
C 406	13.8	72.6	599	9	US-10-972-079-34028	Sequence 34028, A	C 479	13.8	72.6	1356	10	US-11-097-143-16259	Sequence 43591, A
C 407	13.8	72.6	599	9	US-10-972-079-34028	Sequence 34028, A	C 480	13.8	72.6	1395	6	US-10-369-493-43591	Sequence 9, Appli
C 408	13.8	72.6	600	9	US-10-956-157-7272	Sequence 7272, Ap	C 481	13.8	72.6	1404	3	US-09-804-551B-9	Sequence 19, Appl
C 409	13.8	72.6	602	4	US-09-925-065A-296301	Sequence 296301,	C 482	13.8	72.6	1451	6	US-10-283-423-19	Sequence 19, Appl
C 410	13.8	72.6	606	4	US-09-925-065A-436624	Sequence 436624,	C 483	13.8	72.6	1451	6	US-10-213-821-19	Sequence 19, Appl
C 411	13.8	72.6	607	4	US-09-925-065A-817644	Sequence 817644,	C 484	13.8	72.6	1451	7	US-10-736-048-19	Sequence 19, Appl
C 412	13.8	72.6	620	4	US-09-925-065A-646609	Sequence 646609,	C 485	13.8	72.6	1452	8	US-10-489-425-59	Sequence 59, Appl
C 413	13.8	72.6	638	5	US-10-027-632-209545	Sequence 209545,	C 486	13.8	72.6	1554	7	US-10-425-114-1363	Sequence 1363, Ap
C 414	13.8	72.6	638	6	US-10-027-632-209545	Sequence 209545,	C 487	13.8	72.6	1575	9	US-10-450-763-7099	Sequence 7099, Ap
C 415	13.8	72.6	644	7	US-10-424-539-91398	Sequence 91398, A	C 488	13.8	72.6	1589	5	US-10-087-192-1751	Sequence 1751, Ap
C 416	13.8	72.6	645	9	US-10-487-901-826	Sequence 826, App	C 489	13.8	72.6	1627	8	US-10-425-115-66930	Sequence 66930, A
C 417	13.8	72.6	646	4	US-09-925-065A-60501	Sequence 60501, A	C 490	13.8	72.6	1630	7	US-10-403-571-89	Sequence 89, Appl
C 418	13.8	72.6	650	5	US-10-027-632-242742	Sequence 242742,	C 491	13.8	72.6	1665	9	US-10-450-763-28569	Sequence 28569, A
C 419	13.8	72.6	650	5	US-10-027-632-242742	Sequence 242742,	C 492	13.8	72.6	1690	8	US-10-425-115-19149	Sequence 19149, A
C 420	13.8	72.6	650	6	US-10-027-632-242742	Sequence 242742,	C 493	13.8	72.6	1755	6	US-10-369-493-24301	Sequence 24301, A
C 421	13.8	72.6	650	6	US-10-027-632-242742	Sequence 242742,	C 494	13.8	72.6	1956	3	US-09-854-761-13883	Sequence 13883, A
C 422	13.8	72.6	654	5	US-10-106-698-1453	Sequence 1453, Ap	C 495	13.8	72.6	2011	3	US-09-825-489-11	Sequence 11, Appl
C 423	13.8	72.6	655	5	US-10-027-632-257853	Sequence 257853,	C 496	13.8	72.6	2103	7	US-10-437-963-31475	Sequence 31475, A
C 424	13.8	72.6	663	5	US-10-027-632-257853	Sequence 257853,	C 497	13.8	72.6	2128	7	US-10-437-963-86520	Sequence 86520, A
C 425	13.8	72.6	663	5	US-10-027-632-230356	Sequence 230356,	C 498	13.8	72.6	2202	4	US-09-925-065A-725286	Sequence 725286,
C 426	13.8	72.6	663	6	US-10-027-632-230356	Sequence 230356,	C 499	13.8	72.6	2202	4	US-09-925-065A-725287	Sequence 725287,
C 427	13.8	72.6	668	4	US-09-925-065A-719915	Sequence 719915,	C 500	13.8	72.6	2210	5	US-10-027-632-263144	Sequence 263144,
C 428	13.8	72.6	668	4	US-09-925-065A-719916	Sequence 719916,							
C 429	13.8	72.6	672	4	US-09-925-065A-922842	Sequence 922842,							
C 430	13.8	72.6	672	4	US-09-925-065A-947181	Sequence 947181,							
C 431	13.8	72.6	672	8	US-10-653-047-6637	Sequence 6637, Ap							
C 432	13.8	72.6	673	3	US-09-764-891-1670	Sequence 1670, Ap							
C 433	13.8	72.6	673	5	US-10-205-428-146	Sequence 146, App							
C 434	13.8	72.6	693	7	US-10-335-977-3737	Sequence 3737, Ap							
C 435	13.8	72.6	704	6	US-10-369-493-37060	Sequence 37060, A							
C 436	13.8	72.6	705	9	US-10-487-901-2979	Sequence 2979, Ap							
C 437	13.8	72.6	719	7	US-10-398-221-1377	Sequence 1377, Ap							
C 438	13.8	72.6	726	5	US-10-027-632-123918	Sequence 123918,							
C 439	13.8	72.6	726	6	US-10-027-632-123918	Sequence 123918,							
C 440	13.8	72.6	735	9	US-10-487-901-6744	Sequence 6744, Ap							
C 441	13.8	72.6	756	8	US-10-425-115-19151	Sequence 19151, A							
C 442	13.8	72.6	756	4	US-09-925-065A-8622	Sequence 8622, Ap							
C 443	13.8	72.6	796	4	US-09-925-065A-8623	Sequence 8623, Ap							
C 444	13.8	72.6	796	4	US-09-925-065A-8624	Sequence 8624, Ap							
C 445	13.8	72.6	846	7	US-10-282-122A-31040	Sequence 31040, A							
C 446	13.8	72.6	872	7	US-10-425-114-44918	Sequence 44918, A							
C 447	13.8	72.6	889	3	US-09-764-891-8360	Sequence 8360, Ap							
C 448	13.8	72.6	889	3	US-09-764-891-8361	Sequence 8361, Ap							
C 449	13.8	72.6	889	5	US-10-205-428-785	Sequence 785, App							
C 450	13.8	72.6	889	5	US-10-205-428-786	Sequence 786, App							
C 451	13.8	72.6	903	5	US-10-027-632-121510	Sequence 121510,							
C 452	13.8	72.6	903	5	US-10-027-632-121511	Sequence 121511,							
C 453	13.8	72.6	903	6	US-10-027-632-121510	Sequence 121510,							
C 454	13.8	72.6	903	6	US-10-027-632-121511	Sequence 121511,							
C 455	13.8	72.6	929	7	US-10-424-599-63357	Sequence 63357, A							
C 456	13.8	72.6	957	5	US-10-027-632-121435	Sequence 121435,							
C 457	13.8	72.6	957	6	US-10-027-632-121435	Sequence 121435,							
C 458	13.8	72.6	969	6	US-10-369-493-24179	Sequence 24179, A							
C 459	13.8	72.6	993	6	US-10-188-359-86	Sequence 86, Appl							
C 460	13.8	72.6	993	9	US-10-956-157-2037	Sequence 2037, Ap							
C 461	13.8	72.6	1031	8	US-10-425-115-73200	Sequence 73200, A							

ALIGNMENTS

RESULT 1
US-10-352-806A-2
; Sequence 2, Application US/10352806A
; Publication No. US20030170617A1
; GENERAL INFORMATION:
; APPLICANT: PASIOSKE, BRITAN L.
; TITLE OF INVENTION: CRUDE BIOLOGICAL DERIVATIVES COMPETENT FOR NUCLEIC ACID
; TITLE OF INVENTION: DETECTION
; FILE REFERENCE: AMBI:0790S
; CURRENT APPLICATION NUMBER: US/10352.806A
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/352,402
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-352-806A-2
Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. NO. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CCCGTAATCGGCTAATC 19

Db 1 CCCCTGAATGCGGCTAATC 19
|||||

RESULT 2

US-10-829-474-1
; Sequence 1, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-1

Query Match 100.0%; Score 19; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||

Db 1 CCCCTGAATGCGGCTAATC 19
|||||

RESULT 3

US-10-829-474-14
; Sequence 14, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-14

Query Match 100.0%; Score 19; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||

Db 1 CCCCTGAATGCGGCTAATC 19
|||||

RESULT 4

US-10-829-474-15
; Sequence 15, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.

; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-15

Query Match 100.0%; Score 19; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||

Db 2 CCCCTGAATGCGGCTAATC 20
|||||

RESULT 5

US-10-829-474-16
; Sequence 16, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-16

Query Match 100.0%; Score 19; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||

Db 7 CCCCTGAATGCGGCTAATC 25
|||||

RESULT 6

US-10-332-123-70
; Sequence 70, Application US/10332123
; Publication No. US20040072239A1
; GENERAL INFORMATION:
; APPLICANT: RENAUD, Patricia
; APPLICANT: GUILLOT, Emmanuelle
; APPLICANT: MABILAT, Claude
; APPLICANT: VACHON, Carole
; APPLICANT: LACROIX, Bruno
; APPLICANT: VERNET, Guy
; APPLICANT: ARMAND, Marie-Astrid
; APPLICANT: LAFFAIRE, Philippe
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
; FILE REFERENCE: 114502
; CURRENT APPLICATION NUMBER: US/10/332,123
; CURRENT FILING DATE: 2003-09-24

; PRIOR APPLICATION NUMBER: PCT/FR01/02191
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: FR00-08839
 ; PRIOR FILING DATE: 2000-07-06
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 70
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Poliovirus type 2
 US-10-332-123-70

Query Match 100.0%; Score 19; DB 7; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
 |||||
 Db 7 CCCCTGAATGGGCTAATC 25

RESULT 7
 US-10-332-123-72
 ; Sequence 72, Application US/10332123
 ; Publication No. US20040072239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RENAUD, Patricia
 ; APPLICANT: GUILLOT, Emmanuelle
 ; APPLICANT: MABILAT, Claude
 ; APPLICANT: VACHON, Carole
 ; APPLICANT: LACROIX, Bruno
 ; APPLICANT: VERNET, Guy
 ; APPLICANT: ARMAND, Marie-Astrid
 ; APPLICANT: LAFFAIRE, Philippe
 ; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
 ; FILE REFERENCE: 114502
 ; CURRENT APPLICATION NUMBER: US/10/332,123
 ; PRIOR FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: PCT/FR01/02191
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR FILING DATE: 2000-07-06
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 72
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Coxsackievirus A21
 US-10-332-123-72

Query Match 100.0%; Score 19; DB 7; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
 |||||
 Db 6 CCCCTGAATGGGCTAATC 24

RESULT 8
 US-10-332-123-74
 ; Sequence 74, Application US/10332123
 ; Publication No. US20040072239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RENAUD, Patricia
 ; APPLICANT: GUILLOT, Emmanuelle
 ; APPLICANT: MABILAT, Claude
 ; APPLICANT: VACHON, Carole
 ; APPLICANT: LACROIX, Bruno
 ; APPLICANT: VERNET, Guy
 ; APPLICANT: ARMAND, Marie-Astrid
 ; APPLICANT: LAFFAIRE, Philippe

; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
 ; FILE REFERENCE: 114502
 ; CURRENT APPLICATION NUMBER: US/10/332,123
 ; CURRENT FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: PCT/FR01/02191
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: FR00-08839
 ; PRIOR FILING DATE: 2000-07-06
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 74
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Echovirus 12
 US-10-332-123-74

Query Match 100.0%; Score 19; DB 7; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
 |||||
 Db 11 CCCCTGAATGGGCTAATC 29

RESULT 9
 US-10-408-519-1
 ; Sequence 1, Application US/10408519
 ; Publication No. US20030228683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Kan-Hung
 ; APPLICANT: Shih, Yu-Hau
 ; APPLICANT: Tsai, Chuan-Mei
 ; APPLICANT: Wang, Yih-Weng
 ; APPLICANT: Hsiao, Hsiung
 ; APPLICANT: Bair, Chi-Horng
 ; APPLICANT: Wang, Shin-Hwan
 ; TITLE OF INVENTION: BIOMOLECULE-BOUND SUBSTRATES
 ; FILE REFERENCE: 12674-002002
 ; CURRENT APPLICATION NUMBER: US/10/408,519
 ; CURRENT FILING DATE: 2003-04-07
 ; PRIOR APPLICATION NUMBER: US 09/522,417
 ; PRIOR FILING DATE: 2000-03-09
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 52
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe from 5' ends of enterovirus genes
 US-10-408-519-1

Query Match 100.0%; Score 19; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
 |||||
 Db 34 CCCCTGAATGGGCTAATC 52

RESULT 10
 US-10-332-123-54
 ; Sequence 54, Application US/10332123
 ; Publication No. US20040072239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RENAUD, Patricia
 ; APPLICANT: GUILLOT, Emmanuelle
 ; APPLICANT: MABILAT, Claude
 ; APPLICANT: VACHON, Carole
 ; APPLICANT: LACROIX, Bruno

```

; APPLICANT: RENAUD, Patricia
; APPLICANT: GUILLOT, Emmanuelle
; APPLICANT: MABILAT, Claude
; APPLICANT: VACHON, Carole
; APPLICANT: LACROIX, Bruno
; APPLICANT: VERNET, Guy
; APPLICANT: ARMAND, Marie-Astrid
; APPLICANT: LAFFAIRE, Philippe
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
; TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
; FILE REFERENCE: 114502
; CURRENT APPLICATION NUMBER: US/10/332,123
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: PCT/FR01/02191
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: P000-08839
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Echovirus (X77708)
US-10-332-123-55

Query Match          100.0%; Score 19; DB 7; Length 525;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGGCTAATC 19
    |||||
Db 391 CCCTGAATCGGCTAATC 409

RESULT 13
US-10-760-048-67
; Sequence 67, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 67
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-760-048-67

Query Match          100.0%; Score 19; DB 9; Length 660;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGGCTAATC 19
    |||||
Db 373 CCCTGAATCGGCTAATC 391

RESULT 14
US-10-614-283-1
; Sequence 1, Application US/10614283
; Publication No. US20050112095A1
; GENERAL INFORMATION:
; APPLICANT: HSU, TSU-AN
; APPLICANT: WU, TZONG-YUAN
; APPLICANT: LEE, JIN-CHING
; TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN
; TITLE OF INVENTION: EXPRESSION

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; FILE REFERENCE: 08842.0002-00000
; CURRENT APPLICATION NUMBER: US/10/614,283
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/394,269
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-10-614-283-1

Query Match      100.0%; Score 19; DB 9; Length 709;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 420 CCCCTGAATCGGCTAATC 438

RESULT 15
US-10-839-729-21
; Sequence 21, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 743
; TYPE: DNA
; ORGANISM: Mahoney Strain Poliovirus Type I
US-10-839-729-21

Query Match      100.0%; Score 19; DB 8; Length 743;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 448 CCCCTGAATCGGCTAATC 466

RESULT 16
US-10-489-136-10
; Sequence 10, Application US/10489136
; Publication No. US20050014150A1
; GENERAL INFORMATION:
; APPLICANT: Atabekov, Joseph
; APPLICANT: Dorokhov, Yuri
; APPLICANT: Skulachev, Maxim
; APPLICANT: Ivanov, Peter
; APPLICANT: Gleba, Yuri
; TITLE OF INVENTION: IDENTIFICATION OF EUKARYOTIC INTERNAL RIBOSOME ENTRY SITE (IRES)
; FILE REFERENCE: 9286.30
; CURRENT APPLICATION NUMBER: US/10/489,136
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: PCT/EP02/09844
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: DE 101 43 238.0
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 10
; LENGTH: 745
; TYPE: DNA
; ORGANISM: Poliovirus
US-10-489-136-10

Query Match      100.0%; Score 19; DB 8; Length 745;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 454 CCCCTGAATCGGCTAATC 472

RESULT 17
US-09-884-586A-3
; Sequence 3, Application US/09884586A
; Publication No. US20030046716A1
; GENERAL INFORMATION:
; APPLICANT: Echelard, Yann
; APPLICANT: Meade, Harry M.
; APPLICANT: Eichner, Wolfram
; APPLICANT: Sommermeyer, Klaus
; TITLE OF INVENTION: TRANSGENICALLY PRODUCED PLATELET DERIVED
; TITLE OF INVENTION: GROWTH FACTOR
; FILE REFERENCE: 10275-120001
; CURRENT APPLICATION NUMBER: US/09/884,586A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/212,406
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-586A-3

Query Match      100.0%; Score 19; DB 3; Length 2076;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 1203 CCCCTGAATCGGCTAATC 1221

RESULT 18
US-10-136-819-7
; Sequence 7, Application US/10136819
; Publication No. US20030166593A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific gen
; FILE REFERENCE: 6627-Pat198
; CURRENT APPLICATION NUMBER: US/10/136,819
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/287,423
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 7399
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-136-819-7

Query Match      100.0%; Score 19; DB 6; Length 7399;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCCCTGAATGCGGCTAATC 19
Db 454 CCCCTGAATGCGGCTAATC 472

RESULT 19
US-10-408-456-4
; Sequence 4, Application US/10408456
; Publication No. US20040013648A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-4

Query Match 100.0%; Score 19; DB 6; Length 10448;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 1427 CCCCTGAATGCGGCTAATC 1445

RESULT 20
US-10-408-456-5
; Sequence 5, Application US/10408456
; Publication No. US20040013648A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 11058
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-5

Query Match 100.0%; Score 19; DB 6; Length 11058;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 3699 CCCCTGAATGCGGCTAATC 3717

RESULT 21
US-10-408-456-34
; Sequence 34, Application US/10408456
; Publication No. US20040013648A1

; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 11622
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-34

Query Match 100.0%; Score 19; DB 6; Length 11622;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 7130 CCCCTGAATGCGGCTAATC 7148

RESULT 22
US-10-873-573-7
; Sequence 7, Application US/10873573
; Publication No. US20050002907A1
; GENERAL INFORMATION:
; APPLICANT: ROHLL, JONATHAN
; APPLICANT: MITRAPHANOUS, KYRI
; APPLICANT: MISKIN, JAMES
; APPLICANT: KINGSMAN, SUSAN MARIE
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 674523-2016.1
; CURRENT APPLICATION NUMBER: US/10/873,573
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 10/408,456
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 11622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-873-573-7

Query Match 100.0%; Score 19; DB 8; Length 11622;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 7130 CCCCTGAATGCGGCTAATC 7148

RESULT 23
US-10-829-474-10
; Sequence 10, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF

APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
OTHER INFORMATION: RNA
US-10-829-474-10

Query Match 94.7%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAATC 19
|||||
Db 1 CCCTGAATGGCGCTAATC 18

RESULT 24

US-10-829-474-11
Sequence 11, Application US/10829474
Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
OTHER INFORMATION: RNA
US-10-829-474-11

Query Match 94.7%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGCGCTAAT 18
|||||
Db 1 CCCTGAATGGCGCTAAT 18

RESULT 25

US-09-802-110B-105
Sequence 105, Application US/09802110B
Publication No. US20030082535A1
GENERAL INFORMATION:
APPLICANT: Leushner, James
Dunn, May
LaCroix, Jean-Michel
TITLE OF INVENTION: METHOD, COMPOSITIONS AND KIT FOR
DETECTION AND IDENTIFICATION OF MICROORGANISMS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson LLP
STREET: PO Box 5068
CITY: Dillon
STATE: CO

COUNTRY: US
ZIP: 80435
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/802,110B
FILING DATE: 07-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-058-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 468-6600
TELEFAX: (970) 468-0104
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-09-802-110B-105

Query Match 94.7%; Score 18; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGCGCTAAT 18
|||||
Db 8 CCCTGAATGGCGCTAAT 25

RESULT 26

US-10-104-611-31
Sequence 31, Application US/10104611
Publication No. US20020160976A1
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,611
FILING DATE: 22-Mar-2002
CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/221,816B
 ; FILING DATE: 01-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7960-030
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 627 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: RNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
 US-10-104-611-31

Query Match 91.6%; Score 17.4; DB 5; Length 627;
 Best Local Similarity 78.9%; Pred. No. 23;
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19
 DB 457 CCCUGAAGCGGCUAAC 475

RESULT 27
 US-10-112-547-31
 ; Sequence 31, Application US/10112547
 ; Publication No. US20020160977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miles, Vincent J.
 ; Mathews, Michael B.
 ; Katze, Michael G.
 ; Witherell, Gary
 ; Watson, Julia C.
 ; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
 ; OF VIRAL REPLICATION
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036/2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/112,547
 ; FILING DATE: 28-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/221,816B
 ; FILING DATE: 01-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7960-030
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 627 base pairs

QY 1 CCCCTGAATGGCGTAATC 19
 DB 457 CCCUGAAGCGGCUAAC 475

; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: RNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
 US-10-112-547-31

Query Match 91.6%; Score 17.4; DB 5; Length 627;
 Best Local Similarity 78.9%; Pred. No. 23;
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19
 DB 457 CCCUGAAGCGGCUAAC 475

RESULT 28
 US-10-112-241-31
 ; Sequence 31, Application US/10112241
 ; Publication No. US20020165194A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miles, Vincent J.
 ; Mathews, Michael B.
 ; Katze, Michael G.
 ; Witherell, Gary
 ; Watson, Julia C.
 ; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
 ; OF VIRAL REPLICATION
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036/2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/112,241
 ; FILING DATE: 28-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/221,816B
 ; FILING DATE: 01-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7960-030
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 627 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: RNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
 US-10-112-241-31

Query Match 91.6%; Score 17.4; DB 5; Length 627;
 Best Local Similarity 78.9%; Pred. No. 23;
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19
 DB 457 CCCUGAAGCGGCUAAC 475

RESULT 29
US-10-109-368-31
; Sequence 31, Application US/10109368
; Publication No. US20030144226A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-109-368-31

Query Match 91.6%; Score 17.4; DB 6; Length 627;
Best Local Similarity 78.9%; Pred. No. 23;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 457 CCCUGAUGCGCUAAC 475

RESULT 30
US-10-867-798-31
; Sequence 31, Application US/10867798
; Publication No. US20040254140A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/867,798
FILING DATE: 14-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/109,368
FILING DATE: 27-Mar-2002
APPLICATION NUMBER: US/08/221,816
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-867-798-31

Query Match 91.6%; Score 17.4; DB 8; Length 627;
Best Local Similarity 78.9%; Pred. No. 23;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 457 CCCUGAUGCGCUAAC 475

RESULT 31
US-10-829-474-6
; Sequence 6, Application US/10829474
; Publication No. US2005023905A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-6

Query Match 89.5%; Score 17; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTAA 17
Db 1 CCCTGAATGCGGCTAA 17

RESULT 32

US-10-829-474-7

; Sequence 7, Application US/10829474

; Publication No. US20050239055A1

; GENERAL INFORMATION:

; APPLICANT: Genetics & IVF

; APPLICANT: MARIANI, Brian D.

; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES

; FILE REFERENCE: 043956-0121

; CURRENT APPLICATION NUMBER: US/10/829,474

; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral

; OTHER INFORMATION: RNA

US-10-829-474-7

Query Match 89.5%; Score 17; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAATC 19
Db 1 CCTGAATGCGGCTAATC 17

RESULT 33

US-10-829-474-9

; Sequence 9, Application US/10829474

; Publication No. US20050239055A1

; GENERAL INFORMATION:

; APPLICANT: Genetics & IVF

; APPLICANT: MARIANI, Brian D.

; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES

; FILE REFERENCE: 043956-0121

; CURRENT APPLICATION NUMBER: US/10/829,474

; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 9

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral

; OTHER INFORMATION: RNA

US-10-829-474-9

Query Match 89.5%; Score 17; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
Db 1 CCCTGAATGCGGCTAAT 17

RESULT 34

US-10-829-474-13

; Sequence 13, Application US/10829474

; Publication No. US20050239055A1

; GENERAL INFORMATION:

; APPLICANT: Genetics & IVF

; APPLICANT: MARIANI, Brian D.

; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES

; FILE REFERENCE: 043956-0121

; CURRENT APPLICATION NUMBER: US/10/829,474

; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral

; OTHER INFORMATION: RNA

US-10-829-474-13

Query Match 89.5%; Score 17; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
Db 1 CCCTGAATGCGGCTAAT 17

RESULT 35

US-10-938-005-2

; Sequence 2, Application US/10938005

; Publication No. US20050048475A1

; GENERAL INFORMATION:

; APPLICANT: Paul, John H.

; APPLICANT: Casper, Erica T.

; APPLICANT: Patterson, Stacey S.

; TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus

; FILE REFERENCE: USF-114XC621

; CURRENT APPLICATION NUMBER: US/10/938,005

; CURRENT FILING DATE: 2004-09-10

; PRIOR APPLICATION NUMBER: 10/857,109

; PRIOR FILING DATE: 2004-05-28

; PRIOR APPLICATION NUMBER: 10/179,082

; PRIOR FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: 60/301,218

; PRIOR FILING DATE: 2001-06-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer Ent P2 (JP128)

US-10-938-005-2

Query Match 89.5%; Score 17; DB 8; Length 24;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTAA 17
Db 8 CCCTGAATGCGGCTAA 24

RESULT 36

US-10-767-701-7988

; Sequence 7988, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 7988
; LENGTH: 1216
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS23029_1
US-10-767-701-7988

Query Match 89.5%; Score 17; DB 7; Length 1216;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
|||||
Db 789 CCCTGAATGCGGCTAAT 805
|||||

RESULT 37

US-10-911-318-74/c
; Sequence 74, Application US/10911318
; Publication No. US20050130186A1
; GENERAL INFORMATION:
; APPLICANT: We Gene Technologies, Inc.
; TITLE OF INVENTION: MENINGITIS DETECTION CHIP AND FABRICATION METHOD THEREOF AND
; TITLE OF INVENTION: METHOD OF DETECTING MENINGITIS AND PRIMER SET FOR MENINGITIS
; TITLE OF INVENTION: DETECTION
; FILE REFERENCE: 12333-US-PA
; CURRENT APPLICATION NUMBER: US/10/911,318
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: TW 92135134
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 74
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-911-318-74

Query Match 86.3%; Score 16.4; DB 9; Length 19;
Best Local Similarity 94.4%; Pred. No. 67;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
|||
Db 19 CCCAGAATGCGGCTAATC 2
|||

RESULT 38

US-10-829-474-12
; Sequence 12, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-12

Query Match 84.2%; Score 16; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18
|||||
Db 1 CCTGAATGCGGCTAAT 16
|||||

RESULT 39

US-10-425-115-173355
; Sequence 173355, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 173355
; LENGTH: 359
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_89681C.1
US-10-425-115-173355

Query Match 84.2%; Score 16; DB 8; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTGAATGCGGCTAATC 19
|||||
Db 173 CTGAATGCGGCTAATC 188
|||||

RESULT 40

US-10-437-963-33914
; Sequence 33914, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33914
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37981C.1
US-10-437-963-33914

Query Match 83.2%; Score 15.8; DB 7; Length 1110;

```
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||
Db 538 CCCCTGAGTGCAGCTAATC 556

RESULT 41
US-10-437-963-33913/c
; Sequence 33913, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33913
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37980C.1
US-10-437-963-33913

Query Match 83.2%; Score 15.8; DB 7; Length 1275;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||
Db 411 CCCCTGAGTGCAGCTAATC 393

RESULT 42
US-10-282-122A-19830/c
; Sequence 19830, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
```

```
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19830
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Enterobacter cloacae
US-10-282-122A-19830

Query Match 83.2%; Score 15.8; DB 7; Length 1326;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||
Db 621 CACCTGAATGCGGCAATC 603

RESULT 43
US-10-179-082A-2
; Sequence 2, Application US/10179082A
; Publication No. US20030186222A1
; GENERAL INFORMATION:
; APPLICANT: Paul, John H
; TITLE OF INVENTION: RAPID DETECTION OF ENTEROVIRUSES IN ENVIRONMENTAL SAMPLES BY NASB
; FILE REFERENCE: USF-114XC6
; CURRENT APPLICATION NUMBER: US/10/179,082A
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Enterovirus sp.
US-10-179-082A-2

Query Match 81.1%; Score 15.4; DB 6; Length 24;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAA 17
||||| ||| |||||
Db 8 CCCCGGAATGCGGCTAA 24

RESULT 44
US-09-974-300-5975
; Sequence 5975, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
```



```
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1549
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1549

Query Match      81.1%; Score 15.4; DB 3; Length 32193;
Best Local Similarity 94.1%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAA 17
    |||||
Db 2571 CCCCTGAATGCGGCTAA 2555

RESULT 50
US-10-092-154-1549/c
; Sequence 1549, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1549
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1549

Query Match      81.1%; Score 15.4; DB 5; Length 32193;
Best Local Similarity 94.1%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAA 17
    |||||
Db 2571 CCCCTGAATGCGGCTAA 2555

RESULT 51
US-10-829-474-8
; Sequence 8, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
;

; Patent No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 90608
; LENGTH: 197
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52831C.1
US-10-424-599-90608

Query Match      78.9%; Score 15; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGCGGCTAATC 19
    |||||
Db 65 TGAATGCGGCTAATC 79

RESULT 53
US-10-425-115-89087
; Sequence 89087, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 89087
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_181248C.1
US-10-425-115-89087

Query Match      78.9%; Score 15; DB 8; Length 415;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAA 17
    |||||
Db 174 CCTGAATGCGGCTAA 188
```

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RESULT 54
US-10-282-122A-20329
; Sequence 20329, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20329
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-282-122A-20329

Query Match 78.9%; Score 15; DB 7; Length 534;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGCGGCTAATC 19
Db 62 TGAATGCGGCTAATC 76

; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 35873
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Chicken 19866894262226_1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(125)
; OTHER INFORMATION: n is any nucleotide
US-10-972-079-35873

Query Match 78.9%; Score 15; DB 9; Length 599;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGCGGCTAATC 19
Db 520 TGAATGCGGCTAATC 534

RESULT 56
US-10-027-632-261979
; Sequence 261979, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261979
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261979

Query Match 78.9%; Score 15; DB 5; Length 969;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTGAATCGGCTAAT 18
Db 81 CTGAATCGGCTAAT 95

RESULT 57
US-10-027-632-261980
; Sequence 261980, Application US/10027632
; Publication No. US20020198371A1
```

```
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
```

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; TITLE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261980
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261980

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```

Query Match      78.9%; Score 15; DB 5; Length 959;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  CTGAATCGGCTAAT 18
          |||||
Db      81  CTGAATCGGCTAAT 95

```

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RESULT 58
US-10-027-632-261981
; Sequence 261981, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261981
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261981

```

Query Match 78.9%; Score 15; DB 5; Length 969;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CTGAATGGGCTAAT 18
      |||||
Db 81 CTGAATGGGCTAAT 95

RESULT 59
US-10-027-632-261979
; Sequence 261979, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261979
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261979

```

```

Query Match          78.9%;   Score 15;   DB 6;   Length 969;
Best Local Similarity 100.0%;   Pred. NO. 5.2e+02;
Matches 15;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      4   CTGAATGCGGCTAAT 18
          |||||
Db      81   CTGAATGCGGCTAAT 95

RESULT 60
US-10-027-632-261980
; Sequence 261980, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMERIZATION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

```

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261980
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261980

Query Match 78.9%; Score 15; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTGAATGCGGCTAAT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 81 CTGAATGCGGCTAAT 95

RESULT 61
US-10-027-632-261981
; Sequence 261981, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261981
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261981

Query Match 78.9%; Score 15; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTGAATGCGGCTAAT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 81 CTGAATGCGGCTAAT 95

RESULT 62
US-10-437-963-38285
; Sequence 38285, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)H
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 38285
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41936C.1
US-10-437-963-38285

Query Match 78.9%; Score 15; DB 7; Length 1458;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAA 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1383 CCTGAATGCGGCTAA 1397

RESULT 63
US-10-450-763-29581
; Sequence 29581, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 29581
; LENGTH: 2780
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1409)..(2074)
; OTHER INFORMATION: 94% homologous to Escherichia coli L-asparagine permease (L-
; OTHER INFORMATION: asparagine transport protein), accession number D90785, Smith-
; OTHER INFORMATION: Waterman Score=1059.
US-10-450-763-29581

Query Match 78.9%; Score 15; DB 9; Length 2780;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 239 TGAATGCGGCTAATC 253

RESULT 64
US-10-719-900-576555
; Sequence 576555, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Wei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808

; OTHER INFORMATION: Located on chromosome 6
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 112298313
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 96016
US-10-674-124A-10734

Query Match 77.9%; Score 14.8; DB 8; Length 295;
Best Local Similarity 88.9%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGGCTAAT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 27 CCCTGAATGCACTAAT 10

RESULT 59

US-10-437-963-66461/c
; Sequence 66461, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 66461
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6740C.1
US-10-437-963-66461

Query Match 77.9%; Score 14.8; DB 7; Length 354;
Best Local Similarity 88.9%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGGCTAAT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 92 CCCTCAATGGGCTAAT 75

RESULT 70

US-10-424-599-81916
; Sequence 81916, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 81916
; LENGTH: 405

; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(405)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_44988C.1
US-10-424-599-81916

Query Match 77.9%; Score 14.8; DB 7; Length 405;
Best Local Similarity 88.9%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGGCTAAT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 380 CCCTGAATGGGCGAAT 397

RESULT 71

US-10-240-425-991/c
; Sequence 991, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 991
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AI922821
US-10-240-425-991

Query Match 77.9%; Score 14.8; DB 7; Length 537;
Best Local Similarity 88.9%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGGCTAATC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 162 CCCTGAACGGCGCTAATC 145

RESULT 72

US-09-925-065A-152961/c
; Sequence 152961, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 152961
 ; LENGTH: 595
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-152961

Query Match 77.9%; Score 14.8; DB 4; Length 595;
 Best Local Similarity 88.9%; Pred. No. 6.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
 |||||
 Db 433 CACTGAATGGGCTAATC 416

RESULT 73
 US-09-925-065A-886331/c
 ; Sequence 886331, Application US/09925065A
 ; Publication No. US20050228172A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 886331
 ; LENGTH: 612
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-886331

Query Match 77.9%; Score 14.8; DB 4; Length 612;
 Best Local Similarity 88.9%; Pred. No. 6.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
 |||||
 Db 445 CCCTGAAGGCGGCTAATC 428

RESULT 74
 US-10-425-115-112682/c
 ; Sequence 112682, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 112682
 ; LENGTH: 635
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_34256C.1
 US-10-425-115-112682

Query Match 77.9%; Score 14.8; DB 8; Length 635;
 Best Local Similarity 88.9%; Pred. No. 6.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
 |||||
 Db 527 CCCTGAAGGCGGCTAACC 510

RESULT 75
 US-10-238-075-384
 ; Sequence 384, Application US/10238075
 ; Publication No. US20030148324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: I.N.S.E.R.M.
 ; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
 ; FILE REFERENCE: B.coli, and biological uses of these polynucleotides and of thei
 ; CURRENT APPLICATION NUMBER: US/10/238,075
 ; CURRENT FILING DATE: 2002-09-10
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 1576
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 384
 ; LENGTH: 708
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 US-10-238-075-384

Query Match 77.9%; Score 14.8; DB 6; Length 708;
 Best Local Similarity 88.9%; Pred. No. 6.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTAAT 18
 |||||
 Db 643 GCCTGAATGCGGCAAT 660

RESULT 76
 US-10-437-963-80579/c
 ; Sequence 80579, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 80579
 ; LENGTH: 714
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa

	US-10-027-963-80579	PAT_MRT4530_8018C.1	Score 14.8; DB 7; Length 714;	Indels 0; Gaps 0;
	Query Match	77.9%;	Best Local Similarity	88.9%; Pred. No. 6.6e+02;
	Matches	16; Conservative	0; Mismatches	2; Indels
	Qy	1 CCCTGAATGCGGCTAAT 18		
	Db	446 CCCTTCRATGCGGCTAAT 429		
	RESULT 77	US-10-027-632-18639	Sequence 18639, Application US/10027632	
		Publication No.	US20020198371A1	
		GENERAL INFORMATION:		
		APPLICANT:	Wang, David C.	
		TITLE OF INVENTION:	Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome	
		FILE REFERENCE:	108827.129	
		CURRENT APPLICATION NUMBER:	US/10/027,632	
		CURRENT FILING DATE:	2002-04-30	
		PRIOR APPLICATION NUMBER:	US 60/218,006	
		PRIOR FILING DATE:	2000-07-12	
		PRIOR APPLICATION NUMBER:	US 60/198,676	
		PRIOR FILING DATE:	2000-04-20	
		PRIOR APPLICATION NUMBER:	US 60/193,483	
		PRIOR FILING DATE:	2000-03-29	
		PRIOR APPLICATION NUMBER:	US 60/185,218	
		PRIOR FILING DATE:	2000-02-24	
		PRIOR APPLICATION NUMBER:	US 60/167,363	
		PRIOR FILING DATE:	1999-11-23	
		PRIOR APPLICATION NUMBER:	US 60/156,358	
		PRIOR FILING DATE:	1999-09-28	
		PRIOR APPLICATION NUMBER:	US 60/146,002	
		PRIOR FILING DATE:	1999-08-09	
		NUMBER OF SEQ ID NOS:	325720	
		SOFTWARE:	FastSeq for Windows Version 4.0	
		SEQ ID NO	18639	
		LENGTH:	719	
		TYPE:	DNA	
		ORGANISM:	Human	
		US-10-027-632-18639		
		Query Match	77.9%;	Score 14.8; DB 5; Length 719;
		Best Local Similarity	88.9%;	Pred. No. 6.6e+02;
		Matches	16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
		Qy	2 CCCTGAATGCGGCTAATC 19	
		Db	160 CCCTGAATGCGGCTGTGC 177	
		RESULT 78	US-10-027-632-18639	
		Sequence 18639, Application US/10027632		
		Publication No.	US20030204075A9	
		GENERAL INFORMATION:		
		APPLICANT:	Wang, David C.	
		TITLE OF INVENTION:	Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome	
		FILE REFERENCE:	108827.129	
		CURRENT APPLICATION NUMBER:	US/10/027,632	
		CURRENT FILING DATE:	2002-04-30	
		PRIOR APPLICATION NUMBER:	US 60/218,006	
		PRIOR FILING DATE:	2000-07-12	
		PRIOR APPLICATION NUMBER:	US 60/198,676	
		PRIOR FILING DATE:	2000-04-20	
		PRIOR APPLICATION NUMBER:	US 60/193,483	
		PRIOR FILING DATE:	2000-03-29	
		PRIOR APPLICATION NUMBER:	US 60/185,218	
		PRIOR FILING DATE:	2000-02-24	
		PRIOR APPLICATION NUMBER:	US 60/167,363	
		PRIOR FILING DATE:	1999-11-23	
		PRIOR APPLICATION NUMBER:	US 60/156,358	
		PRIOR FILING DATE:	1999-09-28	
		PRIOR APPLICATION NUMBER:	US 60/146,002	
		PRIOR FILING DATE:	1999-08-09	
		NUMBER OF SEQ ID NOS:	325720	
		SOFTWARE:	FastSeq for Windows Version 4.0	
		SEQ ID NO	18639	
		LENGTH:	719	
		TYPE:	DNA	
		ORGANISM:	Human	
		US-10-027-632-18639		
		Query Match	77.9%;	Score 14.8; DB 5; Length 719;
		Best Local Similarity	88.9%;	Pred. No. 6.6e+02;
		Matches	16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
		Qy	2 CCCTGAATGCGGCTAATC 19	
		Db	160 CCCTGAATGCGGCTGTGC 177	
		RESULT 79	US-10-006-285-246/c	
		Sequence 246, Application US/10006285		
		Publication No.	US20030165854A1	
		GENERAL INFORMATION:		
		APPLICANT:	Mary Jane Cunningham	
		APPLICANT:	Matthew R. Kaser	
		TITLE OF INVENTION:	MARKER GENES RESPONDING TO TREATMENT WITH TOXINS	
		FILE REFERENCE:	PA-0039 US	
		CURRENT APPLICATION NUMBER:	US/10/006,285	
		CURRENT FILING DATE:	2001-12-05	
		NUMBER OF SEQ ID NOS:	514	
		SOFTWARE:	PERL Program	
		SEQ ID NO	246	
		LENGTH:	767	
		TYPE:	DNA	
		ORGANISM:	Rattus norvegicus	
		FEATURE:		
		NAME/KEY:	misc feature	
		OTHER INFORMATION:	Incyte ID No. US20030165854A1 211417_Rn.1	
		US-10-006-285-246		
		Query Match	77.9%;	Score 14.8; DB 6; Length 767;
		Best Local Similarity	88.9%;	Pred. No. 6.7e+02;
		Matches	16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
		Qy	2 CCCTGAATGCGGCTAATC 19	
		Db	476 CCCTGACTGTGGCTAATC 459	
		RESULT 80	US-10-027-632-154375/c	

;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 154375
;; LENGTH: 810
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-154375

Query Match 77.9%; Score 14.8; DB 5; Length 810;
Best Local Similarity 88.9%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
|||||
Db 575 CCCTGAATGCGGCTAATC 558

RESULT 81

US-10-027-632-154375/c
;; Sequence 154375, Application US/10027632
;; Publication No. US20030204075A9
;; GENERAL INFORMATION:

;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; TITLE OF INVENTION: Polymorphisms in the Human Genome
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 154375
;; LENGTH: 810
;; TYPE: DNA
;; ORGANISM: Human

US-10-027-632-154375

Query Match 77.9%; Score 14.8; DB 6; Length 810;
Best Local Similarity 88.9%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
|||||
Db 575 CCCTGAATGCGGCTAATC 558

RESULT 82

US-11-097-143-12548
;; Sequence 12548, Application US/11097143
;; Publication No. US20050208558A1
;; GENERAL INFORMATION:
;; APPLICANT: Venter, J. Craig
;; APPLICANT: et al.

;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;; FILE REFERENCE: CL000728
;; CURRENT APPLICATION NUMBER: US/11/097,143
;; CURRENT FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12548
;; LENGTH: 925
;; TYPE: DNA
;; ORGANISM: DROSOPHILA

US-11-097-143-12548

Query Match 77.9%; Score 14.8; DB 10; Length 925;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
|||||
Db 675 CTCTGAATGCGGCTAATC 692

RESULT 83

US-10-027-632-262260
;; Sequence 262260, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:

;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; TITLE OF INVENTION: Polymorphisms in the Human Genome
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 262260
;; LENGTH: 926
;; TYPE: DNA
;; ORGANISM: Human

US-10-027-632-262260

Query Match 77.9%; Score 14.8; DB 5; Length 926;

Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | |
Db 311 CCCTGAAAGCGGCTTATC 328

RESULT 84

US-10-027-632-262261
; Sequence 262261, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262261
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-262261

Query Match 77.9%; Score 14.8; DB 5; Length 926;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | |
Db 311 CCCTGAAAGCGGCTTATC 328

RESULT 85

US-10-027-632-262260
; Sequence 262260, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262260
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-262260

Query Match 77.9%; Score 14.8; DB 6; Length 926;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | |
Db 311 CCCTGAAAGCGGCTTATC 328

RESULT 86

US-10-027-632-262261
; Sequence 262261, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262261
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-262261

Query Match 77.9%; Score 14.8; DB 6; Length 926;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | |
Db 311 CCCTGAAAGCGGCTTATC 328

RESULT 87

US-10-437-963-56313/c
; Sequence 56313, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

Qy 1 CCCCTGAATGGGCTAAT 18
Db 1751 CCCCTGAAAGCAGCTAAT 1768

RESULT 91
 US-10-632-257412
 ; Sequence 257412, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 257412
 ; LENGTH: 1929
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-257412

Query Match 77.9%; Score 14.8; DB 6; Length 1929;
 Best Local Similarity 88.9%; Pred. No. 7.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
 |||||
 Db 1751 CCCCTGAATCGGCTAAT 1768

RESULT 92
 US-10-437-963-11634/c
 ; Sequence 11634, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; Title of Invention: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 11634
 ; LENGTH: 2079
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_1783C.1
 US-10-437-963-11634

Query Match 77.9%; Score 14.8; DB 7; Length 2079;
 Best Local Similarity 88.9%; Pred. No. 7.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
 |||||
 Db 530 CCCTTCATCGGCTAAT 513

RESULT 93
 US-10-437-963-81682/c
 ; Sequence 81682, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; Title of Invention: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 81682
 ; LENGTH: 2256
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_81184C.1
 US-10-437-963-81682

Query Match 77.9%; Score 14.8; DB 7; Length 2256;
 Best Local Similarity 88.9%; Pred. No. 7.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
 |||||
 Db 1991 CCCTTCATCGGCTAAT 1974

RESULT 94
 US-10-437-963-68811/c
 ; Sequence 68811, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; Title of Invention: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 68811
 ; LENGTH: 2508
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_6953C.1
 US-10-437-963-68811

Query Match 77.9%; Score 14.8; DB 7; Length 2508;
 Best Local Similarity 88.9%; Pred. No. 7.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18

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Db      806 CCCTCAATGGCGCTAAT 789
|||||
Query Match      77.9%; Score 14.8; DB 7; Length 2525;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 95
US-10-437-963-87164/c
; Sequence 87164, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 87164
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_86136C.1
US-10-437-963-87164

Query Match      77.9%; Score 14.8; DB 7; Length 2525;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 CCCTCAATGGCGCTAAT 18
|||||
Db      1363 CCCTCAATGGCGCTAAT 1346

RESULT 96
US-11-097-143-35308
; Sequence 35308, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35308
; LENGTH: 2534
```

```
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-35308

Query Match      77.9%; Score 14.8; DB 10; Length 2534;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 CCCTCAATGGCGCTAAT 18
|||||
Db      1922 CGCTTGAATGGCGCTAAT 1939

RESULT 97
US-10-437-963-56314/c
; Sequence 56314, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 56314
; LENGTH: 2549
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58237C.1
US-10-437-963-56314

Query Match      77.9%; Score 14.8; DB 7; Length 2549;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 CCCTCAATGGCGCTAAT 18
|||||
Db      2404 CCCTCAATGGCGCTAAT 2387

RESULT 98
US-10-437-963-58797/c
; Sequence 58797, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 58797
; LENGTH: 2775
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:29:05 ; Search time 413.942 Seconds
(Without alignments)
105.905 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19

Sequence: 1 cccctgaatgcggtaatc 19

Scoring table: IDENTITY_NUC

Gapop 10.0., Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database: Published Applications NA New:

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	20	12	US-11-119-231-99
2	19	100.0	25	12	US-11-119-231-98
3	19	100.0	28	12	US-11-119-231-47
4	19	100.0	28	12	US-11-119-231-95
5	19	100.0	72	7	US-10-886-517A-3
6	19	100.0	117	7	US-10-886-517A-41
7	19	100.0	117	7	US-10-886-517A-49
8	19	100.0	117	7	US-10-886-517A-59
9	19	100.0	117	7	US-10-886-517A-61
10	19	100.0	117	7	US-10-886-517A-65
11	19	100.0	118	7	US-10-886-517A-62
12	19	100.0	118	7	US-10-886-517A-63
13	19	100.0	118	7	US-10-886-517A-64
14	19	100.0	118	7	US-10-886-517A-66
15	19	100.0	118	7	US-10-886-517A-67
16	19	100.0	118	7	US-10-886-517A-68
17	19	100.0	118	7	US-10-886-517A-69
18	19	100.0	118	7	US-10-886-517A-70
19	19	100.0	118	7	US-10-886-517A-71
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					Sequence 70, Appl
					Sequence 71, Appl

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22	18	94.7	73	7	US-10-886-517A-5	Sequence 5, Appl
23	18	94.7	73	7	US-10-886-517A-6	Sequence 6, Appl
24	18	94.7	73	7	US-10-886-517A-11	Sequence 11, Appl
25	17.4	91.6	72	7	US-10-886-517A-1	Sequence 1, Appl
26	17.4	91.6	72	7	US-10-886-517A-2	Sequence 2, Appl
27	17.4	91.6	118	7	US-10-886-517A-29	Sequence 29, Appl
28	17.4	91.6	118	7	US-10-886-517A-30	Sequence 30, Appl
29	17.4	91.6	118	7	US-10-886-517A-31	Sequence 31, Appl
30	17.4	91.6	118	7	US-10-886-517A-33	Sequence 33, Appl
31	17.4	91.6	118	7	US-10-886-517A-34	Sequence 34, Appl
32	17.4	91.6	118	7	US-10-886-517A-36	Sequence 36, Appl
33	17.4	91.6	118	7	US-10-886-517A-37	Sequence 37, Appl
34	17.4	91.6	119	7	US-10-886-517A-28	Sequence 28, Appl
35	17.4	91.6	119	7	US-10-886-517A-35	Sequence 35, Appl
36	17.4	91.6	119	7	US-10-886-517A-39	Sequence 39, Appl
37	17.4	91.6	119	7	US-10-886-517A-42	Sequence 42, Appl
38	17.4	91.6	119	7	US-10-886-517A-44	Sequence 44, Appl
39	17.4	91.6	119	7	US-10-886-517A-47	Sequence 47, Appl
40	17.4	91.6	119	7	US-10-886-517A-51	Sequence 51, Appl
41	17.4	91.6	119	7	US-10-886-517A-55	Sequence 55, Appl
42	17.4	91.6	119	7	US-10-886-517A-56	Sequence 56, Appl
43	17.4	91.6	119	7	US-10-886-517A-58	Sequence 58, Appl
44	17.4	91.6	120	7	US-10-886-517A-53	Sequence 60, Appl
45	17.4	91.6	415	7	US-10-886-517A-53	Sequence 53, Appl
46	17.4	91.6	627	12	US-11-195-109-31	Sequence 21, Appl
47	17.4	91.6	627	12	US-11-195-109-31	Sequence 31, Appl
48	17	89.5	73	7	US-10-886-517A-7	Sequence 7, Appl
49	17	89.5	73	7	US-10-886-517A-12	Sequence 12, Appl
50	16.4	86.3	118	7	US-10-886-517A-48	Sequence 48, Appl
51	15.8	83.2	118	7	US-10-886-517A-32	Sequence 32, Appl
52	15.8	83.2	118	7	US-10-886-517A-38	Sequence 38, Appl
53	15.8	83.2	118	7	US-10-886-517A-40	Sequence 40, Appl
54	15.8	83.2	118	7	US-10-886-517A-43	Sequence 43, Appl
55	15.8	83.2	118	7	US-10-886-517A-45	Sequence 45, Appl
56	15.8	83.2	118	7	US-10-886-517A-46	Sequence 46, Appl
57	15.8	83.2	118	7	US-10-886-517A-50	Sequence 50, Appl
58	15.8	83.2	118	7	US-10-886-517A-52	Sequence 52, Appl
59	15.8	83.2	118	7	US-10-886-517A-57	Sequence 57, Appl
60	15.8	83.2	119	7	US-10-886-517A-54	Sequence 54, Appl
61	15.4	81.1	175673	12	US-11-121-086-55	Sequence 55, Appl
62	14.8	77.9	32	8	US-10-939-294A-8358	Sequence 8358, Ap
63	14.8	77.9	32	8	US-10-939-294A-20728	Sequence 20728, A
64	14.8	77.9	48	8	US-10-939-294A-332	Sequence 332, App
65	14.8	77.9	48	8	US-10-939-294A-1620	Sequence 1620, Ap
66	14.8	77.9	64	8	US-10-939-294A-2653	Sequence 2653, Ap
67	14.8	77.9	64	8	US-10-939-294A-2701	Sequence 2701, Ap
68	14.8	77.9	201	8	US-10-939-294A-38314	Sequence 38314, A
69	14.8	77.9	595	6	US-09-925-065A-152961	Sequence 152961, A
70	14.8	77.9	612	6	US-09-925-065A-886331	Sequence 886331, A
71	14.8	77.9	1946	8	US-10-750-185-37125	Sequence 37125, A
72	14.8	77.9	1946	8	US-10-750-185-37125	Sequence 37125, A
73	14.8	77.9	2139	7	US-10-932-182A-80809	Sequence 80809, A
74	14.8	77.9	2139	7	US-10-932-182A-80809	Sequence 80809, A
75	14.8	77.9	137935	8	US-10-935-561-13278	Sequence 13278, A
76	14.8	77.9	150481	12	US-11-112-908-37	Sequence 37, Appl
77	14.8	77.9	171162	12	US-11-112-908-38	Sequence 38, Appl
78	14.8	77.9	358847	7	US-10-330-773-305	Sequence 305, App
79	14.4	75.8	459	6	US-09-925-065A-253192	Sequence 253192, A
80	14.4	75.8	585	6	US-09-925-065A-692313	Sequence 692313, A
81	14.4	75.8	1638	8	US-10-750-185-50407	Sequence 50407, A
82	14.4	75.8	1638	8	US-10-750-185-50407	Sequence 50407, A
83	14.4	75.8	70549	7	US-10-330-773-413	Sequence 413, App
84	14.4	75.8	173120	9	US-11-114-798-55	Sequence 55, Appl
85	14.4	75.8	182303	12	US-11-121-086-45	Sequence 45, Appl
86	14.2	74.7	451	6	US-09-925-065A-84313	Sequence 84313, A
87	14.2	74.7	514	6	US-09-925-065A-740536	Sequence 740536, A
88	14.2	74.7	534	6	US-09-925-065A-84290	Sequence 84290, A
89	14.2	74.7	535	6	US-09-925-065A-380735	Sequence 380735, A
90	14.2	74.7	535	6	US-09-925-065A-605576	Sequence 605576, A
91	14.2	74.7	543	6	US-09-925-065A-153402	Sequence 153402, A
92	14.2	74.7	548	6	US-09-925-065A-430404	Sequence 430404, A
93	14.2	74.7	548	6	US-09-925-065A-430405	Sequence 430405, A

c 94	14.2	74.7	573	9	US-11-096-568A-8418	Sequence 8418, Ap	c 167	13.8	72.6	2202	6	US-09-925-065A-725287	Sequence 725287,
c 95	14.2	74.7	577	6	US-09-925-065A-442742	Sequence 442742,	168	13.8	72.6	2226	7	US-10-932-182A-5447	Sequence 5447, Ap
c 96	14.2	74.7	587	6	US-09-925-065A-740537	Sequence 740537,	169	13.8	72.6	2226	7	US-10-932-182A-5447	Sequence 5447, Ap
c 97	14.2	74.7	592	6	US-09-925-065A-123839	Sequence 123839,	170	13.8	72.6	2266	6	US-09-925-065A-23650	Sequence 23650, A
c 98	14.2	74.7	609	6	US-09-925-065A-361613	Sequence 361613,	c 171	13.8	72.6	2817	6	US-09-925-065A-669289	Sequence 669289,
c 99	14.2	74.7	609	6	US-09-925-065A-361614	Sequence 361614,	c 172	13.8	72.6	2817	6	US-09-925-065A-669290	Sequence 669290,
c 100	14.2	74.7	648	6	US-09-925-065A-390368	Sequence 390368,	c 173	13.8	72.6	3594	8	US-10-775-169-317	Sequence 317, App
c 101	14.2	74.7	649	6	US-09-925-065A-330535	Sequence 330535,	c 174	13.8	72.6	4261	12	US-11-122-329-112	Sequence 112, App
c 102	14.2	74.7	665	6	US-09-925-065A-93414	Sequence 93414, A	c 175	13.8	72.6	5605	9	US-11-253-881-7	Sequence 7, Appli
c 103	14.2	74.7	669	6	US-09-925-065A-778189	Sequence 778189,	c 176	13.8	72.6	34603	7	US-10-330-773-597	Sequence 597, App
c 104	14.2	74.7	771	6	US-09-925-065A-68422	Sequence 68422, A	c 177	13.8	72.6	71594	7	US-10-330-773-738	Sequence 738, App
c 105	14.2	74.7	771	6	US-09-925-065A-68423	Sequence 68423, A	c 178	13.8	72.6	91576	8	US-10-995-561-13461	Sequence 13461, A
c 106	14.2	74.7	771	6	US-09-925-065A-68423	Sequence 68423, A	c 179	13.8	72.6	204803	8	US-10-928-446A-181	Sequence 181, App
c 107	14.2	74.7	1218	8	US-10-454-437-393	Sequence 393, App	c 180	13.8	72.6	91576	8	US-10-928-446A-181	Sequence 181, App
c 108	14.2	74.7	1248	7	US-10-932-182A-39	Sequence 39, Appli	c 181	13.8	72.6	218821	12	US-11-121-086-31	Sequence 31, Appli
c 109	14.2	74.7	1248	7	US-10-932-182A-39	Sequence 39, Appli	c 182	13.8	72.6	348101	7	US-10-330-773-122	Sequence 122, App
c 110	14.2	74.7	1297	6	US-09-925-065A-31739	Sequence 31739, A	c 183	13.8	72.6	645179	8	US-10-995-561-13293	Sequence 13293, A
c 111	14.2	74.7	1297	6	US-09-925-065A-31740	Sequence 31740, A	c 184	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 112	14.2	74.7	1346	6	US-09-925-065A-86422	Sequence 86422, A	c 185	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 113	14.2	74.7	1346	6	US-09-925-065A-86423	Sequence 86423, A	c 186	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 114	14.2	74.7	1672	8	US-10-750-185-59975	Sequence 59975, A	c 187	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 115	14.2	74.7	2217	8	US-09-925-065A-699467	Sequence 699467, A	c 188	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 116	14.2	74.7	2732	8	US-10-750-185-41642	Sequence 41642, A	c 189	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 117	14.2	74.7	2732	8	US-10-750-623-41642	Sequence 41642, A	c 190	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 118	14.2	74.7	2906	8	US-10-750-185-43438	Sequence 43438, A	c 191	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 119	14.2	74.7	2906	8	US-10-750-623-43438	Sequence 43438, A	c 192	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 120	14.2	74.7	3769	8	US-10-750-185-25076	Sequence 25076, A	c 193	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 121	14.2	74.7	3769	8	US-10-750-623-25076	Sequence 25076, A	c 194	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
c 122	14.2	74.7	48986	12	US-11-124-367A-5003	Sequence 5003, Ap	c 195	13.4	70.5	25	7	US-10-932-182A-141074	Sequence 141074,
c 123	14.2	74.7	75782	7	US-10-330-773-772	Sequence 772, App	c 196	13.4	70.5	25	7	US-10-932-182A-141074	Sequence 141074,
c 124	14.2	74.7	146733	7	US-10-330-773-387	Sequence 387, App	c 197	13.4	70.5	25	12	US-11-121-849-465224	Sequence 465224,
c 125	14.2	74.7	156297	12	US-11-121-086-65	Sequence 65, Appli	c 198	13.4	70.5	231	7	US-10-932-182A-80546	Sequence 80546, A
c 126	13.8	72.6	500	6	US-09-925-065A-487214	Sequence 487214,	c 199	13.4	70.5	231	7	US-10-932-182A-80546	Sequence 80546, A
c 127	13.8	72.6	508	6	US-09-925-065A-213946	Sequence 213946,	c 200	13.4	70.5	332	6	US-09-925-065A-160447	Sequence 160447,
c 128	13.8	72.6	542	6	US-09-925-065A-494214	Sequence 494214,	c 201	13.4	70.5	358	6	US-09-925-065A-192455	Sequence 192455,
c 129	13.8	72.6	547	6	US-09-925-065A-251345	Sequence 251345,	c 202	13.4	70.5	376	6	US-09-925-065A-791376	Sequence 791376,
c 130	13.8	72.6	548	6	US-09-925-065A-199315	Sequence 199315, A	c 203	13.4	70.5	379	6	US-09-925-065A-746414	Sequence 746414,
c 131	13.8	72.6	548	6	US-09-925-065A-199316	Sequence 199316, A	c 204	13.4	70.5	380	6	US-09-925-065A-112583	Sequence 112583,
c 132	13.8	72.6	548	6	US-09-925-065A-199317	Sequence 199317, A	c 205	13.4	70.5	417	6	US-09-925-065A-917514	Sequence 917514,
c 133	13.8	72.6	548	6	US-09-925-065A-199318	Sequence 199318, A	c 206	13.4	70.5	417	6	US-09-925-065A-917515	Sequence 917515,
c 134	13.8	72.6	550	6	US-09-925-065A-374022	Sequence 374022,	c 207	13.4	70.5	444	6	US-09-925-065A-426571	Sequence 426571,
c 135	13.8	72.6	564	6	US-09-925-065A-157232	Sequence 157232,	c 208	13.4	70.5	445	6	US-09-925-065A-754703	Sequence 754703,
c 136	13.8	72.6	569	6	US-09-925-065A-434002	Sequence 434002,	c 209	13.4	70.5	451	6	US-10-623-155-211	Sequence 211, App
c 137	13.8	72.6	573	6	US-09-925-065A-274574	Sequence 274574,	c 210	13.4	70.5	471	6	US-09-925-065A-252379	Sequence 252379,
c 138	13.8	72.6	576	6	US-09-925-065A-163903	Sequence 163903,	c 211	13.4	70.5	485	6	US-09-925-065A-852158	Sequence 852158,
c 139	13.8	72.6	581	6	US-09-925-065A-440003	Sequence 440003,	c 212	13.4	70.5	491	6	US-09-925-065A-852912	Sequence 852912,
c 140	13.8	72.6	581	6	US-09-925-065A-440004	Sequence 440004,	c 213	13.4	70.5	528	6	US-09-925-065A-599766	Sequence 599766,
c 141	13.8	72.6	581	6	US-09-925-065A-440005	Sequence 440005,	c 214	13.4	70.5	561	6	US-09-925-065A-437247	Sequence 437247,
c 142	13.8	72.6	591	6	US-09-925-065A-530517	Sequence 530517,	c 215	13.4	70.5	577	6	US-09-925-065A-437902	Sequence 437902,
c 143	13.8	72.6	602	6	US-09-925-065A-296301	Sequence 296301,	c 216	13.4	70.5	577	6	US-09-925-065A-437903	Sequence 437903,
c 144	13.8	72.6	602	6	US-10-750-185-1025	Sequence 1025, Ap	c 217	13.4	70.5	577	6	US-09-925-065A-905595	Sequence 905595,
c 145	13.8	72.6	602	8	US-10-750-185-3591	Sequence 3591, Ap	c 218	13.4	70.5	581	6	US-09-925-065A-873888	Sequence 873888,
c 146	13.8	72.6	602	8	US-10-750-623-1025	Sequence 1025, Ap	c 219	13.4	70.5	581	6	US-09-925-065A-577662	Sequence 577662,
c 147	13.8	72.6	602	8	US-10-750-623-3591	Sequence 3591, Ap	c 220	13.4	70.5	586	6	US-09-925-065A-46637	Sequence 46637, A
c 148	13.8	72.6	606	6	US-09-925-065A-436624	Sequence 436624,	c 221	13.4	70.5	609	6	US-09-925-065A-813607	Sequence 813607,
c 149	13.8	72.6	606	6	US-09-925-065A-817644	Sequence 817644,	c 222	13.4	70.5	618	6	US-09-925-065A-128964	Sequence 128964,
c 150	13.8	72.6	620	6	US-09-925-065A-646609	Sequence 646609,	c 223	13.4	70.5	620	6	US-09-925-065A-492503	Sequence 492503,
c 151	13.8	72.6	646	6	US-09-925-065A-60501	Sequence 60501, A	c 224	13.4	70.5	630	6	US-09-925-065A-427568	Sequence 427568,
c 152	13.8	72.6	668	6	US-09-925-065A-719915	Sequence 719915,	c 225	13.4	70.5	643	6	US-09-925-065A-863074	Sequence 863074,
c 153	13.8	72.6	668	6	US-09-925-065A-719916	Sequence 719916,	c 226	13.4	70.5	643	6	US-09-925-065A-863075	Sequence 863075,
c 154	13.8	72.6	672	6	US-09-925-065A-922842	Sequence 922842,	c 227	13.4	70.5	810	6	US-09-925-065A-23114	Sequence 23114, A
c 155	13.8	72.6	672	6	US-09-925-065A-947181	Sequence 947181,	c 228	13.4	70.5	810	6	US-09-925-065A-23115	Sequence 23115, A
c 156	13.8	72.6	796	6	US-09-925-065A-8622	Sequence 8622, Ap	c 229	13.4	70.5	913	6	US-09-925-065A-709534	Sequence 709534,
c 157	13.8	72.6	796	6	US-09-925-065A-8623	Sequence 8623, Ap	c 230	13.4	70.5	913	6	US-09-925-065A-709535	Sequence 709535,
c 158	13.8	72.6	1249	6	US-09-925-065A-8624	Sequence 8624, Ap	c 231	13.4	70.5	1290	9	US-11-096-568A-10052	Sequence 10052, A
c 159	13.8	72.6	1249	6	US-09-925-065A-715166	Sequence 715166,	c 232	13.4	70.5	1587	7	US-10-932-182A-82256	Sequence 82256, A
c 160	13.8	72.6	1728	8	US-10-750-185-39169	Sequence 39169, A	c 233	13.4	70.5	1587	7	US-10-932-182A-82256	Sequence 82256, A
c 161	13.8	72.6	1728	8	US-10-750-185-39169	Sequence 39169, A	c 234	13.4	70.5	1798	8	US-10-750-185-37688	Sequence 37688, A
c 162	13.8	72.6	1896	8	US-10-750-185-44889	Sequence 44889, A	c 235	13.4	70.5	1798	8	US-10-750-185-37688	Sequence 37688, A
c 163	13.8	72.6	1896	8	US-10-750-623-34989	Sequence 34989, A	c 236	13.4	70.5	3171	7	US-10-501-035-189	Sequence 189, Appli
c 164	13.8	72.6	2186	8	US-10-750-185-36969	Sequence 36969, A	c 237	13.4	70.5	3171	9	US-11-264-046-2	Sequence 2, Appli
c 165	13.8	72.6	2186	8	US-10-750-623-36969	Sequence 36969, A	c 238	13.4	70.5	3205	7	US-10-649-591-7	Sequence 7, Appli
c 166	13.8	72.6	2202	6	US-09-925-065A-725286	Sequence 725286,	c 239	13.4	70.5	3205	12	US-11-090-739-121	Sequence 121, App

240	13.4	70.5	3205	12	US-11-186-284-17	Sequence 17, Appl	C 313	13.2	69.5	533	6	US-09-925-065A-9569	Sequence 9569, Ap
241	13.4	70.5	3781	9	US-11-096-568A-33272	Sequence 33272, A	C 314	13.2	69.5	533	6	US-09-925-065A-9570	Sequence 9570, Ap
242	13.4	70.5	4405	8	US-10-750-185-58770	Sequence 58770, A	C 315	13.2	69.5	536	6	US-09-925-065A-188708	Sequence 188708, Ap
243	13.4	70.5	4405	8	US-10-750-623-58770	Sequence 58770, A	C 316	13.2	69.5	537	6	US-09-925-065A-490381	Sequence 490381, Ap
244	13.4	70.5	12561	12	US-11-124-367A-5110	Sequence 5110, Ap	C 317	13.2	69.5	537	6	US-09-925-065A-490382	Sequence 490382, Ap
245	13.4	70.5	24458	7	US-10-330-773-450	Sequence 450, Appl	C 318	13.2	69.5	537	6	US-09-925-065A-490383	Sequence 490383, Ap
246	13.4	70.5	38059	9	US-11-129-861-4	Sequence 4, Appl	C 319	13.2	69.5	537	6	US-09-925-065A-490384	Sequence 490384, Ap
247	13.4	70.5	69885	8	US-10-995-561-13490	Sequence 13490, A	C 320	13.2	69.5	542	6	US-09-925-065A-40661	Sequence 40661, A
248	13.4	70.5	61331	8	US-10-995-561-13501	Sequence 13501, A	C 321	13.2	69.5	542	6	US-09-925-065A-40662	Sequence 40662, A
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ALIGNMENTS

RESULT 1

US-11-119-231-99
 ; Sequence 99, Application US/11119231
 ; Publication No. US2006000352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lipkin, W. Ian
 ; APPLICANT: Jingyue, Ju
 ; APPLICANT: Thomas, Briesse
 ; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
 ; FILE REFERENCE: 0575/71310-A
 ; CURRENT APPLICATION NUMBER: US/11/119,231
 ; CURRENT FILING DATE: 2005-04-28
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 99
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL SEQUENCE
 ; FEATURE:
 ; OTHER INFORMATION: Forward Primer for Enterovirus A/B 702/495
 US-11-119-231-99

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 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-11-119-231-98
; Sequence 98, Application US/11119231
; Publication No. US20060003352A1
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. Ian
; APPLICANT: Jingyue, Ju
; APPLICANT: Thomas, Briese
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
; FILE REFERENCE: 0575/71310-A
; CURRENT APPLICATION NUMBER: US/11/119,231
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
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; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Forward Primer for Enterovirus A/B 702/495
US-11-119-231-98

Query Match 100.0%; Score 19; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 CCCCTGAATGGCGCTAATC 24

RESULT 3

US-11-119-231-47
; Sequence 47, Application US/11119231
; Publication No. US20060003352A1
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. Ian
; APPLICANT: Jingyue, Ju
; APPLICANT: Thomas, Briese
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
; FILE REFERENCE: 0575/71310-A
; CURRENT APPLICATION NUMBER: US/11/119,231
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
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US-11-119-231-47

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RESULT 4

US-11-119-231-95
; Sequence 95, Application US/11119231
; Publication No. US20060003352A1
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. Ian

; APPLICANT: Jingyue, Ju
; APPLICANT: Thomas, Briese
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
; FILE REFERENCE: 0575/71310-A
; CURRENT APPLICATION NUMBER: US/11/119,231
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 131
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US-11-119-231-95

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Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCCCTGAATGGCGCTAATC 19
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RESULT 5

US-10-886-517A-3
; Sequence 3, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 72
; TYPE: DNA
; ORGANISM: enterovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)...(28)
; OTHER INFORMATION: n = A, T, C or G
US-10-886-517A-3

Query Match 100.0%; Score 19; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.39; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19
Db 41 CCCCTGAATGGCGCTAATC 59

RESULT 6

US-10-886-517A-41
; Sequence 41, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 117
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-41

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 7
US-10-886-517A-49
; Sequence 49, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 117
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-49

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 8
US-10-886-517A-59
; Sequence 59, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 117
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-59

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 9
US-10-886-517A-61
; Sequence 61, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; APPLICANT: LEE, MING-CHOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 117
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-61

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 10
US-10-886-517A-65
; Sequence 65, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 117
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-65

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 11
US-10-886-517A-62
; Sequence 62, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; APPLICANT: LEE, MING-CHOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 117
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-62

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 60 CCCCTGAATCGGCTAATC 78
```

```
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-62

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 12
US-10-886-517A-63
; Sequence 63, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-63

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 13
US-10-886-517A-64
; Sequence 64, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-64

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 14
US-10-886-517A-66
; Sequence 66, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-66

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 15
US-10-886-517A-67
; Sequence 67, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-67

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 16
US-10-886-517A-68
; Sequence 68, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
```

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; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-68

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
Db      61 CCCCTGAATCGGCTAATC 79

RESULT 17
US-10-886-517A-69
; Sequence 69, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-69

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
Db      61 CCCCTGAATCGGCTAATC 79

RESULT 18
US-10-886-517A-70
; Sequence 70, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
```

```
US-10-886-517A-70

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
Db      61 CCCCTGAATCGGCTAATC 79

RESULT 19
US-10-886-517A-71
; Sequence 71, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-71

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
Db      61 CCCCTGAATCGGCTAATC 79

RESULT 20
US-11-155-478A-137
; Sequence 137, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 810
; TYPE: DNA
; ORGANISM: human Enterovirus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(810)
; OTHER INFORMATION: human Enterovirus
; OTHER INFORMATION: strain Coxsakiavirus B1
; OTHER INFORMATION: accession number m16560
US-11-155-478A-137
```

Query Match 100.0%; Score 19; DB 12; Length 810;
 Best Local Similarity 100.0%; Pred. No. 0.51; 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
 |||||
 Db 4 CCCCTGAATGCGGCTAATC 22

RESULT 21

US-10-886-517A-4
 ; Sequence 4, Application US/10886517A
 ; Publication No. US20060008810A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEE, MING-CHOU
 ; APPLICANT: KONG, LILLY
 ; APPLICANT: GROEN, JAN
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 ; FILE REFERENCE: FOCs-003
 ; CURRENT APPLICATION NUMBER: US/10/886,517A
 ; CURRENT FILING DATE: 2004-07-06
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 73
 ; TYPE: DNA
 ; ORGANISM: human rhinovirus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (5)...(5)
 ; OTHER INFORMATION: n = T
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (11)...(11)
 ; OTHER INFORMATION: n = G or C
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (12)...(12)
 ; OTHER INFORMATION: n = C or T
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (14)...(14)
 ; OTHER INFORMATION: n = A, C, or G
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (15)...(15)
 ; OTHER INFORMATION: n = C
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (16)...(16)
 ; OTHER INFORMATION: n = G or A
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (19)...(19)
 ; OTHER INFORMATION: n = T
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (28)...(28)
 ; OTHER INFORMATION: n = A, T, C, or G
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (30)...(30)
 ; OTHER INFORMATION: n = T
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (31)...(31)
 ; OTHER INFORMATION: n = G
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (33)...(33)
 ; OTHER INFORMATION: n = G
 ; FEATURE:

; NAME/KEY: misc feature
 ; LOCATION: (59)...(59)
 ; OTHER INFORMATION: n = C
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (61)...(61)
 ; OTHER INFORMATION: n = T
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (62)...(62)
 ; OTHER INFORMATION: n = A or T
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (65)...(65)
 ; OTHER INFORMATION: n = A or C
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (66)...(66)
 ; OTHER INFORMATION: n = C
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (67)...(67)
 ; OTHER INFORMATION: n = C
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (68)...(68)
 ; OTHER INFORMATION: n = C or T
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (69)...(69)
 ; OTHER INFORMATION: n = A or G
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (70)...(70)
 ; OTHER INFORMATION: n = C or G
 ; US-10-886-517A-4

Query Match 94.7%; Score 18; DB 7; Length 73;
 Best Local Similarity 94.7%; Pred. No. 1.5;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
 |||||
 Db 42 CCCCTGAATGCGGCTAATC 60

RESULT 22

US-10-886-517A-5
 ; Sequence 5, Application US/10886517A
 ; Publication No. US20060008810A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEE, MING-CHOU
 ; APPLICANT: KONG, LILLY
 ; APPLICANT: GROEN, JAN
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 ; FILE REFERENCE: FOCs-003
 ; CURRENT APPLICATION NUMBER: US/10/886,517A
 ; CURRENT FILING DATE: 2004-07-06
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 73
 ; TYPE: DNA
 ; ORGANISM: enterovirus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (5)...(5)
 ; OTHER INFORMATION: n = C or T
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (11)...(11)
 ; OTHER INFORMATION: n = G

```
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)...(12)
OTHER INFORMATION: n = C
FEATURE:
NAME/KEY: misc feature
LOCATION: (14)...(14)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)...(15)
OTHER INFORMATION: n = A
FEATURE:
NAME/KEY: misc feature
LOCATION: (16)...(16)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc feature
LOCATION: (19)...(19)
OTHER INFORMATION: n = A
FEATURE:
NAME/KEY: misc feature
LOCATION: (28)...(28)
OTHER INFORMATION: n = A, T, C or G
FEATURE:
NAME/KEY: misc feature
LOCATION: (30)...(30)
OTHER INFORMATION: n = A or G
FEATURE:
NAME/KEY: misc feature
LOCATION: (31)...(31)
OTHER INFORMATION: n = G or T
FEATURE:
NAME/KEY: misc feature
LOCATION: (33)...(33)
OTHER INFORMATION: n = A or G
FEATURE:
NAME/KEY: misc feature
LOCATION: (59)...(59)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc feature
LOCATION: (61)...(61)
OTHER INFORMATION: n = C
FEATURE:
NAME/KEY: misc feature
LOCATION: (62)...(62)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc feature
LOCATION: (65)...(65)
OTHER INFORMATION: n = C
FEATURE:
NAME/KEY: misc feature
LOCATION: (66)...(66)
OTHER INFORMATION: n = C or T
FEATURE:
NAME/KEY: misc feature
LOCATION: (67)...(67)
OTHER INFORMATION: n = A or G
FEATURE:
NAME/KEY: misc feature
LOCATION: (68)...(68)
OTHER INFORMATION: n = C
FEATURE:
NAME/KEY: misc feature
LOCATION: (69)...(69)
OTHER INFORMATION: n = G
FEATURE:
NAME/KEY: misc feature
LOCATION: (70)...(70)
OTHER INFORMATION: n = G
US-10-896-517A-5
```

```
Query Match 94.7%; Score 18; DB 7; Length 73;
Best Local Similarity 94.7%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 42 CCCCTGAATCGGCTAANC 60

RESULT 23
US-10-886-517A-6
; Sequence 6, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: F0CS-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 73
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: n = A, T, or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)...(11)
; OTHER INFORMATION: n = G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)...(12)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)...(15)
; OTHER INFORMATION: n = T, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)...(16)
; OTHER INFORMATION: n = A, G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)...(28)
; OTHER INFORMATION: n = A, T, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)...(30)
; OTHER INFORMATION: n = A, C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)...(31)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (33)...(33)
; OTHER INFORMATION: n = T, G or C
```

```

;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)...(59)
; OTHER INFORMATION: n = A, C or G
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61)...(61)
; OTHER INFORMATION: n = A, T or G
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)...(62)
; OTHER INFORMATION: n = A or T
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)...(65)
; OTHER INFORMATION: n = A or C
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (66)...(66)
; OTHER INFORMATION: n = A, G, or C
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (67)...(67)
; OTHER INFORMATION: n = T, G or C
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (68)...(68)
; OTHER INFORMATION: n = C or T
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (69)...(69)
; OTHER INFORMATION: n = A or G
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)...(70)
; OTHER INFORMATION: n = C or G
;
US-10-886-517A-6

Query Match      94.7%; Score 18; DB 7; Length 73;
Best Local Similarity 94.7%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 42 CCCCTGAATGCGGCTAANC 60

RESULT 24
US-10-886-517A-11
; Sequence 11, Application US/10886517A
; Publication No. US20060008910A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIROSES
; FILE REFERENCE: F0CS-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 73
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(11)

```

```

;
; OTHER INFORMATION: n = G or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)...(12)
; OTHER INFORMATION: n = C or T
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: n = A, C or G
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)...(15)
; OTHER INFORMATION: n = C
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)...(16)
; OTHER INFORMATION: n = G or A
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: n = T
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)...(28)
; OTHER INFORMATION: n = A, T, C or G
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)...(30)
; OTHER INFORMATION: n = T
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (31)...(31)
; OTHER INFORMATION: n = G
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33)...(33)
; OTHER INFORMATION: n = G
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)...(59)
; OTHER INFORMATION: n = C
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61)...(61)
; OTHER INFORMATION: n = T
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)...(62)
; OTHER INFORMATION: n = A or T
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)...(65)
; OTHER INFORMATION: n = A or C
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (66)...(66)
; OTHER INFORMATION: n = C
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (67)...(67)
; OTHER INFORMATION: n = C
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (68)...(68)
; OTHER INFORMATION: n = C or T
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (69)...(69)
; OTHER INFORMATION: n = A or G
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)...(70)
; OTHER INFORMATION: n = C or G

```

US-10-886-517A-11

Query Match 94.7%; Score 18; DB 7; Length 73;
Best Local Similarity 94.7%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | | |
Db 42 CCCCTGAATGGCGCTAACC 50

RESULT 25

US-10-886-517A-1
; Sequence 1, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 28
; OTHER INFORMATION: n = A,T,C or G
US-10-886-517A-1

Query Match 91.6%; Score 17.4; DB 7; Length 72;
Best Local Similarity 94.7%; Pred. No. 3.2;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | | |
Db 41 CCCCTGAATGGCGCTAACC 59

RESULT 26

US-10-886-517A-2
; Sequence 2, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 72
; TYPE: RNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)...(28)
; OTHER INFORMATION: n = A,U,C or G
US-10-886-517A-2

Query Match 91.6%; Score 17.4; DB 7; Length 72;

Best Local Similarity 78.9%; Pred. No. 3.2;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | | |
Db 41 CCCUGAAGCGGCUACC 59

RESULT 27

US-10-886-517A-29
; Sequence 29, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-29

Query Match 91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | | |
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 28

US-10-886-517A-30
; Sequence 30, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-30

Query Match 91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | | |
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 29

US-10-886-517A-31
; Sequence 31, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:

```
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-31

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 30
US-10-886-517A-33
; Sequence 33, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-33

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 31
US-10-886-517A-34
; Sequence 34, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 118
; TYPE: DNA
US-10-886-517A-34

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 32
US-10-886-517A-36
; Sequence 36, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-36

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 33
US-10-886-517A-37
; Sequence 37, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-37

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 34
US-10-886-517A-38
; Sequence 38, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 118
; TYPE: DNA
US-10-886-517A-38

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79
```

```
US-10-886-517A-28
; Sequence 28, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-28
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      62 CCCCTGAATCGGCTAACC 80

RESULT 35
US-10-886-517A-35
; Sequence 35, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-35
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      62 CCCCTGAATCGGCTAACC 80

US-10-886-517A-39
; Sequence 39, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-39
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      62 CCCCTGAATCGGCTAACC 80

US-10-886-517A-42
; Sequence 42, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-42
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      62 CCCCTGAATCGGCTAACC 80

US-10-886-517A-44
; Sequence 44, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-44
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      62 CCCCTGAATCGGCTAACC 80

US-10-886-517A-46
; Sequence 46, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-46
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      62 CCCCTGAATCGGCTAACC 80
```

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Db      62 CCCCTGAATCGCGCTAACC 80

RESULT 39
US-10-886-517A-47
; Sequence 47, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886.517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-47

Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCCTGAATCGCGCTAATC 19
        |||||
Db      62 CCCCTGAATCGCGCTAACC 80

RESULT 40
US-10-886-517A-51
; Sequence 51, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886.517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-51

Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCCTGAATCGCGCTAATC 19
        |||||
Db      62 CCCCTGAATCGCGCTAACC 80

RESULT 41
US-10-886-517A-55
; Sequence 55, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES

```

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 Db 62 CCCCTGAATCGGCTAACC 80

RESULT 44

US-10-886-517A-60
 ; Sequence 60, Application US/10886517A

; Publication No. US20060008810A1

; GENERAL INFORMATION:

; APPLICANT: LEE, MING-CHOU

; APPLICANT: KONG, LILLY

; APPLICANT: GROEN, JAN

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

; FILE OF INVENTION: RHINOVIRES

; FILE REFERENCE: FOCs-003

; CURRENT APPLICATION NUMBER: US/10/886.517A

; CURRENT FILING DATE: 2004-07-06

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 60

; LENGTH: 119

; TYPE: DNA

; ORGANISM: human rhinovirus

US-10-886-517A-60

Query Match 91.6%; Score 17.4; DB 7; Length 119;

Best Local Similarity 94.7%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 Db 62 CCCCTGAATCGGCTAACC 80

RESULT 45

US-10-886-517A-53

; Sequence 53, Application US/10886517A

; Publication No. US20060008810A1

; GENERAL INFORMATION:

; APPLICANT: LEE, MING-CHOU

; APPLICANT: KONG, LILLY

; APPLICANT: GROEN, JAN

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

; FILE OF INVENTION: RHINOVIRES

; FILE REFERENCE: FOCs-003

; CURRENT APPLICATION NUMBER: US/10/886.517A

; CURRENT FILING DATE: 2004-07-06

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 53

; LENGTH: 120

; TYPE: DNA

; ORGANISM: human rhinovirus

US-10-886-517A-53

Query Match 91.6%; Score 17.4; DB 7; Length 120;

Best Local Similarity 94.7%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 Db 62 CCCCTGAATCGGCTAACC 80

RESULT 46

US-10-886-517A-21

; Sequence 21, Application US/10886517A

; Publication No. US20060008810A1

; GENERAL INFORMATION:

; APPLICANT: LEE, MING-CHOU

; APPLICANT: KONG, LILLY

; APPLICANT: GROEN, JAN

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

; FILE OF INVENTION: RHINOVIRES

; FILE REFERENCE: FOCs-003

; CURRENT APPLICATION NUMBER: US/10/886.517A

; CURRENT FILING DATE: 2004-07-06

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21

; LENGTH: 415

; TYPE: DNA

; ORGANISM: human rhinovirus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1, 23, 24, 25, 26, 27, 28, 29, 31, 32, 33, 34, 35, 44, 60,

; LOCATION: 61, 135, 136, 137, 138, 139, 167, 203, 224, 225, 231, 232,

; LOCATION: 284, 346, 390

; OTHER INFORMATION: n = A, T, C or G

US-10-886-517A-21

Query Match 91.6%; Score 17.4; DB 7; Length 415;

Best Local Similarity 94.7%; Pred. No. 4;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 Db 297 CCCCTGAATCGGCTAACC 315

RESULT 47

US-11-195-109-31

; Sequence 31, Application US/11195109

; Publication No. US20050285975A1

; GENERAL INFORMATION:

; APPLICANT: Miles, Vincent J.

; APPLICANT: Mathews, Michael B.

; APPLICANT: Katze, Michael G.

; APPLICANT: Witherell, Gary

; APPLICANT: Watson, Julia C.

; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION

; TITLE OF INVENTION: OF VIRAL REPLICATION

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/195,109

FILING DATE: 01-Aug-2005

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: US/10/867,798

FILING DATE: 14-Jun-2004

APPLICATION NUMBER: US/10/109,368

FILING DATE: 27-Mar-2002

APPLICATION NUMBER: US/08/221,816

FILING DATE: 01-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Cotuzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7960-030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-11-195-109-31

Query Match 91.6%; Score 17.4; DB 12; Length 627;
Best Local Similarity 78.9%; Pred. No. 4.1;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||:||||:||||:|
Db 457 CCCUGAUGCGCUAAC 475

RESULT 48

US-10-886-517A-7
; Sequence 7, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 73
; TYPE: DNA

ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: n = A, T or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)...(11)
; OTHER INFORMATION: n = G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)...(12)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)...(15)
; OTHER INFORMATION: n = T, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)...(16)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23)...(29)
; OTHER INFORMATION: n = A, C, T or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)...(30)

; OTHER INFORMATION: n = A, C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)...(31)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (33)...(33)
; OTHER INFORMATION: n = T, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52)...(52)
; OTHER INFORMATION: n = A, C, T or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59)...(59)
; OTHER INFORMATION: n = A, G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (61)...(61)
; OTHER INFORMATION: n = A, T or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (62)...(62)
; OTHER INFORMATION: n = A or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65)...(65)
; OTHER INFORMATION: n = A or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (66)...(66)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67)...(67)
; OTHER INFORMATION: n = T, G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (68)...(68)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (69)...(69)
; OTHER INFORMATION: n = A or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70)...(70)
; OTHER INFORMATION: n = C or G
US-10-886-517A-7

Query Match 89.5%; Score 17; DB 7; Length 73;
Best Local Similarity 89.5%; Pred. No. 5.5;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||||:|||||:|
Db 42 CCCCTGAATGGCGCTAATC 60

RESULT 49

US-10-886-517A-12
; Sequence 12, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06

```

; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 73
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)...(11)
; OTHER INFORMATION: n = G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)...(12)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)...(15)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)...(16)
; OTHER INFORMATION: n = G or A
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23)...(29)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)...(30)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)...(31)
; OTHER INFORMATION: n = G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (33)...(33)
; OTHER INFORMATION: n = G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52)...(52)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59)...(59)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (61)...(61)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (62)...(62)
; OTHER INFORMATION: n = A or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65)...(65)
; OTHER INFORMATION: n = A or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (66)...(66)

```

```

; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67)...(67)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (68)...(68)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (69)...(69)
; OTHER INFORMATION: n = A or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70)...(70)
; OTHER INFORMATION: n = C or G
; US-10-886-517A-12

Query Match      89.5%   Score 17;   DB 7;   Length 73;
Best Local Similarity 89.5%;   Pred. No. 5.5;
Matches 17;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      1  CCCCTGAATCGGCTAATC 19
         |||||
Db      42  CCCCTGAATGCGCTAANC 60

RESULT 50
US-10-886-517A-48
; Sequence 48, Application US/10886517A
; Publication No. US200600810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 78, 89, 92, 110
; OTHER INFORMATION: n = A,T,C or G
; US-10-886-517A-48

Query Match      86.3%   Score 16.4;   DB 7;   Length 118;
Best Local Similarity 89.5%;   Pred. No. 13;
Matches 17;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      1  CCCCTGAATCGGCTAATC 19
         |||||
Db      61  CCCCTGAATGCGCTAANC 79

RESULT 51
US-10-886-517A-32
; Sequence 32, Application US/10886517A
; Publication No. US200600810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003

```

```
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-32

Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 52
US-10-886-517A-38
; Sequence 38, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-38

Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 53
US-10-886-517A-40
; Sequence 40, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-40

Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 54
US-10-886-517A-43
; Sequence 43, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-43

Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 55
US-10-886-517A-45
; Sequence 45, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-45

Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 56
US-10-886-517A-46
; Sequence 46, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
```

```

; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: F0CS-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-46

```

```
Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. NO. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGTGGCTAACC 79

```

RESULT 57
US-10-886-517A-50
; Sequence 50, Application US/10886517A
; Publication No. US2006008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPO
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: F0CS-003
; CURRENT APPLICATION NUMBER: US/10/886
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Fast-SEQ for Windows Version
; SEQ ID NO 50
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-50

```

```
Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 CCCCTGAATGCGGCTAATC 19
|||||
D'b 61 CCCCTGAATGTGGCTAAC 79

```

RESULT 58
US-10-886-517A-52
; Sequence 52, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: F0CS-003
; CURRENT APPLICATION NUMBER: US/10/886.517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-52

```

Query Match 83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGCTAATC 19
db 61 CCCTGAATGTGGCTAAC 79

```

RESULT 59
US-10-886-517A-57
; Sequence 57, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886.517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: 92
; OTHER INFORMATION: n = A,T,C or G
US-10-886-517A-57

```

```
Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. NO. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Caps 0;
```

Qy 1 CCCCTGAATGCGGCTAATC 19
|||
Db 61 CCCCTGAATGTGGCTAAC 79

```

RESULT 60
US-10-886-517A-54
; Sequence 54, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: P0CS-003
; CURRENT APPLICATION NUMBER: US/10/886.517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-54

```

Query Match	83.2%	Score 15.8;	DB 7;	Length 119;
Best Local Similarity	89.5%;	Pred. No. 29;		
Matches 17: Conservative	0;	Mismatches	2;	Indels 0;
				Gaps 0;

Qy 1 CCCCTGAATGCGGTAATC 19
||| ||| ||| ||| |||
Db 62 CCCCCGAATGCGGTAACC 80

```
Query Match      77.9%; Score 14.8; DB 8; Length 32;
Best Local Similarity 88.9%; Pred. No. 94;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy	2	CCCTGAATCGGCTAATC	19
Db	23	CCCCGAATCGGCAAATC	6

```
Query Match      77.9%; Score 14.8; DB 8; Length 48;
Best Local Similarity 88.9%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 CCCTGAATGCGGCTAATC 19
 ||| ||| ||| ||| |||
Db 39 CCCCGAATGCGGCAATC 22

RESULT 65
US-10-939-294A-1620
; Sequence 1620, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Turner, Maneesh
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10

; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 3895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1620
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-1620

Query Match 77.9%; Score 14.8; DB 8; Length 48;
Best Local Similarity 88.9%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19
||| ||||| ||||| |||||
Db 26 CCCGAATGCGCAATC 43

RESULT 66
US-10-939-294A-2653/c
; Sequence 2653, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 3895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2653
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-2653

Query Match 77.9%; Score 14.8; DB 8; Length 64;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19
||| ||||| ||||| |||||
Db 39 CCCGAATGCGCAATC 22

RESULT 67
US-10-939-294A-2701/c
; Sequence 2701, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 3895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2701

; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-2701

Query Match 77.9%; Score 14.8; DB 8; Length 64;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19
||| ||||| ||||| |||||
Db 55 CCCGAATGCGCAATC 38

RESULT 68
US-10-995-561-38314/c
; Sequence 38314, Application US/109955561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38314
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-38314

Query Match 77.9%; Score 14.8; DB 8; Length 201;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19
||| ||||| ||||| |||||
Db 21 CCTGAATGCGCCAATC 4

RESULT 69
US-09-925-065A-152961/c
; Sequence 152961, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152961
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-152961

Query Match 77.9%; Score 14.8; DB 6; Length 595;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | | | |
Db 433 CACTGAATGCGGCTAATC 416

RESULT 70

US-09-925-065A-886331/c
; Sequence 886331, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 886331
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-886331

Query Match 77.9%; Score 14.8; DB 6; Length 612;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | | | |
Db 445 CCCTGAAGGCGAGCTAATC 428

RESULT 71

US-10-750-185-37125/c
; Sequence 37125, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37125
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: Bovine 19866880769791
US-10-750-185-37125

Query Match 77.9%; Score 14.8; DB 8; Length 1946;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | | | |
Db 933 CCCTGAATGCGGCTTATC 916

RESULT 72

US-10-750-623-37125/c
; Sequence 37125, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37125
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: Bovine 19866880769791
US-10-750-623-37125

Query Match 77.9%; Score 14.8; DB 8; Length 1946;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | | | |
Db 933 CCCTGAATGCGGCTTATC 916

RESULT 73

US-10-932-182A-80809/c
; Sequence 80809, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80809
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80809

Query Match 77.9%; Score 14.8; DB 7; Length 2139;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | | | |

Db 408 CCTGAATGCGCAGATC 391

RESULT 74

US-10-932-182A-80809/c

; Sequence 80809, Application US/10932182A

; Publication No. US20060046253A1

; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: 030685-043

; CURRENT APPLICATION NUMBER: US/10/932.182A

; CURRENT FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 80809

; LENGTH: 2139

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-10-932-182A-80809

Query Match 77.9%; Score 14.8; DB 7; Length 2139;

Best Local Similarity 88.9%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19

Db 408 CCTGAATGCGCAGATC 391

RESULT 75

US-10-995-561-13278/c

; Sequence 13278, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995.561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13278

; LENGTH: 137935

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(137935)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13278

Query Match 77.9%; Score 14.8; DB 8; Length 137935;

Best Local Similarity 88.9%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19

Db 67700 CCTGAATGCGCCCAATC 67683

RESULT 76

US-11-112-908-37/c

; Sequence 37, Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Davis, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 37

; LENGTH: 150481

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-37

Query Match 77.9%; Score 14.8; DB 12; Length 150481;

Best Local Similarity 88.9%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19

Db 66054 CCTGAATGCGCCCAATC 66037

RESULT 77

US-11-112-908-38/c

; Sequence 38, Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Davis, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 38

; LENGTH: 171162

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-38

Query Match 77.9%; Score 14.8; DB 12; Length 171162;

Best Local Similarity 88.9%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19

Db 138554 CCTGAATGCGCCCAATC 138537

RESULT 78

US-10-330-773-305/c

; Sequence 305, Application US/10330773

; Publication No. US20060040262A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc Malandro

```

; TITLE OF INVENTION: Novel Compositions and Methods. in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 358847
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(358847)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-305

```

```
Query Match          77.9%; Score 14.8; DB 7; Length 358847;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 CCCTGAATGCGGCTAATC 19
|||
Db 252910 CCCTGAATGCACCTAATC 252893

RESULT 79
US-09-925-065A-259192/c
; Sequence 259192, Application US/09925065A
; Publication No. US20040181048A1

```

, APPUNGANI, wang, David G.
, TITLE OF INVENTION: Identification and Mapping of Single
, TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
, FILE REFERENCE: 108827.135
, CURRENT APPLICATION NUMBER: US/09/925,065A
, CURRENT FILING DATE: 2001-08-08
, PRIOR APPLICATION NUMBER: US 60/243,096
, PRIOR FILING DATE: 2000-10-24
, PRIOR APPLICATION NUMBER: US 60/252,147
, PRIOR FILING DATE: 2000-11-20
, PRIOR APPLICATION NUMBER: US 60/250,092
, PRIOR FILING DATE: 2000-11-30
, PRIOR APPLICATION NUMBER: US 60/261,766
, PRIOR FILING DATE: 2001-01-16
, PRIOR APPLICATION NUMBER: US 60/289,846
, PRIOR FILING DATE: 2001-05-09
, NUMBER OF SEQ ID NOS: 957086
, SOFTWARE: FastSEQ for Windows Version 4.0
, SEQ ID NO 259192
, LENGTH: 459

```

US-09-925-065A-259192

```
Query Match          75.8%; Score 14.4; DB 6; Length 459;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 3 CCTGAATGCGGCTAAT 18
Db 45 CCTGAATGCTGCTAAT 30

RESULT 80
US-09-925-065A-692313/c
; Sequence 692313, Application US/09925065A
; Publication No. US20040181048A1

```

; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

```

; CURRENT APPLICATION NUMBER: US/09/925,065A

```

% CURRENT FILING DATE: 2001-08-08
% PRIOR APPLICATION NUMBER: US 60/243,096
% PRIOR FILING DATE: 2000-10-24
% PRIOR APPLICATION NUMBER: US 60/252,147
% PRIOR FILING DATE: 2000-11-20
% PRIOR APPLICATION NUMBER: US 60/250,092
% PRIOR FILING DATE: 2000-11-30
% PRIOR APPLICATION NUMBER: US 60/261,766
% PRIOR FILING DATE: 2001-01-16
% PRIOR APPLICATION NUMBER: US 60/289,846
% PRIOR FILING DATE: 2001-05-09
% NUMBER OF SEQ ID NOS: 957086
% SOFTWARE: fastseq for Windows Version 4.0
% SEQ ID NO 692313
% LENGTH: 585
% TYPE: DNA
% ORGANISM: Homo sapiens
US-09-925-065A-692313

```

```
Query Match          75.8%; Score 14.4; DB 6; Length 585;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 CCCCTGAATGCGGCTA 16
Db 473 CCCCTGAATGCGGCAA 458

```

RESULT 81
US-10-750-185-50407
; Sequence 50407, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFECTION
; FILE REFERENCE: WM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50407
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-50407

```

Query Match 75.8%; Score 14.4; DB 8; Length 1638;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTA 16
|||
Db 1503 CCCCTGAATGCTGCTA 1518

RESULT 82
US-10-750-6233-50407
; Sequence 50407, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom

```
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50407
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Bovine 19866880379342
US-10-750-623-50407

Query Match 75.8%; Score 14.4; DB 8; Length 1638;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTA 16
| | | | | | | | | | | | | | | |
Db 1503 CCCCTGAATGCTGCTA 1518

RESULT 83
US-10-330-773-413/c
; Sequence 413, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: S29452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 70549
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(70549)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-413

Query Match 75.8%; Score 14.4; DB 7; Length 70549;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | |
Db 56056 CTGAATGCAGCTAATC 56041

RESULT 84
US-11-114-798-55
; Sequence 55, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
```

```
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 55
; LENGTH: 173120
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-55

Query Match 75.8%; Score 14.4; DB 9; Length 173120;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTA 16
| | | | | | | | | | | | | | | |
Db 8805 CCCCTGAATGCGGCTA 8820

RESULT 85
US-11-121-086-45
; Sequence 45, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 182303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-45

Query Match 75.8%; Score 14.4; DB 12; Length 182303;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTA 16
| | | | | | | | | | | | | | | |
Db 30719 CCCCTGAATGCGGCTA 30734

RESULT 86
US-09-925-065A-84313/c
; Sequence 84313, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 84313
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-84313

Query Match      74.7%; Score 14.2; DB 6; Length 451;
Best Local Similarity 84.2%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  CCCCTGAATGGCGCTAATC 19
Db      313  CACCTGAATGGCTAGTC 295

RESULT 87
US-09-925-065A-740536
; Sequence 740536, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 740536
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-740536

Query Match      74.7%; Score 14.2; DB 6; Length 514;
Best Local Similarity 84.2%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  CCCCTGAATGGCGCTAATC 19
Db      241  CCCCTGATTACTGCTAATC 259

RESULT 88
US-09-925-065A-84290
; Sequence 84290, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846

```

; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 605576
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-605576

Query Match 74.7%; Score 14.2; DB 6; Length 535;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||| ||||| ||||| |||||
Db 27 CCCCTGAATCGGCTAATC 45

RESULT 91

US-09-925-065A-153402/c
; Sequence 153402, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153402
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-153402

Query Match 74.7%; Score 14.2; DB 6; Length 543;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||| ||||| ||||| |||||
Db 481 CCCAGGAATCGGCTAACC 463

RESULT 92

US-09-925-065A-430404
; Sequence 430404, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 430404
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-430404

Query Match 74.7%; Score 14.2; DB 6; Length 548;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||| ||||| ||||| |||||
Db 31 CCCCTGAATCGGCTAATC 49

RESULT 93

US-09-925-065A-430405
; Sequence 430405, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 430405
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-430405

Query Match 74.7%; Score 14.2; DB 6; Length 548;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||| ||||| ||||| |||||
Db 31 CCCCTGAATCGGCTAATC 49

RESULT 94

US-11-096-568A-8418/c
; Sequence 8418, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01

```

; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8418
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(573)
; OTHER INFORMATION: Ceres S
US-11-096-568A-8418

```

Query Match 74.7%; Score 14.2; DB 9; Length 573;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 1 CCCCTGAATCGGCTAATC 19
Db 405 CCTCTGAATGTGGCTCATC 387

RESULT 95
US-09-925-065A-442742/c
; Sequence 442742, Application US/09925065A
; Publication No. US20040181048A1

```

; CURRENT INVENTION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

```

```

, CURRENT FILING DATE: 2001-08-08
, PRIOR APPLICATION NUMBER: US 60/243,096
, PRIOR FILING DATE: 2000-10-24
, PRIOR APPLICATION NUMBER: US 60/252,147
, PRIOR FILING DATE: 2000-11-20
, PRIOR APPLICATION NUMBER: US 60/250,092
, PRIOR FILING DATE: 2000-11-30
, PRIOR APPLICATION NUMBER: US 60/261,766
, PRIOR FILING DATE: 2001-01-16
, PRIOR APPLICATION NUMBER: US 60/289,846
, PRIOR FILING DATE: 2001-05-09
, NUMBER OF SEQ IDS NOS: 957086
, SOFTWARE: FASTSEQ for Windows Version 4.0
, SEQ ID NO 442742
, LENGTH: 577

```

```

; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-442742

```

Query Match	74.7%	Score 14.2;	DB 6;	Length 577;
Best Local Similarity	84.2%	Pred. No. 2.9e+02;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 60 CCCCCGTATGCGGCTACTC 42

RESULT 96
US-09-925-065A-740537
; Sequence 740537, Application US/09925065A
; Publication No. US20040181048A1

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCES: 108927.135

```

```

; CURRENT APPLICATION NUMBER: US/09/925,065A
;
; CURRENT FILING DATE: 2001-08-08
;
; PRIOR APPLICATION NUMBER: US 60/243,096
;
; PRIOR FILING DATE: 2000-10-24
;
; PRIOR APPLICATION NUMBER: US 60/252,147
;
; PRIOR FILING DATE: 2000-11-20
;

```

; PRIOR FILING DATE: 2000-11-20

```

; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 740537
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-740537

```

Query Match 74.7%; Score 14.2; DB 6; Length 587;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 1 CCCCTGAATCGGCTAATC 19
|||
Db 313 CCCCTGATTACTGCTAATC 331

RESULT 97
US-09-925-065A-123839
; Sequence 123839, Application US/09925065A
; Publication No. US20040181048A1

```

; CURRENT INVENTION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

```

```

, , CURRENT FILING DATE: 2001-08-08
, , PRIOR APPLICATION NUMBER: US 60/243,096
, , PRIOR FILING DATE: 2000-10-24
, , PRIOR APPLICATION NUMBER: US 60/252,147
, , PRIOR FILING DATE: 2000-11-20
, , PRIOR APPLICATION NUMBER: US 60/250,092
, , PRIOR FILING DATE: 2000-11-30
, , PRIOR APPLICATION NUMBER: US 60/261,766
, , PRIOR FILING DATE: 2001-01-16
, , PRIOR APPLICATION NUMBER: US 60/289,846
, , PRIOR FILING DATE: 2001-05-09
, , NUMBER OF SEQ ID NOS: 957086
, , SOFTWARE: FastSEQ for Windows Version 4.0
, , SEQ ID NO 123839
, , LENGTH: 592

```

TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-123839

Query Match 74.7%; Score 14.2; DB 6; Length 592;
Best Local Similarity 84.2%; Pred. NO. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 1 CCCCTGAATGCGGCTAATC 19
|||
Db 192 CCCCTGAATCCTGGTAATC 210

RESULT 98
US-09-925-065A-361613/c
; Sequence 361613, Application US/09925065A
; Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096

```
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361613
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-361613
```

```
Query Match 74.7%; Score 14.2; DB 6; Length 609;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 221 CCCCTGAATCGACTACTC 203
```

RESULT 99

```
US-09-925-065A-361614/c
; Sequence 361614, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361614
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-361614
```

```
Query Match 74.7%; Score 14.2; DB 6; Length 609;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 221 CCCCTGAATCGACTACTC 203
```

RESULT 100

```
US-09-925-065A-390368/c
; Sequence 390368, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390368
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-390368
```

```
Query Match 74.7%; Score 14.2; DB 6; Length 648;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 232 CCCAGAAAGCGTTAATC 214
```

```
Search completed: March 9, 2006, 01:18:52
Job time : 428.942 secs
```

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:12:30 ; Search time 1492.15 Seconds
(without alignments)
595.756 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19

Sequence: 1 ccctggaatggcgtaatc 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	94.7	543	6	CA083939 SCEPAM205
C 2	18	94.7	613	6	CA138671
C 3	18	94.7	631	6	CA187742
C 4	18	94.7	656	6	CA104389
C 5	18	94.7	904	6	CA085581
C 6	17.4	91.6	589	7	CV608160 L AL-aa0
C 7	17	89.5	320	2	BG933318 WSL_3_H09
C 8	17	89.5	392	6	CP771460 DSBFI_19
C 9	17	89.5	554	2	BG933077 WSL_3_H09
C 10	17	89.5	590	6	CA104476 SCJFHR103
C 11	17	89.5	645	6	CA429058 ETH1_2_B0
C 12	17	89.5	696	1	AW680038 WSL_3_H09
C 13	16.4	86.3	118	10	C2476191 d08347-5p
C 14	16.4	86.3	533	9	BH899915 Ots00982
C 15	16.4	86.3	569	6	CA190230
C 16	16.4	86.3	655	8	CA10223 JGI_XZT32
C 17	16.4	86.3	690	6	CA125729 SCRLRL11
C 18	16.4	86.3	760	5	BX867956 BX867956
C 19	16.4	86.3	800	10	AG218963 Drosophil
C 20	16.4	86.3	1104	8	DR126636 49290467
C 21	16	84.2	485	9	CC751821 ZMMBB013
C 22	16	84.2	527	10	CL414924 ZMMBB042

23	16	84.2	547	9	BZ718658
24	16	84.2	595	8	CX698830
25	16	84.2	596	8	CX683834 ydb82g09.
26	16	84.2	632	8	CX691884 ydb36h05.
27	16	84.2	675	8	CX557631 yda39d02.
28	16	84.2	676	8	CX692600 yde83d07.
C 29	16	84.2	784	9	CC751823
C 30	16	84.2	787	9	CC753964
C 31	16	84.2	809	6	CB945315
C 32	16	84.2	838	10	CG038424
33	15.8	83.2	262	2	BE000416
34	15.8	83.2	300	1	AU176457
35	15.8	83.2	361	2	BE405912
36	15.8	83.2	417	3	BJ468982
37	15.8	83.2	422	3	BJ473149
38	15.8	83.2	431	5	BU971174
39	15.8	83.2	443	9	AZ233765
40	15.8	83.2	456	8	DN183928
41	15.8	83.2	463	1	AV932335
42	15.8	83.2	472	6	CA657673
C 43	15.8	83.2	487	1	AV774105
C 44	15.8	83.2	494	9	CC472389
45	15.8	83.2	511	8	DN183756
46	15.8	83.2	513	1	AW585068
C 47	15.8	83.2	525	6	CB884273
C 48	15.8	83.2	525	6	CD026506
C 49	15.8	83.2	544	3	BJ469271
C 50	15.8	83.2	545	11	FR0012843
51	15.8	83.2	546	3	BJ479716
52	15.8	83.2	564	7	CF992378
53	15.8	83.2	564	7	CK037253
54	15.8	83.2	568	1	AU249544
55	15.8	83.2	569	10	CE815985
56	15.8	83.2	570	6	CB212741
57	15.8	83.2	572	2	BE403208
58	15.8	83.2	574	2	BG907934
C 59	15.8	83.2	579	8	CX625718
60	15.8	83.2	581	7	CF954381
61	15.8	83.2	584	6	CA255155
62	15.8	83.2	597	6	CD876322
63	15.8	83.2	598	3	BM135186
64	15.8	83.2	601	6	CB680958
65	15.8	83.2	602	8	DN178545
66	15.8	83.2	627	1	AV933787
67	15.8	83.2	631	10	CB312739
68	15.8	83.2	636	3	BJ469064
69	15.8	83.2	636	6	CB656521
70	15.8	83.2	637	6	CB656403
71	15.8	83.2	648	3	BJ472488
72	15.8	83.2	654	3	BJ469669
73	15.8	83.2	659	1	AJ432460
74	15.8	83.2	662	1	AV933115
75	15.8	83.2	681	6	CA744325
76	15.8	83.2	686	6	CD054348
77	15.8	83.2	695	3	BJ471067
78	15.8	83.2	698	9	BZ008560
79	15.8	83.2	700	8	DN178149
C 80	15.8	83.2	713	9	BH516786
C 81	15.8	83.2	716	6	CA240024
C 82	15.8	83.2	749	7	CB662892
C 83	15.8	83.2	777	7	CO033780
C 84	15.8	83.2	778	6	CB659097
C 85	15.8	83.2	785	6	CB624346
C 86	15.8	83.2	790	6	CB657398
87	15.8	83.2	795	6	CB648104
88	15.8	83.2	796	6	CB624345
C 89	15.8	83.2	800	10	CL746478
C 90	15.8	83.2	810	6	CB655953
91	15.8	83.2	825	6	CB656772
C 92	15.8	83.2	834	6	CB657399
C 93	15.8	83.2	851	6	CB663361
C 94	15.8	83.2	861	7	CK156356
C 95	15.8	83.2	868	6	CF819853

C 96	15.8	83.2	876	6	CB680959	CR346986	245	11	CR346986	CR346986 mte1-80L1
C 97	15.8	83.2	929	6	CF821836	EST699218	169	14.8	77.9	AT868751 tJ93b05.x
C 98	15.8	83.2	941	7	CN512333	AGENCOURT	170	14.8	77.9	BB572879 BB572879
C 99	15.8	83.2	994	7	CO010346	EST798681	171	14.8	77.9	AI565236 th9e12.x
C 100	15.8	83.2	996	2	BE743432	601573680	172	14.8	77.9	AI470419 tJ43e04.x
C 101	15.8	83.2	1001	8	CK114637	EI090819	173	14.8	77.9	CR331167 mte1-6001
C 102	15.8	83.2	1003	7	CK206868	FGAS01847	174	14.8	77.9	AV099619 AV099619
C 103	15.8	83.2	1024	7	CK206942	FGAS01855	175	14.8	77.9	CG632986 OST352167
C 104	15.8	83.2	1034	7	CK207162	FGAS01878	176	14.8	77.9	AV524455 AV524455
C 105	15.8	83.2	1135	3	BQ063512	AGENCOURT	177	14.8	77.9	AX430229 JG1_XG61
C 106	15.8	83.2	1220	10	CL648023	CH2113-159	178	14.8	77.9	AW137507 UI-H-B11-
C 107	15.8	83.2	1261	6	CD254577	AGENCOURT	179	14.8	77.9	CN649096 EG_PSPGRB
C 108	15.8	83.2	1336	6	CX114889	EI092N07	180	14.8	77.9	CR145136 Forward s
C 109	15.4	81.1	58	8	DN955356	it86e04.g	181	14.8	77.9	CO278514 EK130240.
C 110	15.4	81.1	118	9	AZ089499	RPCI-23-4	182	14.8	77.9	EX552579 BX552579
C 111	15.4	81.1	170	10	CW191135	104_613.1	183	14.8	77.9	AZ892884 RPCI-24-2
C 112	15.4	81.1	284	2	BE144147	MRO-HTO16	184	14.8	77.9	AK191345 Mus muscu
C 113	15.4	81.1	356	10	CG612471	OST298727	185	14.8	77.9	AI127566 QC21907.x
C 114	15.4	81.1	403	7	CK936592	CGF100452	186	14.8	77.9	AQ088585 HS_2208.B
C 115	15.4	81.1	430	1	AA219175	zql17f01.s	187	14.8	77.9	CX029433 13i1329.N
C 116	15.4	81.1	442	2	BF858904	RC5-F7019	188	14.8	77.9	AQ088585 HS_2208.B
C 117	15.4	81.1	443	9	BZ183574	CH230-485	189	14.8	77.9	AI137965 tC81b10.x
C 118	15.4	81.1	445	7	CN955933	3433_106-	190	14.8	77.9	AQ581636 RPCI-11-4
C 119	15.4	81.1	461	11	DE056529	OryZias 1	191	14.8	77.9	DN022665 JG1_CAA83
C 120	15.4	81.1	461	5	BY543692	BY543692	192	14.8	77.9	AI900384 sc05a05.Y
C 121	15.4	81.1	490	3	BP392262	BP392262	193	14.8	77.9	CG599934 OST268024
C 122	15.4	81.1	509	9	CE222506	tigr-988-	194	14.8	77.9	CR323965 mte1-50N1
C 123	15.4	81.1	568	7	CN124698	RHOH1_6.H	195	14.8	77.9	AI951548 w36e06.x
C 124	15.4	81.1	640	8	CF442258	EST678603	196	14.8	77.9	CC763600 CH240_4D1
C 125	15.4	81.1	690	8	DR786856	ZM_BF0000	197	14.8	77.9	BH250888 SALK_O106
C 126	15.4	81.1	691	7	CK937081	CGF100451	198	14.8	77.9	CO343135 EP16153.3
C 127	15.4	81.1	692	1	AI873533	wf84e03.x	199	14.8	77.9	AA808971 nv19c02.i
C 128	15.4	81.1	717	9	CE174112	tigr-988-	200	14.8	77.9	BJ636421 BJ636421
C 129	15.4	81.1	746	6	CF447698	EST684043	201	14.8	77.9	CK676629 ZF101-P00
C 130	15.4	81.1	747	6	CF445823	EST682168	202	14.8	77.9	BU381184 B03582009
C 131	15.4	81.1	760	10	AG556749	Mus muscu	203	14.8	77.9	BY188842 BY188842
C 132	15.4	81.1	761	6	CF342050	AGENCOURT	204	14.8	77.9	AI178612 UI-H-B11-
C 133	15.4	81.1	854	7	CO033897	EST813281	205	14.8	77.9	AW134718 AU1-H-B11-
C 134	15.4	81.1	866	5	BQ704899	Bn01_01a2	206	14.8	77.9	AI128330 Q650h02.x
C 135	15.4	81.1	872	5	BN171518	AGENCOURT	207	14.8	77.9	AI148787 Q659a09.x
C 136	15.4	81.1	893	6	CF548005	AGENCOURT	208	14.8	77.9	AI1088714 qal12d02.x
C 137	15.4	81.1	965	11	CNS03KTI	AL248607 Tetradon	209	14.8	77.9	BI135594 F055P20Y
C 138	15.4	81.1	1008	3	BQ050772	AGENCOURT	210	14.8	77.9	BI135594 F055P20Y
C 139	15.4	81.1	1022	10	CL036098	CH216-400	211	14.8	77.9	BO097947 BX097947
C 140	15.4	81.1	1039	11	CNS039HQ	AL233927 Tetradon	212	14.8	77.9	AI097552 q6a0f09.x
C 141	15.4	81.1	1068	3	BN479812	AGENCOURT	213	14.8	77.9	AQ261983 CITBI-E1-
C 142	15.4	81.1	1102	11	CNS038R1	AL232966 Tetradon	214	14.8	77.9	AI970702 w13e02.x
C 143	15.4	81.1	1405	2	BE730376	601563816	215	14.8	77.9	BF461068 UI-M-CG0p
C 144	15.4	81.1	333	9	BZ661537	SALK_O250	216	14.8	77.9	AQ126088 HS_3036.A
C 145	15.4	81.1	375	7	CK095952	UA38BPA09	217	14.8	77.9	AL779679 AL779679
C 146	15.4	81.1	410	10	AG970375	AG970375 Drosophila	218	14.8	77.9	CE730627 tigr-988-
C 147	15.4	81.1	420	8	R92106	YP96d10.s1	219	14.8	77.9	AQ27923 RPCI-23-2
C 148	15.4	81.1	467	6	CF714157	AMGNNUC:N	220	14.8	77.9	CL682161 PRI0133a_
C 149	15.4	81.1	512	1	AW735958	EST336726	221	14.8	77.9	AI740562 w16g06.x
C 150	15.4	81.1	560	1	AJ808629	AJ808629	222	14.8	77.9	AA494514 ne36h05.s
C 151	15.4	81.1	593	10	CL739566	OR_BBa007	223	14.8	77.9	BI244282 EG_PSPGR
C 152	15.4	81.1	598	3	BQ116146	EST601722	224	14.8	77.9	CN650536 EG_PSPGRS
C 153	15.4	81.1	617	1	AV403771	AV403771	225	14.8	77.9	CE634654 tigr-988-
C 154	15.4	81.1	661	3	BI960063	HVSMEN002	226	14.8	77.9	CA350143 UC0809 NC
C 155	15.4	81.1	672	1	AJ793847	AJ793847	227	14.8	77.9	CF834215 DROSOPHIL
C 156	15.4	81.1	759	6	CB166956	BTU602600	228	14.8	77.9	AG960099 Drosophila
C 157	15.4	81.1	801	10	CL662642	PRI0142a_	229	14.8	77.9	AQ573912 nbxb0083C
C 158	15.4	81.1	824	10	CL662642	PRI0142a_	230	14.8	77.9	RA778220 z19e09.s
C 159	15.4	81.1	835	7	CO564696	AGENCOURT	231	14.8	77.9	AI922821 w04d06.x
C 160	15.4	81.1	838	7	CO567950	AGENCOURT	232	14.8	77.9	AW202789 fJ22C04.Y
C 161	15.4	81.1	858	10	CZ321096	ZMWBFO023	233	14.8	77.9	AZ409425 IM0181J01
C 162	15.4	81.1	902	9	AZ203580	SP_O081.B	234	14.8	77.9	AI971512 wr05e07.x
C 163	15.4	81.1	990	1	AV110510	AV110510	235	14.8	77.9	AX242053 Danio rer
C 164	15.4	81.1	1013	2	BF973291	602242213	236	14.8	77.9	AL489676 T_brucei
C 165	15.4	81.1	1069	3	BI551860	603192766	237	14.8	77.9	BE667658 154222.MA
C 166	15.4	81.1	1164	3	CC185536	CH261-129	238	14.8	77.9	AJ711286 AJ711286
C 167	14.8	77.9	41	9	AZ411946	IM0185009	239	14.8	77.9	AL785793 AL785793
C 168	14.8	77.9	175	9	CC795725	SALK_0880	240	14.8	77.9	CE723160 tigr-988-

242	14.8	77.9	9	AZ955764	2M0222D04	AZ955764	2M0222D04	C 315	14.8	77.9	740	9	BZ278712	CH230-451
243	14.8	77.9	555	7	CN694663	CN694663	E0353G08-	316	14.8	77.9	741	10	CL795448	OR_CBA000
244	14.8	77.9	556	8	CN988204	IPCGFrl_1	CN988204	317	14.8	77.9	742	9	CE029972	tigr-g98-
245	14.8	77.9	563	3	AZ055596	RPCI-23-4	AZ055596	318	14.8	77.9	747	5	EX700997	BX700997
246	14.8	77.9	565	3	BJ059717	BJ059717	BJ059717	319	14.8	77.9	747	7	CV512284	KC82a08_Y
247	14.8	77.9	566	3	BJ070137	BJ070137	BJ070137	320	14.8	77.9	748	8	CV474314	JGI_XZG49
248	14.8	77.9	567	1	A1935287	WP16d12.x	A1935287	321	14.8	77.9	748	8	AQ156029	IND500021
249	14.8	77.9	572	8	DT006298	WP032F10	DT006298	322	14.8	77.9	748	9	CK028259	AGENCOURT
250	14.8	77.9	580	6	CB110278	K-EST0151	CB110278	323	14.8	77.9	749	7	DN597221	AGENCOURT
251	14.8	77.9	582	1	AV599249	AV599249	AV599249	C 324	14.8	77.9	750	9	CC003285	PUECT95TD
252	14.8	77.9	584	10	AG926251	Drosophil	AG926251	C 325	14.8	77.9	752	8	CK411312	JGI_XZT28
253	14.8	77.9	586	10	AG923374	Drosophil	AG923374	C 326	14.8	77.9	753	10	CL851044	OR_CBA007
254	14.8	77.9	588	7	CK131326	CH20621.3	CK131326	C 327	14.8	77.9	754	10	AG562056	Mus muscu
255	14.8	77.9	589	8	DT006327	VVG033A04	DT006327	C 328	14.8	77.9	755	10	CL846860	OR_CBA007
256	14.8	77.9	595	7	CN650665	Eg_PSPGRS	CN650665	C 329	14.8	77.9	760	8	DN023695	JGI_CAA4A
257	14.8	77.9	598	10	CE535032	tigr-g98-	CE535032	C 330	14.8	77.9	763	8	DN023694	JGI_CAA4A
258	14.8	77.9	599	9	AZ291021	RPCI-23-1	AZ291021	C 331	14.8	77.9	764	9	BZ372626	ie69h07_b
259	14.8	77.9	600	10	AG924507	Drosophil	AG924507	C 332	14.8	77.9	766	9	BZ773948	mcv82h11.
260	14.8	77.9	603	10	CL266204	PHCRC-GT-	CL266204	C 333	14.8	77.9	766	10	AG480043	Mus muscu
261	14.8	77.9	610	8	DT008426	VVG055F04	DT008426	C 334	14.8	77.9	770	8	CK829104	JGI_CAAK6
262	14.8	77.9	617	5	CA012931	HT06004r	CA012931	C 335	14.8	77.9	775	5	EX105784	BX105784
263	14.8	77.9	620	9	CT720334	CH240_7J1	CT720334	C 336	14.8	77.9	778	2	BG916759	BG916759
264	14.8	77.9	621	7	CK968614	4084180_B	CK968614	C 337	14.8	77.9	783	1	AT1517505	AT1517505
265	14.8	77.9	622	10	CE747872	tigr-g98-	CE747872	C 338	14.8	77.9	783	5	BM963551	BM963551
266	14.8	77.9	623	6	CB111276	K-EST0152	CB111276	C 339	14.8	77.9	783	9	BM608003	BM608003
267	14.8	77.9	623	10	CL621457	OR_BBA001	CL621457	C 340	14.8	77.9	786	6	CD100362	AGENCOURT
268	14.8	77.9	634	1	A1513338	GH26511.5	A1513338	C 341	14.8	77.9	789	10	AG362352	Mus muscu
269	14.8	77.9	639	3	BO173414	Eg_PSPGR_0	BO173414	C 342	14.8	77.9	794	8	CK345864	JGI_XZT43
270	14.8	77.9	639	3	BO241771	TaE05001A	BO241771	C 343	14.8	77.9	794	8	AG362352	Mus muscu
271	14.8	77.9	640	8	CK370623	JGI_XZT55	CK370623	C 344	14.8	77.9	796	6	CB206331	AGENCOURT
272	14.8	77.9	641	1	AV274320	AV274320	AV274320	C 345	14.8	77.9	805	10	CL928532	OA_ABA003
273	14.8	77.9	646	5	EX773414	EX773414	EX773414	C 346	14.8	77.9	806	10	CL804065	OA_ABA003
274	14.8	77.9	648	1	A1055707	coau0004N	A1055707	C 347	14.8	77.9	816	2	BF670143	BF670143
275	14.8	77.9	648	8	CK341808	JGI_XZT46	CK341808	C 348	14.8	77.9	816	9	BH507255	BH507255
276	14.8	77.9	649	8	CK345963	JGI_XZT43	CK345963	C 349	14.8	77.9	821	9	CC087506	CC087506
277	14.8	77.9	651	5	BU625080	UI-H-FGI-	BU625080	C 350	14.8	77.9	823	5	BU334146	BU334146
278	14.8	77.9	651	9	AZ955752	UI-H-FGI-	AZ955752	C 351	14.8	77.9	825	8	DN107112	DN107112
279	14.8	77.9	651	10	AG047975	Pan trogl	AG047975	C 352	14.8	77.9	826	2	BE906428	BE906428
280	14.8	77.9	652	2	BH535557	BH535557	BH535557	C 353	14.8	77.9	830	10	AY407843	Mus muscu
281	14.8	77.9	655	10	CL570964	UI-H-FGI-	CL570964	C 354	14.8	77.9	832	5	EX782764	EX782764
282	14.8	77.9	656	3	BM984775	UI-H-FGI-	BM984775	C 355	14.8	77.9	837	11	CR812452	GR0AAA36C
283	14.8	77.9	658	6	CA307182	UI-H-FGI-	CA307182	C 356	14.8	77.9	838	5	BU343598	BU343598
284	14.8	77.9	659	8	CA411311	JGI_XZT28	CA411311	C 357	14.8	77.9	845	6	CB199535	AGENCOURT
285	14.8	77.9	661	3	BI604028	603243841	BI604028	C 358	14.8	77.9	859	10	CG928397	CG928397
286	14.8	77.9	661	5	BM689223	UI-H-FGI-	BM689223	C 359	14.8	77.9	860	6	CA471371	AGENCOURT
287	14.8	77.9	662	9	AO644975	RPCI93-Dp	AO644975	C 360	14.8	77.9	860	6	CA471371	AGENCOURT
288	14.8	77.9	664	9	BH738406	BOMQ35TR	BH738406	C 361	14.8	77.9	861	7	CO881848	BowGen_10
289	14.8	77.9	677	10	CZ700617	OC_BA001	CZ700617	C 362	14.8	77.9	861	7	CO881848	BowGen_10
290	14.8	77.9	680	6	CA446467	UI-H-FGI-	CA446467	C 363	14.8	77.9	868	6	CB574745	AGENCOURT
291	14.8	77.9	680	10	CE402740	tigr-g98-	CE402740	C 364	14.8	77.9	870	10	CG976368	CG976368
292	14.8	77.9	682	10	CM158168	104_561_1	CM158168	C 365	14.8	77.9	871	5	BQ736366	BQ736366
293	14.8	77.9	683	10	CE815010	tigr-g98-	CE815010	C 366	14.8	77.9	873	9	AZ529396	AZ529396
294	14.8	77.9	692	10	CL596795	OB_BA005	CL596795	C 367	14.8	77.9	877	8	DR732749	DR732749
295	14.8	77.9	696	7	CN604421	USDA_FF_1	CN604421	C 368	14.8	77.9	886	5	EX433740	EX433740
296	14.8	77.9	697	7	CR580529	CR580529	CR580529	C 369	14.8	77.9	887	8	CV967186	CV967186
297	14.8	77.9	699	10	AG298311	Mus muscu	AG298311	C 370	14.8	77.9	888	10	CZ953010	CZ953010
298	14.8	77.9	698	1	AI387486	GHI8030.5	AI387486	C 371	14.8	77.9	891	7	DN029257	JGI_CAA43
299	14.8	77.9	699	9	B2165108	CH230-377	B2165108	C 372	14.8	77.9	895	7	CV292253	ao601-12m
300	14.8	77.9	702	7	CV508738	kc75g01.y	CV508738	C 373	14.8	77.9	895	7	CN321683	AGENCOURT
301	14.8	77.9	702	10	CL852151	OR_CBA008	CL852151	C 374	14.8	77.9	911	10	CG052122	PUIH75TD
302	14.8	77.9	705	9	BH928557	odi77a01.	BH928557	C 375	14.8	77.9	914	5	BU857015	AGENCOURT
303	14.8	77.9	706	9	BH979064	ode71e06	BH979064	C 376	14.8	77.9	915	2	BE194539	HVSMNH008
304	14.8	77.9	709	6	CF133289	WHE4356_C	CF133289	C 377	14.8	77.9	915	7	CK417409	AUF_IpInt
305	14.8	77.9	712	7	CK797340	AGENCOURT	CK797340	C 378	14.8	77.9	918	10	CZ858532	OC_BA025
306	14.8	77.9	715	7	CK714313	ZF201-P00	CK714313	C 379	14.8	77.9	920	10	CG920682	MEBK080TR
307	14.8	77.9	722	8	CK418682	JGI_XZG65	CK418682	C 380	14.8	77.9	923	10	AG902453	Oryza sat
308	14.8	77.9	725	10	CL909579	OA_ABA000	CL909579	C 381	14.8	77.9	926	11	CNS040AZ	AL299780
309	14.8	77.9	726	7	CR373915	CR373915	CR373915	C 382	14.8	77.9	930	9	CC069698	Tetraodon
310	14.8	77.9	727	9	BH962522	odi48e10	BH962522	C 383	14.8	77.9	939	11	CNS0546Z	AL320372
311	14.8	77.9	730	8	DN898422	nap33c01.	DN898422	C 384	14.8	77.9	944	10	AG876213	Oryza sat
312	14.8	77.9	732	10	CL765009	OR_BBA013	CL765009	C 385	14.8	77.9	953	10	CNS027EP	AL184606
313	14.8	77.9	737	7	CN055457	Salamande	CN055457	C 386	14.8	77.9	962	10	DU014218	Tetraodon
314	14.8	77.9	738	7	CR565974	CR565974	CR565974	C 387	14.8	77.9	965	10	CG870756	ZMMB0C028
											970	8	CV921669	PHrphc_07

388	14.8	77.9	975	5	BU911821	BU911821 AGENCOURT	461	14.4	75.8	539	1	AL925630	AL925630 AL925630
389	14.8	77.9	977	10	AG867779	AG867779 Oryza sat	462	14.4	75.8	541	6	CD569927	CD569927 EESTeg02
390	14.8	77.9	988	10	CZ995518	CZ995518 183668 To	C 463	14.4	75.8	543	3	BJ012157	BJ012157
391	14.8	77.9	1012	10	CL099115	CL099115 ISB1-32E3	C 464	14.4	75.8	547	3	BI999130	BI999130 1031070H0
392	14.8	77.9	1028	9	BH175566	BH175566 BMJV83TR	C 465	14.4	75.8	549	2	BE758836	BE758836 an 3084 A
C 393	14.8	77.9	1050	8	DN783532	DN783532 93003109	C 466	14.4	75.8	550	3	BJ873867	BJ873867
C 394	14.8	77.9	1055	10	CL285172	CL285172 ZNMVBB062	467	14.4	75.8	550	6	CD972535	CD972535 QAE23A02
C 395	14.8	77.9	1061	9	CC307774	CC307774 TAM32-18J	468	14.4	75.8	556	6	CA071040	CA071040 SCCAM100
C 396	14.8	77.9	1064	11	CNS048WA	AL279811 Tetradon	469	14.4	75.8	560	1	AW967194	AW967194 EST379268
397	14.8	77.9	1067	10	CNS00AKJ	AL056061 Drosophill	470	14.4	75.8	561	6	CB968362	CB968362 EESTef73
398	14.8	77.9	1078	11	CNS05FRL	AL353570 Tetradon	471	14.4	75.8	561	6	CD974000	CD974000 QAE40011
C 399	14.8	77.9	1101	10	CNS00G56	AL071448 Drosophill	C 472	14.4	75.8	562	10	CL517190	CL517190 PHCRC-GT-
C 400	14.8	77.9	1101	10	CNS014YR	AL104781 Drosophill	473	14.4	75.8	567	9	AQ307864	AQ307864 HS 2199 A
401	14.8	77.9	1103	8	DN663574	DN663574 CPW14-P07	C 474	14.4	75.8	567	11	DE046845	DE046845 Oryzias 1
402	14.8	77.9	1156	8	DR046133	DR046133 FP-9 P08	475	14.4	75.8	573	6	CD974157	CD974157 QAE42010
403	14.8	77.9	1171	8	DR046059	DR046059 FP-8 H06	476	14.4	75.8	575	2	BF895320	BF895320 IL0-WT021
404	14.8	77.9	1203	3	BQ277749	BQ277749 AGENCOURT	477	14.4	75.8	577	3	BI577998	BI577998 REV1785.5
405	14.8	77.9	1226	9	CC200990	CC200990 CH261-134	478	14.4	75.8	586	6	CA172813	CA172813 SCUTS103
406	14.8	77.9	1378	8	DN676524	DN676524 CPW93-A09	479	14.4	75.8	594	6	CF818827	CF818827 EST696209
407	14.8	77.9	1388	5	BU150187	BU150187 AGENCOURT	480	14.4	75.8	599	9	CC956935	CC956935 BOIFP29TR
408	14.8	77.9	1452	8	DN659817	DN659817 CEC43-B10	481	14.4	75.8	601	7	CO443223	CO443223 M2CCL1006
409	14.8	77.9	1461	4	AK087319	AK087319 Mus muscu	482	14.4	75.8	603	10	CW063436	CW063436 104 309 1
410	14.8	77.9	2075	4	AK009193	AK009193 Mus muscu	483	14.4	75.8	604	10	CW458000	CW458000 EED5001F2
C 411	14.8	77.9	2181	4	AK081300	AK081300 Mus muscu	484	14.4	75.8	605	5	BM441235	BM441235 BM441235
C 412	14.8	77.9	2314	4	AK089301	AK089301 Mus muscu	485	14.4	75.8	605	11	DE049603	DE049603 Oryzias 1
C 413	14.8	77.9	2853	10	CL949051	CL949051 OrlFBSB002	486	14.4	75.8	607	6	CB408128	CB408128 IPG001C02
C 414	14.8	77.9	3859	4	AK031340	AK031340 Mus muscu	C 487	14.4	75.8	607	10	CW284148	CW284148 104 760 1
415	14.8	77.9	4347	4	AK019848	AK019848 Mus muscu	488	14.4	75.8	614	6	CD346201	CD346201 EESTef90
416	14.8	77.9	4864	4	CR858274	CR858274 Pongo pyg	489	14.4	75.8	615	8	CV744084	CV744084 JGI-ANBT1
417	14.4	75.8	143	8	DN361287	DN361287 LIB3627-0	C 490	14.4	75.8	616	1	AI757288	AI757288 EESTeal14
418	14.4	75.8	154	1	AW849369	AW849369 IL3-CY021	491	14.4	75.8	623	10	CW784399	CW784399 SP_Bb001
C 419	14.4	75.8	185	10	CW100072	CW100072 104 467 1	492	14.4	75.8	627	8	DT012847	DT012847 VH044F06
C 420	14.4	75.8	284	10	CL229038	CL229038 ZNMVBB014	C 493	14.4	75.8	629	7	CV670071	CV670071 LCPE04EX0
C 421	14.4	75.8	287	6	CD154501	CD154501 MLI-0036T	C 494	14.4	75.8	631	11	DE066977	DE066977 Oryzias 1
C 422	14.4	75.8	302	6	CD140350	CD140350 MGI-0067G	C 495	14.4	75.8	632	9	AZ246131	AZ246131 RPCI-23-1
423	14.4	75.8	306	6	CD196399	CD196399 MSI-0094G	C 496	14.4	75.8	633	7	CO596495	CO596495 DGB-128j1
C 424	14.4	75.8	302	6	CB636844	CB636844 OSJNEA02M	C 497	14.4	75.8	634	11	CR130872	CR130872 Forward 8
C 425	14.4	75.8	325	1	AA786371	AA786371 15a03a1.f	498	14.4	75.8	635	1	AU261149	AU261149 AU261149
C 426	14.4	75.8	335	8	H51561	H51561 yo34a03.a1	499	14.4	75.8	635	6	CA179372	CA179372 SCSSGT107
C 427	14.4	75.8	367	1	AA113768	AA113768 zn65906.s	500	14.4	75.8	637	10	CW149115	CW149115 104_548_1
428	14.4	75.8	372	1	AW955727	AW955727 EST376797							
429	14.4	75.8	396	9	AQ027634	AQ027634 CIT-HSP-2							
430	14.4	75.8	399	1	AU069063	AU069063 AU069063							
431	14.4	75.8	410	6	CB803847	CB803847 AMGNNUC-S							
432	14.4	75.8	418	2	BF588142	BF588142 PMI_38_CO							
C 433	14.4	75.8	423	10	CG955510	CG955510 MBEGK35TR							
434	14.4	75.8	434	9	AQ697140	AQ697140 HS 5528 A							
C 435	14.4	75.8	435	3	BP895692	BP895692 BP895692							
436	14.4	75.8	437	1	AA271056	AA271056 va95e09.r							
C 437	14.4	75.8	443	10	CW185416	CW185416 104 603_1							
C 438	14.4	75.8	449	1	AU179238	AU179238 AU179238							
C 439	14.4	75.8	456	3	BJ054677	BJ054677 BJ054677							
C 440	14.4	75.8	458	1	AI327661	AI327661 e0f12a1.f							
C 441	14.4	75.8	459	5	CG2870	CG2870							
C 442	14.4	75.8	459	5	CG3726	CG3726							
443	14.4	75.8	463	9	B41428	B41428 HS-1053-B1-							
C 444	14.4	75.8	466	1	AA784934	AA784934 C83726 rabb							
445	14.4	75.8	467	9	BZ177144	BZ177144 CH230-397							
446	14.4	75.8	472	11	CNS03K2R	AL247644 Tetradon							
447	14.4	75.8	475	9	AQ412625	AQ412625 RPCI-11-1							
448	14.4	75.8	478	2	BM700363	BM700363 BM700363							
449	14.4	75.8	496	10	AG967565	AG967565 Drosophill							
C 450	14.4	75.8	500	3	BU007823	BU007823 BU007823							
C 451	14.4	75.8	500	9	BZ122180	BZ122180 CH230-461							
452	14.4	75.8	515	3	BM481442	BM481442 533681 MA							
C 453	14.4	75.8	519	6	CD077371	CD077371 MA3-0001U							
454	14.4	75.8	519	9	AZ193345	AZ193345 SP 1023 A							
455	14.4	75.8	526	6	CB719879	CB719879 AMGNNUC-U							
C 456	14.4	75.8	533	3	BI672125	BI672125 ft34h02.x							
C 457	14.4	75.8	534	6	CD192055	CD192055 MSI-0074T							
C 458	14.4	75.8	534	6	CD192084	CD192084 MSI-0074T							
459	14.4	75.8	535	8	CX455630	CX455630 JGI XZG53							
C 460	14.4	75.8	536	5	BQ804135	BQ804135 PTAEST198							

ALIGNMENTS

RESULT 1
CA083939/c

LOCUS SCEPAM2056D03.g AM2 Saccharum officinarum cDNA clone SCEPAM2056D03
DEFINITION 543 bp mRNA linear EST 23-SEP-2003
5', mRNA sequence.

ACCESSION CA083939
VERSION CA083939.1 GI:34937250
KEYWORDS EST.

SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

REFERENCE 1 (bases 1 to 543)
Vettore A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br

AUTHORS Vettore A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P

REFERENCE 1 (bases 1 to 543)
Vettore A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
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Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br

Plate: 056 row: D column: 03
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .543
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCBPAM2056D03"
/lab_host="DH10B"
/clone_lib="AM2"
/note="Organ: Apical meristem and tissues surrounding of immature plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Apical meristem and tissues surrounding of immature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 543;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTCGAATGGCGCTAATC 19

Db 256 CCTCGAATGGCGCTAATC 239

RESULT 2

CA138671
LOCUS SCQRT2029D06.g RT2 Saccharum officinarum cDNA clone SCQRT2029D06
5', mRNA sequence.
CA138671
VERSION CA138671.1 GI:35029882
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

1 (bases 1 to 613)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at

<http://www.bcccenter.fcav.unesp.br>

Plate: 029 row: D column: 06

Seq primer: T7 Promoter Primer.

Location/Qualifiers

FEATURES

1. .613
/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCQRT2029D06"

/lab_host="DH10B"

/clone_lib="RT2"

/note="Organ: Root tips(0.3cm-long) from adult plants;

Vector: pSport1; Site 1: SalI; Site 2: NotI; An

unidirectional cDNA library generated from [Root

tips(0.3cm-long) from adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 613;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTCGAATGGCGCTAATC 19

Db 490 CCTCGAATGGCGCTAATC 507

RESULT 3

CA187742/c
LOCUS SCUTST3130H04.g ST3 Saccharum officinarum cDNA clone SCUTST3130H04
5', mRNA sequence.
CA187742
ACCESSION CA187742.1 GI:35128938
VERSION CA187742.1 GI:35128938
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
1 (bases 1 to 631)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at

<http://www.bcccenter.fcav.unesp.br>

Plate: 130 row: H column: 04

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1. .631
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/mol_type="mRNA"

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/lab_host="DH10B"

/clone_lib="ST3"

/note="Organ: Fourth apical stalk internodes of adult

plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An

unidirectional cDNA library generated from [Fourth apical

stalk internodes of adult plants]. cDNA was prepared from

polyA+ mRNA using SuperScript Plasmid System Kit

(Invitrogen). The double-strand cDNAs were fractionated

in a sepharose CL-2B 40cm-columns and fragments sizing

between 0.8 and 1.5 Kb were directionally cloned into the

vector. Details of each source of RNA and library

construction can be obtained at

<http://sucet.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 631;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2  CCCTGAATGCGGCTAATC 19
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Db      349 CCCTGAATGCGGCTAATC 332

RESULT 4
CA104389/c
LOCUS      656 bp      mRNA      linear      EST 23-SEP-2003
DEFINITION SCJFHR1033A07.g HRI Saccharum officinarum cDNA clone SCJFHR1033A07
5', mRNA sequence.
ACCESSION CA104389
VERSION    CA104389.1 GI:34957696
KEYWORDS   EST.
SOURCE     Saccharum officinarum
ORGANISM   Saccharum officinarum

REFERENCE 1 (bases 1 to 656)
AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE     The libraries that made SUCEST
JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT   Centro de Biologia Molecular e Engenharia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parruda@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian Clone Collection Center (BCCC) at
          http://www.bcccenter.fcav.unicamp.br
          Plate: 033 row: A column: 07
          Seq primer: T7 Promoter Primer.
          Location/Qualifiers
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                        /mol_type="mRNA"
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                        /clone="SCJFHR1033A07"
                        /lab_host="DH10B"
                        /clone_lib="HRI"
                        /note="Organ: seedlings inoculated with Herbaspirillum
                        rubrisubalbicans; Vector: pSport1; Site_1: SalI; Site_2:
                        NotI; An unidirectional cDNA library generated from
                        [seedlings inoculated with Herbaspirillum
                        rubrisubalbicans]. cDNA was prepared from polyA+ mRNA
                        using SuperScript Plasmid System Kit (Invitrogen). The
                        double-strand cDNAs were fractionated in a sepharose
                        CL-2B 40cm-columns and fragments sizing between 0.8 and
                        1.5 Kb were directionally cloned into the vector. Details
                        of each source of RNA and library construction can be
                        obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match      94.7%; Score 18; DB 6; Length 656;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  CCCTGAATGCGGCTAATC 19
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Db      269 CCCTGAATGCGGCTAATC 252

RESULT 5
CA085581
LOCUS      904 bp      mRNA      linear      EST 23-SEP-2003
DEFINITION SCULAM2093D05.b AM2 Saccharum officinarum cDNA clone SCULAM2093D05
3', mRNA sequence.
ACCESSION CA085581
VERSION    CA085581.1 GI:34938888

KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 904)
AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE     The libraries that made SUCEST
JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT   Centro de Biologia Molecular e Engenharia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parruda@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian Clone Collection Center (BCCC) at
          http://www.bcccenter.fcav.unicamp.br
          Plate: 033 row: D column: 05
          Seq primer: SP6 Promoter primer.
          Location/Qualifiers
FEATURES             source
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                        /organism="Saccharum officinarum"
                        /mol_type="mRNA"
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                        /clone="SCJLAM2093D05"
                        /lab_host="DH10B"
                        /clone_lib="AM2"
                        /note="Organ: Apical meristem and tissues surrounding of
                        immature plants; Vector: pSport1; Site_1: SalI; Site_2:
                        NotI; An unidirectional cDNA library generated from
                        [Apical meristem and tissues surrounding of immature
                        plants]. cDNA was prepared from polyA+ mRNA using
                        SuperScript Plasmid System Kit (Invitrogen). The
                        double-strand cDNAs were fractionated in a sepharose
                        CL-2B 40cm-columns and fragments sizing between 0.8 and
                        1.5 Kb were directionally cloned into the vector. Details
                        of each source of RNA and library construction can be
                        obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match      94.7%; Score 18; DB 6; Length 904;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  CCCTGAATGCGGCTAATC 19
      |||||||
Db      525 CCCTGAATGCGGCTAATC 542

RESULT 6
CV608160
LOCUS      589 bp      mRNA      linear      EST 22-OCT-2004
DEFINITION L_AL-aaa07f02.b1 Hc6AS_M Ajellomyces capsulatus cDNA 3', mRNA
sequence.
ACCESSION CV608160
VERSION    CV608160.1 GI:54595742
KEYWORDS   EST.
SOURCE     Ajellomyces capsulatus
ORGANISM   Ajellomyces capsulatus

REFERENCE 1 (bases 1 to 589)
AUTHORS   Magrini,V., Sil,A., Goldman,W. and Mardis,R.
TITLE     Genomic Resources for Histoplasma Sequencing Mardis/WashU
JOURNAL   Histoplasma capsulatum Sequencing Project
COMMENT    Unpublished (2004)
           Contact: Vincent Magrini
           Mardis/Goldman/Sil Genomic Resources for Histoplasma Sequencing
           Washington University School of Medicine

KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 904)
AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE     The libraries that made SUCEST
JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT   Centro de Biologia Molecular e Engenharia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parruda@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian Clone Collection Center (BCCC) at
          http://www.bcccenter.fcav.unicamp.br
          Plate: 033 row: D column: 05
          Seq primer: SP6 Promoter primer.
          Location/Qualifiers
FEATURES             source
    source            1..904
                        /organism="Saccharum officinarum"
                        /mol_type="mRNA"
                        /db_xref="taxon:4547"
                        /clone="SCJLAM2093D05"
                        /lab_host="DH10B"
                        /clone_lib="AM2"
                        /note="Organ: Apical meristem and tissues surrounding of
                        immature plants; Vector: pSport1; Site_1: SalI; Site_2:
                        NotI; An unidirectional cDNA library generated from
                        [Apical meristem and tissues surrounding of immature
                        plants]. cDNA was prepared from polyA+ mRNA using
                        SuperScript Plasmid System Kit (Invitrogen). The
                        double-strand cDNAs were fractionated in a sepharose
                        CL-2B 40cm-columns and fragments sizing between 0.8 and
                        1.5 Kb were directionally cloned into the vector. Details
                        of each source of RNA and library construction can be
                        obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match      94.7%; Score 18; DB 6; Length 904;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  CCCTGAATGCGGCTAATC 19
      |||||||
Db      525 CCCTGAATGCGGCTAATC 542

RESULT 6
CV608160
LOCUS      589 bp      mRNA      linear      EST 22-OCT-2004
DEFINITION L_AL-aaa07f02.b1 Hc6AS_M Ajellomyces capsulatus cDNA 3', mRNA
sequence.
ACCESSION CV608160
VERSION    CV608160.1 GI:54595742
KEYWORDS   EST.
SOURCE     Ajellomyces capsulatus
ORGANISM   Ajellomyces capsulatus

REFERENCE 1 (bases 1 to 589)
AUTHORS   Magrini,V., Sil,A., Goldman,W. and Mardis,R.
TITLE     Genomic Resources for Histoplasma Sequencing Mardis/WashU
JOURNAL   Histoplasma capsulatum Sequencing Project
COMMENT    Unpublished (2004)
           Contact: Vincent Magrini
           Mardis/Goldman/Sil Genomic Resources for Histoplasma Sequencing
           Washington University School of Medicine

KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 589)
AUTHORS   Magrini,V., Sil,A., Goldman,W. and Mardis,R.
TITLE     Genomic Resources for Histoplasma Sequencing Mardis/WashU
JOURNAL   Histoplasma capsulatum Sequencing Project
COMMENT    Unpublished (2004)
           Contact: Vincent Magrini
           Mardis/Goldman/Sil Genomic Resources for Histoplasma Sequencing
           Washington University School of Medicine

```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: vmagrini@watson.wustl.edu
 Contact Vincent Magrini (vmagrini@watson.wustl.edu) for further
 information relating to organism, libraries, or clone availability.
 Seq primer: M13 reverse.

FEATURES

source

Location/Qualifiers

1. .589

/organism="Ajellomyces capsulatus"

/mol_type="mRNA"

/strain="G186A-S"

/db_xref="taxon:5037"

/dev_stage="Mycelia"

/lab_host="GC10"

/clone_lib="Hc6AS M"

/note="Vector: pCR4-TOPO; Site 1: EcoRI flanks TA cloning site; Site 2: EcoRI flanks TA cloning site; polyA mRNA was captured with oligo d(T) magnetic beads and eluted. AAGCAGTGTAACACGACGAGTACTTTTTTTTTTTTNN was used for priming reverse transcription in the presence of SuperScript II RTase. The 5' primer (5' GCGCGGCTAATACGACTACTATAGG) annealed to cytosine nucleosides added by terminal transferase to the 5' end of the transcript. Amplification during the PCR used primers 5' AAGCAGTGTAACACGACGAGA and 5' GCGCGTAAACGACTACTATAGG and Clone-TECH Taq DNA polymerase. PCR products between 500 and 2,000 bp were size-fractionated from 0.7% LE/TAE agarose and cloned into the Topo TA site of Invitrogen plasmid vector pCR4-TOPO."

ORIGIN

Query Match 91.6%; Score 17.4; DB 7; Length 589;
 Best Local Similarity 94.7%; Pred. No. 2.1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19

Db 273 CCCCTGAATGGCGCTAATC 291

RESULT 7

BG933318

LOCUS

DEFINITION WS1_3_H09_b2_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA linear EST 07-JUN-2001

ACCESSION BG933318

VERSION BG933318.1

KEYWORDS GI:14328450

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 320)

AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt,L.H.

TITLE An EST database from Sorghum: water-stressed plants

JOURNAL Unpublished (2000)

COMMENT Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV

High quality sequence stop: 308

POLYA=No.

Location/Qualifiers

FEATURES

source

1. .320

/organism="Sorghum bicolor"

/mol_type="mRNA"

/db_xref="taxon:4558"

/clone_lib="Water-stressed 1 (WS1)"

/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

ORIGIN

Query Match 89.5%; Score 17; DB 2; Length 320;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAAT 18

Db 287 CCCTGAATGGCGCTAAT 303

RESULT 8

CF771460

LOCUS

DEFINITION

CF771460

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sorghum bicolor (sorghum)

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 392)

AUTHORS Cordonnier-Pratt,M.-M., Zhang,D., McCartor,K., Nguyen,H.T. and Pratt,L.H.

TITLE An EST Database from Sorghum: Subtracted pre-flowering drought

JOURNAL stressed leaf tissues

COMMENT Unpublished (2003)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Library constructed at Texas Tech University by Deshui Zhang in the

Laboratory of Dr. Henry Nguyen. Sequencing was done in the

Laboratory for Genomics and Bioinformatics, University of Georgia.

Sequence ends have been trimmed to exclude vector and regions below

Phred quality 16. Three-prime sequences are presented as their

reverse complement and have been trimmed to exclude polyA.

Seq primer: T7 (TAATACGACTCACTATAGG)

POLYA=Yes.

Location/Qualifiers

1. .392

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="Tx7000"

/db_xref="taxon:4558"

/clone="DSBF1_19_G07_A010"

/dev_stage="Pre-flowering"

/lab_host="ElectroMax DH10B (BRL)"

/clone_lib="Drought-stressed before flowering"

/note="Organ: Leaf; Vector: pBluescriptSK-; Site 1: XhoI; Site 2: EcoRI; The library was prepared from polyA+ RNA

from leaves harvested from pre-flowering, drought-stressed

Sorghum bicolor, cv. TX7000. Double-stranded cDNA was

cloned unidirectionally using the Unizap system from

Stratagene. After amplification, the library was

subtracted by re-association hybridization. Inserts can be

excised with XhoI and EcoRI."

```

ORIGIN
Query Match      89.5%; Score 17; DB 6; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
|||||
Db 167 CCCTGAATGCGGCTAAT 183
|||||

RESULT 9
BG933077      554 bp mRNA linear EST 07-JUN-2001
LOCUS
DEFINITION WSI_3_H09.b1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA
sequence.
VERSION BG933077.1 GI:14328209
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 554)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
Pratt,L.H.
TITLE An EST database from Sorghum: water-stressed plants
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence start: 13
High quality sequence stop: 543
POLYA=No.

FEATURES
source Location/Qualifiers
1..554
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site1: XhoI;
Site2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

ORIGIN
Query Match      89.5%; Score 17; DB 2; Length 554;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
|||||
Db 282 CCCTGAATGCGGCTAAT 298
|||||

RESULT 10
CA104476      590 bp mRNA linear EST 23-SEP-2003
LOCUS
DEFINITION SCUFHR1033A07.b HR1 Saccharum officinarum cDNA clone SCUFHR1033A07
3', mRNA sequence.
ACCESSION CA104476
VERSION CA104476.1 GI:34957783
KEYWORDS EST.

Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 590)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCRST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 033 row: A column: 07
Seq primer: SP6 Promoter primer.
Location/Qualifiers
1..590
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCUFHR1033A07"
/lab_host="DH10B"
/clone_lib="HR1"
/note="Organ: seedlings inoculated with Herbaspirillum
rubrisubalbicans; Vector: pSPORT1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
[seedlings inoculated with Herbaspirillum
rubrisubalbicans]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match      89.5%; Score 17; DB 6; Length 590;
Best Local Similarity 94.4%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
|||||
Db 525 CCCTGAATGCGGCTAATC 542
|||||

RESULT 11
CD429058      645 bp mRNA linear EST 03-JUN-2003
LOCUS
DEFINITION ETH1_2_B02.b1_A002 Ethylene-treated seedlings Sorghum bicolor cDNA
clone ETH1_2_B02_A002 3', mRNA sequence.
ACCESSION CD429058
VERSION CD429058.1 GI:31344701
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 645)
AUTHORS Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R.,
Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P.,
Olaseinde,O., Eastman,A. and Pratt,L.H.
TITLE An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
(ACC)-treated seedlings
JOURNAL Unpublished (2003)

```

COMMENT

Other ESTs: ETH1_2_B02_g1_A002
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.
 Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
 POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..645

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="BTx623"

/db_xref="taxon:4558"

/clone="ETH1_2_B02_A002"

/lab_host="DH10B-TI phage-resistant E. coli"

/clone_lib="Ethylene-treated seedlings"

/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The

library was prepared from polyA+ RNA from seedlings grown

in hydroponic culture. At 8 days of age, medium was

supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic

acid (ACC) to induce endogenous ethylene (ETH) production.

Roots and shoots were harvested after 27 and 72 hr and

material from both time points was combined prior to RNA

isolation. Double-stranded cDNA was cloned

unidirectionally into different DraIII sites of the

pME18S-FL3 vector (5'-prime DraIII site is CACTGTTG,

3'-prime DraIII site is CACCATGTG). XhoI excises the cDNA

insert."

ORIGIN

Query Match 89.5%; Score 17; DB 6; Length 645;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18

|||||

Db 372 CCCTGAATGCGGCTAAT 388

|||||

RESULT 12

AW680038

LOCUS

DEFINITION WS1_3_H09_g1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA

sequence.

ACCESSION AW680038

VERSION AW680038.1 GI:7553818

KEYWORDS EST.

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

REFERENCE 1 (bases 1 to 696)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and

Pratt, L.H.

An EST database from Sorghum: water-stressed plants

Unpublished (2000)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

FEATURES

source

Location/Qualifiers

1..118

100.0%; Pred. No. 3.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18

|||||

Db 269 CCCTGAATGCGGCTAAT 285

|||||

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.

Seq primer: T7

High quality sequence start: 71

High quality sequence stop: 696

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..696

/organism="Sorghum bicolor"

/mol_type="mRNA"

/db_xref="taxon:4558"

/note="Organ: Mix of 5-week old plants on days 7 & 8 after

water was withheld; Vector: Lambda Zap; Site 1: XhoI;

Site 2: EcoRI; The library was made from polyA+ RNA in the

cloning vector lambda ZAP II. Clones to be sequenced were

prepared by mass excision."

ORIGIN

Query Match 89.5%; Score 17; DB 1; Length 696;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18

|||||

Db 269 CCCTGAATGCGGCTAAT 285

|||||

RESULT 13

CZ476191/c

LOCUS

DEFINITION d08347-5prime Exelixis P element XP insertions Drosophila

melanogaster genomic Sequence recovered from 5' end of P element,

genomic survey sequence.

ACCESSION CZ476191

VERSION CZ476191.1 GI:62970314

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

REFERENCE 1 (bases 1 to 118)

Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,

Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,

Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,

Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,

Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,

Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,

Swimmer, C., Koczynski, C., Duyk, G., Winberg, M.L. and Margolis, J.

A complementary transposon tool kit for Drosophila melanogaster

using P and piggyBac

Nat. Genet. 36 (3), 283-287 (2004)

14981521

Contact: Roger A Hoskins

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA

Tel: 510 486 4015

Fax: 510 486 6798

Email: Rhoskins@lbl.gov

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P

element.

The P element insertion position is 111 in the 118 bases. This

insertion position refers to the first base of the 8 base target

recognition sequence.

Class: transposon insertion site.

FEATURES

source

Location/Qualifiers

1..118

/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis P element XP insertions"
/note="Vector: P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsyncy balancer. New insertions were collected in vias from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 118;
Best Local Similarity 94.4%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGGCTAAT 18
| | | | | | | | | | | | | | | | | |
Db 103 CCCTGAATCGGCTAAT 86

RESULT 14

BH899915
LOCUS
DEFINITION Ota00982 Ostreococcus tauri genomic shotgun library Ostreococcus tauri genomic clone ota04c08.g 5', genomic survey sequence.

ACCESSION BH899915
VERSION BH899915.1 GI:22551410
KEYWORDS GSS.
SOURCE Ostreococcus tauri
ORGANISM Ostreococcus tauri

REFERENCE 1 (bases 1 to 533)
AUTHORS Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales; Mamiellaceae; Ostreococcus.
Derelle, E., Ferraz, C., Lagoda, P., Eychenie, S., Cooke, R., Regad, F., Sabau, X., Courties, C., Delseny, M., Demaille, J., Picard, A. and Moreau, H.

TITLE DNA libraries for sequencing the genome of Ostreococcus tauri (Chlorophytae, Prasinophyceae): the smallest free-living eukaryotic cell

JOURNAL J. Phycol. 38 (6), 1150-1156 (2002)
COMMENT Contact: Moreau H
Laboratoire Arago
CNRS UMR 7628
BP 44, Avenue Fontaule, 66651 Banyuls sur mer, France
Tel: (33)468887309
Fax: (33)468887398
Email: h.moreau@obs-banyuls.fr
Seq primer: reverse
Class: shotgun.

FEATURES

Location/Qualifiers
source
1..533
/organism="Ostreococcus tauri"
/mol_type="genomic DNA"
/strain="OTTH0595"
/db_xref="taxon:70448"
/clone_lib="Ostreococcus tauri genomic shotgun library"
/note="Vector: Bluescript; Site 1: EcoRV; Site 2: EcoRV;
Shotgun library prepared after sonication of the genomic DNA. Blunt ligation in EcoRV site of Bluescript. Size selection of the inserts after agarose electrophoresis between 1 and 3 Kb."

ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 533;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCCTGAATCGGCTAAT 18
| | | | | | | | | | | | | | | | | |
Db 500 CCCTGAATCGGCTACT 517

RESULT 15

CA190230/c
LOCUS
DEFINITION CA190230.1 Lr1 Saccharum officinarum cDNA clone SCCCLR1C10E02 5', mRNA sequence.

ACCESSION CA190230
VERSION CA190230.1 GI:35134178
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 569)
AUTHORS Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>
Plate: C10 row: E column: 02
Seq primer: T7 Promoter Primer.
Location/Qualifiers
source
1..569
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone_lib="SCCCLR1C10E02"
/lab_host="DH108"
/clone_lib="Lr1"
/notes="Organ: Leaf roll from field grown adult plants (large insert library); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from leaf roll from field grown adult plants (large insert library). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

FEATURES

Location/Qualifiers
source
1..569
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone_lib="SCCCLR1C10E02"
/lab_host="DH108"
/clone_lib="Lr1"
/notes="Organ: Leaf roll from field grown adult plants (large insert library); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from leaf roll from field grown adult plants (large insert library). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 86.3%; Score 16.4; DB 6; Length 569;
Best Local Similarity 94.4%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATCGGCTAATC 19
| | | | | | | | | | | | | | | | | |
Db 299 CCCTGAATCGGCTAATC 282

RESULT 16

CX410223
LOCUS
DEFINITION JGI_XZT32869.rev NIH XGC tropAd5 Xenopus tropicalis cDNA clone IMAGE:7609044 3', mRNA sequence.
ACCESSION CX410223

```

VERSION
KEYWORDS
SOURCE
ORGANISM
CX410223.1 GI:57190925
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 655)
Richardson, P., Lucas, S., Rohrer, D., Dettler, J.C., Ng, D.C.,
Brookstein, P., and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI.XZT32869.fwd
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicalis.berkeley.edu/home
cDNA Library Preparation: Richard M. Harland Laboratory, University
of California, Berkeley
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.rev'
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Poly-A: Based upon the presence of a run of 14 or more T residues
at the beginning of the sequence, this clone was polyadenylated.
The resulting Poly-T sequence has been removed.
Plate: XZT 0341 row: i column: 10
High quality sequence stop: 503
POLYA=Yes.
FEATURES
source
Location/Qualifiers
1..655
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE.7609044"
/tissue_type="whole embryo"
/dev_stages="Tadpole (st. 36-41)"
/lab_host="E. coli XL1-Blue derivative, Stratagene
Electrofen-Blue"
/clone_lib="NIH XGC tropTads"
/notes="Vector: PCS108; Site 1: SalI; Site 2: NotI; Tadpole
library constructed by Russell B. Fletcher in R. Harland's
lab using poly A RNA and oligo dt primers (Invitrogen
SuperScript Plasmid System for cDNA Synthesis and
Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
into vector PCS108
(http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"
ORIGIN
Query Match 86.3%; Score 16.4; DB 8; Length 655;
Best Local Similarity 94.4%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGGCGCTAAT 18
|||||
Db 325 CCCCTGAATGGCGCTAAT 342
|||||

RESULT 17
CA125729/c
LOCUS
DEFINITION SCRLR1110E08.g LR1 Saccharum officinarum cDNA clone SCRLR1110E08
5', mRNA sequence.
ACCESSION CA125729
VERSION CA125729.1 GI:35003921

KEYWORDS
SOURCE
ORGANISM
EST.
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 690)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda, P.
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccnet.fcav.unesp.br
Plate: 110 row: E column: 08
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..690
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCRLR1110E08"
/lab_host="DH10B"
/clone_lib="LR1"
/notes="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN
Query Match 86.3%; Score 16.4; DB 6; Length 690;
Best Local Similarity 94.4%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CCTGTAATGGCGCTAATC 19
|||||
Db 299 CCTGTAATGGCGCTAATC 282
|||||

RESULT 18
BX867956/c
LOCUS
DEFINITION BX867956 tcba Oncorhynchus mykiss cDNA clone tcba0023c.o.02 5prim,
mRNA sequence.
ACCESSION BX867956
VERSION BX867956.1 GI:39991469
KEYWORDS
SOURCE
ORGANISM
Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 760)
Govoroun, M., Guiguen, Y. and Le Gac, P.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
Contact: Guiguen Y
INRA - SCRIBE

```

Campus de beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0023 row: o column: 2
 Seq primer: M13R.

FEATURES

source
 Location/Qualifiers
 1..760

/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcba023c.o.02"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tcba"
/notes="vector: pT7T3D-pac; Rainbow trout multi-tissues -
normalized + 1 subtraction; Clone distribution : AGENAE
Resource centre. Francois Piumi,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Query Match 86.3%; Score 16.4; DB 5; Length 760;
 Best Local Similarity 94.4%; Pred. No. 7.9e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATCGCGCTAATC 19
 Db 510 CCCTGAATCGCGTTAATC 493

RESULT 19

AG218963/c
 LOCUS
 DEFINITION
 Drosophila melanogaster DNA, clone:NP5046-3-1, flanking P[GawB]
 transposon insertion, genomic survey sequence.

AG218963
 VERSION
 AG218963.1 GI:22766383
 KEYWORDS
 GSS.
 SOURCE
 Drosophila melanogaster (fruit fly)

ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
 1 Hayashi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H.,
 Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R.,
 Uemura, T., Yoshihara, M. and Goto, S.

TITLE
 GETDB, a database compiling expression patterns and molecular
 locations of a collection of Gal4 enhancer traps

JOURNAL
 Genesis (2002) In press

REFERENCE
 2 (bases 1 to 800)

AUTHORS
 Hayashi, S.
 Direct Submission
 Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
 Developmental Biology, Laboratory for Morphogenetic Signaling;
 Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan
 (E-mail: shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,
 Fax:81-78-301-3183)

COMMENT
 This clone was isolated from genomic DNA flanking an insertion of
 the P element vector P[GawB] of a Drosophila strain.

FEATURES

source
 Location/Qualifiers
 1..800

/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="NP5046"
/db_xref="taxon:7227"

/chromosome="1"
/map="5C4"
/clone="NP5046-3-1"
/notes="flanking P[GawB] transposon insertion"

Query Match 86.3%; Score 16.4; DB 10; Length 800;
 Best Local Similarity 94.4%; Pred. No. 7.9e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGCGCTAAT 18
 Db 186 CCCTGAATCGCGCAAT 169

RESULT 20

DR126636
 LOCUS

DEFINITION
 Drosophila pseudoobscura 1104 bp mRNA linear EST 15-JUN-2005
 pseudoobscura cDNA clone A19 5', mRNA sequence.

ACCESSION
 DR126636
 VERSION
 DR126636.1 GI:67843334
 KEYWORDS
 EST.

SOURCE
 Drosophila pseudoobscura

ORGANISM
 Drosophila pseudoobscura
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
 1 (bases 1 to 1104)

AUTHORS
 Richards, S., Liu, Y., Bettencourt, B.R., Hradscky, P., Letovsky, S.,
 Nielsen, R., Thornton, K., Hubisz, M.J., Chen, R., Meisel, R.P.,
 Couronne, O., Hua, S., Smith, M.A., Zhang, P., Liu, J., Bussemaker, H.J.,
 van Batenburg, M.F., Howells, S.L., Scherer, S.E., Sodergren, E.,
 Matthews, B.B., Crosby, M.A., Schroeder, A.J., Ortiz-Barrientos, D.,
 Rives, C.M., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D.,
 Wheeler, D.A., Worley, K.C., Havlak, P., Durbin, K.J., Egan, A.,
 Gill, R., Hume, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y.,
 Waldron, L., Verdusco, D., Clerc-Blankenburg, K.P., Dubchak, I.,
 Noor, M.A., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W.,
 Geibart, W., Weinstein, G.M. and Gibbs, R.A.

TITLE
 Comparative genome sequencing of Drosophila pseudoobscura:
 chromosomal, gene, and cis-element evolution

JOURNAL
 Genome Res. 15 (1), 1-18 (2005)

COMMENT
 Contact: Stephen Richards
 Human Genome Sequencing Center
 Baylor College of Medicine
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713-798-6667
 Email: stephen@bcm.tmc.edu

NCBI Trace Archive: 226715407

Insert length: 1750 Std Error: 0.25.

FEATURES
 Location/Qualifiers

1..1104

/organism="Drosophila pseudoobscura"
/mol_type="mRNA"

/db_xref="taxon:7237"
/clone="A19"

/dev_stage="0-18h embryos"
/clone_lib="Drosophila pseudoobscura embryonic cDNA
library"

/notes="Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; oligo
dt priming from poly A+ RNA, directionally cloned"

ORIGIN

Query Match 86.3%; Score 16.4; DB 8; Length 1104;
 Best Local Similarity 94.4%; Pred. No. 8.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGCGCTAAT 18
 Db 740 CCCTGAATCGCGCTAAT 757

```

RESULT 21
CC751821/c
LOCUS
DEFINITION ZMMBB0133A01.r ZMMBBB Zea mays genomic clone ZMMBBB0133A01 3',
genomic survey sequence.
ACCESSION CC751821
VERSION CC751821
KEYWORDS GSS.
SOURCE CC751821.1 GI:32211287
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 485)
AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
and Wing,R.
TITLE Sequencing of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0133 row: A column: 01
Seq primer: M13r
Class: BAC ends.
FEATURES
source
location/Qualifiers
1..485
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0133A01"
/lab_host="DH10B"
/clone_lib="ZMMBBB"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. spp. mays"
ORIGIN
Query Match 84.2%; Score 16; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CCTGAATCGCGCTAAT 18
|||||
Db 199 CCTGAATCGCGCTAAT 184

RESULT 22
CL414924/c
LOCUS
DEFINITION ZMMBB0422D13r ZMMBBB (HindIII) Zea mays genomic clone
ZMMBB0422D13 3', genomic survey sequence.
ACCESSION CL414924
VERSION CL414924
KEYWORDS GSS.
SOURCE CL414924.1 GI:45273060
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 527)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Unpublished (2003)
TITLE Sequencing of the maize genome at PGIR (2003c)
JOURNAL Unpublished (2003)

CONTACT: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Freelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: Sp6
Class: BAC ends
High quality sequence start: 94.
FEATURES
source
location/Qualifiers
1..527
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0422D13"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBB (HindIII)"
/note="Vector: pCUGi; Site_1: HindIII; Site_2: HindIII"
ORIGIN
Query Match 84.2%; Score 16; DB 10; Length 527;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CCTGAATCGCGCTAAT 18
|||||
Db 273 CCTGAATCGCGCTAAT 258

RESULT 23
BZ718658
LOCUS
DEFINITION PUCEY99TD_ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTrA13K17,
genomic survey sequence.
ACCESSION BZ718658
VERSION BZ718658
KEYWORDS GSS.
SOURCE BZ718658.1 GI:28505644
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 547)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
TITLE
JOURNAL
COMMENT Contact: Cathy Whitelaw
TIGR Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES
source
location/Qualifiers
1..547
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTrA13K17"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"
ORIGIN
Query Match 84.2%; Score 16; DB 9; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18
    |||||
Db 408 CCTGAATGCGGCTAAT 423

RESULT 24
CX698830 595 bp mRNA linear EST 19-JAN-2005
LOCUS ydb82909.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
DEFINITION clone ydb82909 5' similar to TR:Q94532 Q94532 PUTATIVE TYPE III
ALCOHOL DEHYDROGENASE. [1] ; mRNA sequence.
ACCESSION CX698830
VERSION CX698830.1 GI:57961723
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoida;
Echinoidea; Euechinoidea; Echinacea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 595)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RppOT
High quality sequence stop: 595.
FEATURES
source
1..595
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="ydd56d01"
/lab_host="DH10B"
/clone_lib="Sea urchin EST Lib1"
/notes="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;
Site 2: SmaI; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMVSPORT6.1 (Invitrogen)"

ORIGIN
Query Match 84.2%; Score 16; DB 8; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAA 17
    |||||
Db 376 CCTGAATGCGGCTAA 391

RESULT 26
CX691884 632 bp mRNA linear EST 19-JAN-2005
LOCUS ydd36h05.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
DEFINITION clone ydd36h05 5' similar to TR:Q9U2M4 Q9U2M4 Y38F1A.6 PROTEIN. [1]
; mRNA sequence.
ACCESSION CX691884
VERSION CX691884.1 GI:57953941
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidea;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center

```

```

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 596)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RppOT
High quality sequence stop: 596.
FEATURES
source
1..596
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="ydd56d01"
/lab_host="DH10B"
/clone_lib="Sea urchin EST Lib1"
/notes="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;
Site 2: SmaI; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMVSPORT6.1 (Invitrogen)"

ORIGIN
Query Match 84.2%; Score 16; DB 8; Length 596;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAA 17
    |||||
Db 376 CCTGAATGCGGCTAA 391

RESULT 26
CX691884 632 bp mRNA linear EST 19-JAN-2005
LOCUS ydd36h05.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
DEFINITION clone ydd36h05 5' similar to TR:Q9U2M4 Q9U2M4 Y38F1A.6 PROTEIN. [1]
; mRNA sequence.
ACCESSION CX691884
VERSION CX691884.1 GI:57953941
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center

```

Seq primer: -28RppOT
 High quality sequence stop: 591.
 Location/Qualifiers
 1. .632
 /organism="Strongylocentrotus purpuratus"
 /mol_type="mRNA"
 /db_xref="taxon:7668"
 /clone="ydd36h05"
 /lab_host="DH10B"
 /clone_lib="Sea urchin EST Lib1"
 /note="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;
 Site 2: SmaI; Arrayed normalized library of full-length
 cDNAs representing blastula stage transcriptome of the sea
 urchin Strongylocentrotus purpuratus, cloned into the
 vector pCMVSPORT6.1 (Invitrogen)"

ORIGIN

Query Match 84.2%; Score 16; DB 8; Length 632;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 CCTGAATGCGGCTAA 17
 |||||
 Db 364 CCTGAATGCGGCTAA 379

RESULT 27

CX557631 675 bp mRNA linear EST 12-JAN-2005
 LOCUS yda39d02.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
 DEFINITION clone yda39d02 5' similar to TR:Q9U2M4 Q9U2M4 Y38F1A.6 PROTEIN. [1]
 ;, mRNA sequence.
 ACCESSION CX557631
 VERSION CX557631.1 GI:57584660
 KEYWORDS EST.
 SOURCE Strongylocentrotus purpuratus
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Euechinoidea; Echinacea; Echinoidea;
 Strongylocentrotidae; Strongylocentrotus.
 REFERENCE 1 (bases 1 to 675)
 AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
 Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
 Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
 Wilson,R.

TITLE

WashU Sea Urchin EST Project
 Unpublished (2004)
 CONTACT: Dr. James A. Coffman
 WASHU Sea Urchin EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 DNA sequencing by: Washington University Genome Sequencing Center
 Seq primer: -28RppOT
 High quality sequence stop: 519.
 Location/Qualifiers
 1. .675
 /organism="Strongylocentrotus purpuratus"
 /mol_type="mRNA"
 /db_xref="taxon:7668"
 /clone="yda39d02"
 /lab_host="DH10B"
 /clone_lib="Sea urchin EST Lib1"
 /note="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;
 Site 2: SmaI; Arrayed normalized library of full-length
 cDNAs representing blastula stage transcriptome of the sea
 urchin Strongylocentrotus purpuratus, cloned into the
 vector pCMVSPORT6.1 (Invitrogen)"

FEATURES

source

Query Match

84.2%; Score 16; DB 8; Length 675;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

source

Oy 2 CCTGAATGCGGCTAA 17
 |||||
 Db 113 CCTGAATGCGGCTAA 128

RESULT 28

CX692600 676 bp mRNA linear EST 19-JAN-2005
 LOCUS yde83d07.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
 DEFINITION clone yde83d07 5' similar to TR:Q9U2M4 Q9U2M4 Y38F1A.6 PROTEIN. [1]
 ;, mRNA sequence.
 ACCESSION CX692600
 VERSION CX692600.1 GI:57954747
 KEYWORDS EST.
 SOURCE Strongylocentrotus purpuratus
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Euechinoidea; Echinacea; Echinoidea;
 Strongylocentrotidae; Strongylocentrotus.
 REFERENCE 1 (bases 1 to 676)
 AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
 Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
 Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
 Wilson,R.

TITLE

JOURNAL

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COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J. and Wing,R.

JOURNAL
COMMENT Sequencing of the maize genome Unpublished (2003)

Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu

PCR Primers
FORWARD: T7
BACKWARD: M13r

Plate: 0133 row: A column: 03

Seq primer: M13r

Class: BAC ends.

Location/Qualifiers
1. 784

FEATURES
source
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0133A03"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/notes="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"
HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 84.2%; Score 16; DB 9; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18
|||||
Db 293 CCTGAATGCGGCTAAT 278

RESULT 30

CC753964/c

LOCUS

DEFINITION ZMMBB01337J07.r ZMMBBb Zea mays genomic clone ZMMBBb01337J07 3', 787 bp DNA linear GSS 25-JUN-2003

genomic sequence.

ACCESSION CC753964

VERSION CC753964.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J. and Wing,R.

JOURNAL
COMMENT Sequencing of the maize genome Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: T7

BACKWARD: M13r

Plate: 0137 row: J column: 07

Seq primer: M13r

Class: BAC ends.

Location/Qualifiers

1. 787
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB01337J07"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/notes="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"
HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 84.2%; Score 16; DB 9; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18
|||||
Db 295 CCTGAATGCGGCTAAT 280

RESULT 31

CB945315

LOCUS

DEFINITION AGENCOURT 13841963 NICHD_XGC_Tad2 Xenopus laevis cDNA clone IMAGE:6933220 5', mRNA sequence.

ACCESSION CB945315

VERSION CB945315.1

KEYWORDS GI:30194442

SOURCE EST.

ORGANISM Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 809)

AUTHORS NCI-CGAP

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: Drs. Donald Brown and Liqun Cai

cDNA Library Preparation: CLONTECH

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM3248 row: b column: 03

High quality sequence stop: 447.

Location/Qualifiers

1. 809

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:6933220"

/dev_stage="metamorphosis stage 62"

/clone_lib="NICHD_XGC_Tad2"

/notes="Organ: Developing tadpole; Vector: pDNR-LIB;

Site 1: SfiI; Site 2: SfiI; 5' and 3' adaptors were used

in cloning as follows: 5' adaptor sequence:

5'-CACGGCCATTATGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGGCGGCATG-TT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.7 kb

(range 0.8-3.0 kb). 15/15 colonies contained inserts by

PCR. This library was enriched for full-length clones and

was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 84.2%; Score 16; DB 6; Length 809;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTA 16
 |||||
 Db 454 CCCCTGAATCGGCTA 469

RESULT 32
 CG038424/c
 LOCUS
 DEFINITION PUFKT95TD ZM_0.6.1.0 KB Zea mays genomic clone ZMBETA0672P22,
 genomic survey sequence.

ACCESSION CG038424
 VERSION CG038424.1 GI:33910580
 KEYWORDS GSS.

SOURCE
 ORGANISM

Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
 AUTHORS

1 (bases 1 to 838)
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
 Bennetzen, J.

TITLE
 JOURNAL
 COMMENT

Maize Genomics Consortium
 Unpublished (2003)
 Other GSSs: PUFKT95TB
 Contact: Cathy Whitelaw
 TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TP
 Class: shared ends.

FEATURES
 source
 1..838

/organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMBETA0672P22"
 /clone_lib="ZM_0.6.1.0 KB"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 Cot selected genomic DNA library"

ORIGIN

Query Match 84.2%; Score 16; DB 10; Length 838;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATCGGCTAAT 18
 |||||
 Db 317 CCTGAATCGGCTAAT 302

RESULT 33
 BE000416
 LOCUS
 DEFINITION MRO-BN0070-120500-021-a06_1 BN0070 Homo sapiens cDNA, mRNA
 sequence.

ACCESSION BE000416
 VERSION BE000416.1 GI:8260636
 KEYWORDS EST.

SOURCE
 ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE
 AUTHORS

1 (bases 1 to 262)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

TITLE
 JOURNAL
 PUBMED
 COMMENT

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=MR0-BN0070-120
 500-021-a06_1&t3=2000-05-12&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 262.

FEATURES
 source

Location/Qualifiers
 1..262
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="EN0070"

/note="Organ: breast normal; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 83.2%; Score 15.8; DB 2; Length 262;
 Best Local Similarity 89.5%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
 |||||

Db 11 CCCCTCAATCGGCTGATC 29
 |||||

RESULT 34
 AUI176457

LOCUS

DEFINITION AUI176457 Rice panicle at flowering stage Oryza sativa (japonica
 cultivar-group) cDNA clone E3017, mRNA sequence.

ACCESSION AUI176457.1 GI:13422398

VERSION AUI176457

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 300)

Sasaki, T. and Yamamoto, K.

Rice cDNA from panicle at flowering stage (2001)

Unpublished (2001)

Contact: Takuji Sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
 305-8602, Japan

Tel: 81-298-38-7441

Fax: 81-298-38-7468

Email: tsasaki@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
 PROJECT = 'RGP'

```

FEATURES
  source
    Location/Qualifiers
      1. 300
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nipponbare"
        /db_xref="taxon:39947"
        /clone="E3017"
        /dev_stage="flowering stage"
        /clone_lib="Rice panicle at flowering stage"
        /note="Organ: panicle; Rice cDNA from panicle at flowering
stage"

ORIGIN
  Query Match      83.2%; Score 15.8; DB 1; Length 300;
  Best Local Similarity 89.5%; Pred. No. 1.5e+03;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 261 CCCCTGAGTGCAGCTAATC 279

RESULT 35
BE405912
LOCUS
DEFINITION
  BE405912 361 bp mRNA linear EST 21-JUL-2000
  WHE0401_g02_g022B Wheat etiolated seedling root cDNA library
  Triticum aestivum cDNA clone WHE0401_g02_g02, mRNA sequence.

ACCESSION
  BE405912
VERSION
  BE405912.1 GI:9365380
KEYWORDS
  EST.
SOURCE
  Triticum aestivum (bread wheat)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Pooideae; Triticeae; Triticum.
  1 (bases 1 to 361)
  Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rauech, C.J.,
  Seaton, C.L. and Tong, J.C.
  The structure and function of the expressed portion of the wheat
  genomes
  Unpublished (2000)
  Contact: Olin Anderson
  US Department of Agriculture, Agriculture Research Service, Pacific
  West Area, Western Regional Research Center
  800 Buchanan Street, Albany, CA 94710, USA
  Tel: 5105595773
  Email: oanderson@pw.usda.gov
  Fax: 5105595818
  Sequence have been trimmed to remove vector sequence and low
  quality sequence with phred score less than 20
  Seq primer: Strategene pBluescript SK reverse primer.

FEATURES
  source
    Location/Qualifiers
      1. 361
        /organism="Triticum aestivum"
        /mol_type="mRNA"
        /cultivar="Chinese Spring"
        /db_xref="taxon:4565"
        /clone="WHE0401_g02_g02"
        /tissue_type="Root"
        /dev_stage="Five day old etiolated seedling"
        /lab_host="E. coli SOLR"
        /clone_lib="Wheat etiolated seedling root cDNA library"
        /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
        Site 1: EcoRI; Site 2: XhoI; Seeds were
        surface-sterilized, germinated and grown aseptically in
        the dark at room temperature on filter paper with water,
        nystatin and cefotaxime in covered crystallization
        dishes. Roots were harvested. The tissue, total RNA, and
        poly(A) RNA were prepared, a cDNA library was made, and
        the cDNA clones were in vivo excised to give phagescript
        phagemids in the TJ Close lab (Choi, Close, Fenton) at the
        University of California, Riverside. Plasmid DNA

```

```

preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

ORIGIN
  Query Match      83.2%; Score 15.8; DB 2; Length 361;
  Best Local Similarity 89.5%; Pred. No. 1.5e+03;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 323 CCCCTGAGTGCAGCTAATC 341

RESULT 36
BJ468982
LOCUS
DEFINITION
  BJ468982 417 bp mRNA linear EST 23-MAY-2002
  K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal12e23 5', mRNA sequence.

ACCESSION
  BJ468982
VERSION
  BJ468982.1 GI:21147486
KEYWORDS
  EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Pooideae; Triticeae; Hordeum.
  1 (bases 1 to 417)
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tehini@genes.nig.ac.jp.
  Location/Qualifiers
    1. 417
      /organism="Hordeum vulgare subsp. vulgare"
      /mol_type="mRNA"
      /cultivar="Haruna Nijo"
      /sub_species="vulgare"
      /db_xref="taxon:112509"
      /clone="baal12e23"
      /tissue_type="top three leaves"
      /dev_stage="adult, heading stage"
      /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
      Nijo adult, heading stage top three leaves"

ORIGIN
  Query Match      83.2%; Score 15.8; DB 3; Length 417;
  Best Local Similarity 89.5%; Pred. No. 1.5e+03;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 232 CCCCTGAGTGCAGCTAATC 250

RESULT 37
BJ473149
LOCUS
DEFINITION
  BJ473149 422 bp mRNA linear EST 23-MAY-2002
  K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal38103 5', mRNA sequence.

ACCESSION
  BJ473149
VERSION
  BJ473149.1 GI:21151652
KEYWORDS
  EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 422)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@genes.nig.ac.jp.

FEATURES
    source
        1..422
            /organism="Hordeum vulgare subsp. vulgare"
            /mol_type="mRNA"
            /cultivar="Haruna Nijo"
            /sub_species="vulgare"
            /db_xref="taxon:112509"
            /clone="baal38103"
            /tissue_type="top three leaves"
            /dev_stage="adult, heading stage"
            /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
            Nijo adult, heading stage top three leaves"

ORIGIN
    Query Match      83.2%; Score 15.8; DB 3; Length 422;
    Best Local Similarity 89.5%; Pred. No. 1.6e+03;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
    ||||| ||| |||||
Db 254 CCCCTGAGTGCAGCTAATC 272

RESULT 38
BU971174
LOCUS
DEFINITION
    HB16N07: BC Hordeum vulgare subsp. vulgare cDNA clone HB16N07
5-PRIME, mRNA sequence.
VERSION
    BU971174.1 GI:24221967
KEYWORDS
    EST.
SOURCE
    Hordeum vulgare subsp. vulgare
    Hordeum vulgare subsp. vulgare
    Hordeum vulgare subsp. vulgare
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Pooidae; Triticeae; Hordeum.
REFERENCE
    1 (bases 1 to 431)
    Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
    Barley ESTs from developing seeds
    Unpublished (2002)
    Contact: Stein Nils
    Molecular Markers Group, Department Genbank
    Institute of Plant Genetics and Crop Plant Research (IPK)
    Corrensstr. 3, 06466, Gatersleben, Germany
    Tel: 039482-5522
    Fax: 039482-5595
    Email: stein@ipk-gatersleben.de
    Insert Length: 431 Std Error: 0.00
    Plate: 16 row: N column: 7
    Seq primer: M13rev.
    Location/Qualifiers
        1..431
            /organism="Hordeum vulgare subsp. vulgare"
            /mol_type="mRNA"
            /cultivar="Barke"
            /sub_species="vulgare"
            /db_xref="GABI:236006"
            /db_xref="taxon:112509"
            /clone="HB16N07"
            /tissue_type="developing caryopsis"

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 422)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@genes.nig.ac.jp.

FEATURES
    source
        1..422
            /organism="Hordeum vulgare subsp. vulgare"
            /mol_type="mRNA"
            /cultivar="Haruna Nijo"
            /sub_species="vulgare"
            /db_xref="taxon:112509"
            /clone="baal38103"
            /tissue_type="top three leaves"
            /dev_stage="adult, heading stage"
            /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
            Nijo adult, heading stage top three leaves"

ORIGIN
    Query Match      83.2%; Score 15.8; DB 3; Length 422;
    Best Local Similarity 89.5%; Pred. No. 1.6e+03;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
    ||||| ||| |||||
Db 254 CCCCTGAGTGCAGCTAATC 272

RESULT 38
BU971174
LOCUS
DEFINITION
    HB16N07: BC Hordeum vulgare subsp. vulgare cDNA clone HB16N07
5-PRIME, mRNA sequence.
VERSION
    BU971174.1 GI:24221967
KEYWORDS
    EST.
SOURCE
    Hordeum vulgare subsp. vulgare
    Hordeum vulgare subsp. vulgare
    Hordeum vulgare subsp. vulgare
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Pooidae; Triticeae; Hordeum.
REFERENCE
    1 (bases 1 to 431)
    Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
    Barley ESTs from developing seeds
    Unpublished (2002)
    Contact: Stein Nils
    Molecular Markers Group, Department Genbank
    Institute of Plant Genetics and Crop Plant Research (IPK)
    Corrensstr. 3, 06466, Gatersleben, Germany
    Tel: 039482-5522
    Fax: 039482-5595
    Email: stein@ipk-gatersleben.de
    Insert Length: 431 Std Error: 0.00
    Plate: 16 row: N column: 7
    Seq primer: M13rev.
    Location/Qualifiers
        1..431
            /organism="Hordeum vulgare subsp. vulgare"
            /mol_type="mRNA"
            /cultivar="Barke"
            /sub_species="vulgare"
            /db_xref="GABI:236006"
            /db_xref="taxon:112509"
            /clone="HB16N07"
            /tissue_type="developing caryopsis"

```

```

/dev_stage="8-15 DAP (days after pollination)"
/clone_host="XL10-Gold"
/clone_lib="BC"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); developing
caryopsis, 8-15 DAP(days after pollination) Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present, as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable."

ORIGIN
    Query Match      83.2%; Score 15.8; DB 5; Length 431;
    Best Local Similarity 89.5%; Pred. No. 1.6e+03;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
    ||||| ||| |||||
Db 249 CCCCTGAGTGCAGCTAATC 267

RESULT 39
AZ233765
LOCUS
DEFINITION
    RPCI-23-99L13.TJ RPCI-23 Mus musculus genomic clone RPCI-23-99L13,
    genomic survey sequence.
ACCESSION
    AZ233765
VERSION
    AZ233765.1 GI:8541811
KEYWORDS
    GSS.
SOURCE
    Mus musculus (house mouse)
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 443)
    Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
    Akinret, B., Levins, M., McGann, S., Teegaye, G., Geer, K., Krol, M., de
    Jong, P. and Fraser, C.M.
    Mouse BAC End Sequences from Library RPCI-23
    Unpublished (1999)
    Other GSSs: RPCI-23-99L13.TV
    Contact: Shaying Zhao
    Department of Eukaryotic Genomics
    The Institute for Genomic Research
    9712 Medical Center Dr., Rockville, MD 20850, USA
    Tel: 301 838 0200
    Fax: 301 838 0208
    Email: szhao@tigr.org
    Clones are derived from the mouse BAC library RPCI-23. For BAC
    library availability, please contact Pieter de Jong
    (pieter@dejong.med.buffalo.edu). Clones may be purchased from
    BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
    or from Resea ch Genetics (info@resgen.com). BAC end page:
    http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html
    Plate: 99 row: L column: 13
    Seq primer: SP6
    Class: BAC ends.
    Location/Qualifiers
        1..443
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="RPCI-23-99L13"
            /sex="Female"
            /lab_host="DH10B"
            /clone_lib="RPCI-23"
            /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
            EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
            brain genomic DNA was isolated and partially digested
            with a combination of EcoRI and EcoRI Methylase. Size

```

selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "

ORIGIN

Query Match 83.2%; Score 15.8; DB 9; Length 443;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||||| ||||| |||||
Db 345 CCCCTAAATGCTGCTAATC 363

RESULT 40

DNI183928
LOCUS HO16114S HO Hordeum vulgare cDNA clone HO16114 5-PRIME, mRNA
DEFINITION DNI183928 456 bp mRNA linear EST 24-FEB-2005
sequence.

ACCESSION DNI183928
VERSION DNI183928.1 GI:60279185
KEYWORDS EST.
SOURCE Hordeum vulgare

ORGANISM

Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 456)

REFERENCE Zierold, U. and Schweitzer, P.
AUTHORS Transcriptome analysis of mlo-mediated resistance in the epidermis
TITLE of barley

JOURNAL

COMMENT Mol. Plant Pathol. (2005) In press
Contact: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5660
Fax: 0049 (0)39482-5595
Email: schweiz@ipk-gatersleben.de
Insert Length: 456 Std Error: 0.00
Plate: 16 row: I column: 14
Seq primer: SK.

FEATURES

source

Location/Qualifiers

1..456
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Ingrid BC mlo-5"
/db_xref="GABI:1094605"
/db_xref="taxon:4513"
/clone="HO16114"
/tissue_type="leaf epidermis, 6 h and 24 h post
inoculation with Blumeria graminis"
/dev_stage="7 d after germination"
/lab_host="XL10-Gold"
/clone_lib="HO"
/note="vector: pBlueScript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of
the clones correspond to cDNA from the fungi B. graminis
hordei and tritici, respectively. Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is
1.2 kb"

ORIGIN

Query Match 83.2%; Score 15.8; DB 8; Length 456;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 227 CCCCTGAGTCAGCTAATC 245
||||| ||||| ||||| |||||

RESULT 41

AV932335

LOCUS

DEFINITION

AV932335 463 bp mRNA linear EST 18-JAN-2002
AV932335 K. Sato unpublished cDNA library, cv. Haruna Niho adult,
heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
clone baal3d09 5', mRNA sequence.

ACCESSION AV932335

VERSION AV932335.1 GI:18228132

KEYWORDS EST.

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 463)

AUTHORS Sato, K., Saisho, D. and Takeda, K.

TITLE Barley EST sequencing project in NIG and Okayama Univ

JOURNAL Unpublished (2002)

COMMENT Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tehini@genes.nig.ac.jp.

Location/Qualifiers

1..463

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Haruna Niho"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="baal3d09"

/tissue_type="top three leaves"

/dev_stage="adult, heading stage"

/clone_lib="K. Sato unpublished cDNA library, cv. Haruna

Niho adult, heading stage top three leaves"

ORIGIN

Query Match 83.2%; Score 15.8; DB 1; Length 463;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

||||| ||||| ||||| |||||

Db 236 CCCCTGAGTCAGCTAATC 254

RESULT 42

CA657673

LOCUS

DEFINITION

CA657673 472 bp mRNA linear EST 24-NOV-2002
wlm0.pk038.i13 wlm0 Triticum aestivum cDNA clone wlm0.pk038.i13 5'
end, mRNA sequence.

ACCESSION CA657673

VERSION CA657673.1 GI:25236198

KEYWORDS EST.

SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 472)

AUTHORS Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hayney, C., Yuan, Z.,

Miao, G., Caraher, N. and Hanafey, M.K.

TITLE Dupont Wheat cDNA Sequence

JOURNAL Unpublished (2002)

COMMENT Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@USA.dupont.com
 Seq primer: M13.

FEATURES

Location/Qualifiers
 1..472
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Stephens"
 /db_xref="taxon:4565"
 /clone="wlm0.pk038.i13"
 /tissue_type="leaf"
 /clone_lib="wlm0"
 /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum L.) seedlings 0 hr after inoculation with Erysiphe graminis f. sp. tritici"

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 472;
 Best Local Similarity 89.5%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19

Db 65 CCCCTGAATGGCGCTAATC 83

RESULT 43

LOCUS AV774105/472 bp mRNA linear EST 18-AUG-2004
 DEFINITION AV774105 Lotus japonicus Pods (20-30 mm in length) Lotus corniculatus var. japonicus cDNA clone MPD061h04_f 3', mRNA sequence.

ACCESSION AV774105.1 GI:45397780

VERSION EST.

KEYWORDS Lotus corniculatus var. japonicus (Lotus japonicus)

SOURCE Lotus corniculatus var. japonicus

ORGANISM Lotus corniculatus var. japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

REFERENCE 1 (bases 1 to 487)

AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

TITLE Characteristics of the Lotus japonicus gene repertoire deduced from large-scale expressed sequence tag (EST) analysis

JOURNAL Plant Mol. Biol. 54 (3), 405-414 (2004)

PUBMED 15284495

COMMENT Contact: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

Location/Qualifiers
 1..487
 /organism="Lotus corniculatus var. japonicus"
 /mol_type="mRNA"
 /isolate="Wiyakojima MG-20"
 /db_xref="taxon:34305"
 /clone="MPD061h04_f"
 /tissue_type="Pods (20-30 mm in length)"
 /clone_lib="Lotus japonicus Pods (20-30 mm in length)"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 83.2%; Score 15.8; DB 1; Length 487;
 Best Local Similarity 89.5%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19

|||||

Db 448 CCCCTGAATGGCTAAAC 430

RESULT 44

LOCUS CC472389/c

DEFINITION CC472389

ACCESSION CC472389

VERSION CC472389

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 494)

AUTHORS Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,

Tsai, W., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,

Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,

Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,

Dalrymple, B. P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Unpublished (2003)

Other GSSs: CH240_296A12.T7

COMMENT Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6

Tel: 604-877-6085

Fax: 604-877-6276

Email: rholt@bccsc.ca

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@bmc.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/orderinginformation.htm). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the

British Columbia Genome Sciences Centre, Canada.

Plate: 296 row: A column: 12

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1..494

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="breed: Hereford"

/db_xref="taxon:9913"

/clone="CH240_296A12"

/sex="Male"

/cell_type="Blood"

/clone_lib="CHORI-240"

/note="vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;

Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC

library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 83.2%; Score 15.8; DB 9; Length 494;

Best Local Similarity 89.5%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19

|||||

Db 468 CCCCTGAATTCGTCTAATC 450

RESULT 45

LOCUS DN183756

DEFINITION DN183756

511 bp mRNA linear EST 24-FEB-2005

HO16J13S HO Hordeum vulgare cDNA clone HO16J13 5-PRIME, mRNA

sequence.

ACCESSION DNL83756
VERSION DNL83756.1 GI:80279013
KEYWORDS EST
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
AUTHORS 1 (bases 1 to 511)
TITLE Zierold, U. and Schweizer, P.
JOURNAL Transcriptional analysis of mlo-mediated resistance in the epidermis of barley
COMMENT Mol. Plant Pathol. (2005) In press
 Contact: Patrick Schweizer
 Transcription Analysis, Cytogenetics Department
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, D-06466 Gatersleben, Germany
 Tel: 0049 (0)39482-5660
 Fax: 0049 (0)39482-5595
 Email: schweiz@ipk-gatersleben.de
 Insert Length: 511 Std Error: 0.00
 Plate: 16 row: J column: 13
 Seq primer: SK.

FEATURES
 source
 1..511
 /organism="Hordeum vulgare"
 /mol_type="mRNA"
 /cultivar="Ingrid BC mlo-5"
 /db_xref="GABI:1094623"
 /db_xref="taxon:4513"
 /clone="H016D13"
 /tissue_type="leaf epidermis, 6 h and 24 h post inoculation with Blumeria graminis"
 /dev_stage="7 d after germination"
 /lab_host="XL10-Gold"
 /clone_lib="HO"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of the clones correspond to cDNA from the fungi B. graminis hordii and tritici, respectively. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 1.2 kb"

ORIGIN
 Query Match 83.2%; Score 15.8; DB 8; Length 511;
 Best Local Similarity 89.5%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CCCCTGAATCGCGCTAATC 19
 ||||| ||||| |||||
 Db 227 CCCCTGAGTGCAGCTAATC 245

RESULT 46
LOCUS AW585068
DEFINITION N211264e MHAM Medicago truncatula/Glomus versiforme mixed EST
ACCESSION AW585068
VERSION AW585068.1 GI:7262122
KEYWORDS EST
SOURCE Medicago truncatula/Glomus versiforme mixed EST library
ORGANISM Eukaryota; mixed EST libraries.
REFERENCE 1 (bases 1 to 513)
AUTHORS Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
TITLE ESTs from roots of Medicago truncatula after colonization with

JOURNAL COMMENT
 Unpublished (2000)
 Contact: Harrison, M.J.
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73401
 Tel: 580-223-5810
 Fax: 580-221-7380
 Email: mjharrison@noble.org
 Other name: MHAM-23b-B04; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysie.tamu.edu/medicago'.
 Seq primer: T3.

FEATURES
 source
 1..513
 /organism="Medicago truncatula/Glomus versiforme mixed EST library"
 /mol_type="mRNA"
 /cultivar="Medicago truncatula genotype A17"
 /db_xref="taxon:119092"
 /clone="MHAM-23C8"
 /tissue_type="roots colonized with Glomus versiforme"
 /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XL0LR"
 /clone_lib="MHAM"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

ORIGIN
 Query Match 83.2%; Score 15.8; DB 1; Length 513;
 Best Local Similarity 89.5%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CCCCTGAATCGCGCTAATC 19
 ||||| ||||| |||||
 Db 254 CCCCTAATCGCTAATC 272

RESULT 47
LOCUS CB884273/c
DEFINITION EST00104 Oryza minuta 101144 subtracted cDNA library Oryza minuta cDNA clone omw1-146 similar to cysteine protease, mRNA sequence.
ACCESSION CB884273
VERSION CB884273.1 GI:46931502
KEYWORDS EST.
SOURCE Oryza minuta
ORGANISM Oryza minuta
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 525)
AUTHORS Cho, S.K., Jeung, J.U., Shim, K.S., Jung, K.W., Kang, K.H., Chung, Y.S., Ok, S.H., Choi, H.C. and Shin, J.S.
TITLE Oryza minuta 101144 subtracted cDNA library
JOURNAL Unpublished (2003)
COMMENT Contact: Sung Ki Cho, Ji Ung Jeung, Kyu Suk Shim, Kwang Wook Jung, Kyung Ho Kang, Young Soo Chung, Sung Han Ok, Hae Chune Choi and Jeong Sheop Shin
 Genetics School of Life Science and Biotechnology, Korea University
 5 Ga, Anam-Dong, Sungbuk-Gu, Seoul, 136-701, Republic of Korea
 Tel: 82 2 3290 3430
 Fax: 82 2 927 9028

Email: jsshin@korea.ac.kr

Seq primer: M13R.

Location/Qualifiers
1..525

FEATURES

source

/organism="Oryza minuta"
/mol_type="mRNA"
/strain="101144"
/db_xref="taxon:63629"
/clone="Omwi-146"
/tissue_type="leaf"
/dev_stage="Wound treatment & vegetative stage"
/clone_lib="Oryza minuta 101144 subtracted cDNA library"
/note="Vector: PCR2.1(Invitrogen); After the suppression subtractive hybridization and MOS (Nucleic Acids Research, Vol 28, No 20, e90), cDNA fragments induced by wound treatment were cloned by TA cloning method, and screened by microarray."

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 525;

Best Local Similarity 89.5%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 488 CCCCTGAGTGCAGCTAATC 470

RESULT 48

LOCUS

DEFINITION CD026506 525 bp mRNA linear EST 01-MAY-2004
Oryza minuta 101144 subtracted cDNA library Oryza minuta
cDNA clone omi-855, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 525)
AUTHORS Cho, S.K., Jeung, J.U., Shim, K.S., Jung, K.W., Kang, K.H., Chung, Y.S.,
Ok, S.H., Choi, H.C. and Shin, J.S.
TITLE Oryza minuta 101144 subtracted cDNA library
JOURNAL Unpublished (2003)
COMMENT Contact: Sung Ki Cho, Ji Ung Jeung, Kyu Suk Shim, Kwang Wook Jung,
Kyung Ho Kang, Young Soo Chung, Sung Han Ok, Hae Chune Choi and
Jeong Sheop Shin

Plant Molecular Genetics

School of Life Science and Biotechnology, Korea University

5 Ga, Anam-Dong, Sungbuk-Gu, Seoul, 136-701, Republic of Korea

Tel: 82 2 3290 3430

Fax: 82 2 927 9028

Email: jsshin@korea.ac.kr

Seq primer: M13R.

Location/Qualifiers

1..525

/organism="Oryza minuta"

/mol_type="mRNA"

/strain="101144"

/db_xref="taxon:63629"

/clone="Omwi-855"

/tissue_type="leaf"

/dev_stage="Wound treatment & vegetative stage"

/clone_lib="Oryza minuta 101144 subtracted cDNA library"

/note="Vector: PCR2.1(Invitrogen); After the suppression subtractive hybridization and MOS (Nucleic Acids Research, Vol 28, No 20, e90), cDNA fragments induced by wound treatment were cloned by TA cloning method, and screened by microarray."

ORIGIN

Query Match

Best Local Similarity 83.2%; Score 15.8; DB 6; Length 525;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 488 CCCCTGAGTGCAGCTAATC 470

RESULT 49

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

1 (bases 1 to 544)

Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1..544

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Haruna Nijo"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="baall3p10"

/tissue_type="top three leaves"

/dev_stage="adult, heading stage"

/clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"

ORIGIN

Query Match

Best Local Similarity 83.2%; Score 15.8; DB 3; Length 544;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 328 CCCCTGAGTGCAGCTAATC 346

RESULT 50

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 545)

Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J.,

Bouchireb, N., Cottage, A., Yeo, G.S., Umrana, Y., Williams, G. and

Genomic survey sequence.

AL004093.1 GI:2449663

GSS: genome survey sequence.

Takifugu rubripes (Fugu rubripes)

Takifugu rubripes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.


```

KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
TITLE The Genomes of Oryza sativa: A History of Duplications
JOURNAL PLOS Biol. 3 (2), e38. (2005)
PUBMED 15685292
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805986
Fax: 86-571-56805984
Email: zhouyan@genomics.org.cn
Seq primer: M3 Forward
High quality sequence stop: 564
POLYA=No.

FEATURES
source Location/Qualifiers
1..564
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="93-11"
/db_xref="taxon:4530"
/tissue_type="whole plant"
/dev stage="tillering"
/clone_lib="Oryza sativa cv. 93-11 tillering whole plant
cDNA library"

ORIGIN
Query Match 83.2%; Score 15.8; DB 7; Length 564;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19
||||| ||| |||||
Db 521 CCCCTGAGTGCAGCTAATC 539

RESULT 54
AU249544 LE Lolium multiflorum cDNA clone LE009H09-5, mRNA
LOCUS AU249544
DEFINITION AU249544 LE Lolium multiflorum cDNA clone LE009H09-5, mRNA
sequence.
ACCESSION AU249544
VERSION AU249544.1 GI:46506813
KEYWORDS EST.
SOURCE Lolium multiflorum (Italian ryegrass)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Poaceae; Poaeae; Lolium.
REFERENCE 1 (bases 1 to 568)
AUTHORS Ikeda,S.
TITLE Lolium multiflorum EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Seiji Yazaki
Japan Grassland Agriculture and Forage Seed Association
Forage Crop Research Institute (FCRI)
Higashiakada 388-5, Nishinasuno, Tochigi 329-2742, Japan
Tel: 81-287-37-6755
Fax: 81-287-37-6757
Email: yazakis@fscs.or.jp
contact:Tadaaki Takamizo (takamizo@affrc.go.jp)

FEATURES
source Location/Qualifiers
1..568
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BatXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 83.2%; Score 15.8; DB 10; Length 569;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19
||||| ||| |||||
Db 261 CCCCTGAGTGCAGCTAATC 279

RESULT 56
CB212741
LOCUS CB212741
DEFINITION OML03021 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',

```

```

National Institute of Livestock and Grassland Science, Nishinasuno
Resistance gene analog.
Location/Qualifiers
1..568
/organism="Lolium multiflorum"
/mol_type="mRNA"
/db_xref="taxon:4521"
/clone="LE009H09-5"
/tissue_type="Leaf"
/clone_lib="LE"

ORIGIN
Query Match 83.2%; Score 15.8; DB 1; Length 568;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19
||||| ||| |||||
Db 533 CCCCTGAGTGCAGCTAATC 551

RESULT 55
CE815985
LOCUS CE815985
DEFINITION tigr-gss-dog-17000318393613 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE815985
VERSION CE815985.1 GI:37157005
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 569)
AUTHORS Kirkness,B.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source Location/Qualifiers
1..569
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BatXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 83.2%; Score 15.8; DB 10; Length 569;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19
||||| ||| |||||
Db 261 CCCCTGAGTGCAGCTAATC 279

RESULT 56
CB212741
LOCUS CB212741
DEFINITION OML03021 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',

```

```

mRNA sequence.
ACCESSION CB212741
VERSION CB212741.1 GI:28258832
KEYWORDS EST.
SOURCE Oryza minuta
ORGANISM Oryza minuta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 570)
REFERENCE
AUTHORS Shin, J.S.
TITLE Oryza minuta HybriZAP-2.1 XR library
JOURNAL Unpublished (2003)
COMMENT Contact: Jeong Sheop Shin
Plant Molecular Genetics
Graduate School of Biotechnology, University of Korea
136-701 Anam-dong 5/I Seoul, Korea
Tel: 00 82 2 3290 3430
Fax: 00 82 2 927 9028
Email: jshin@kucn.ac.kr.
FEATURES
source
1..570
Location/Qualifiers
/organism="Oryza minuta"
/mol_type="mRNA"
/db_xref="taxon:63629"
/dev_stage="4-weeks after germination"
/clone_libs="Oryza minuta HybriZAP-2.1 XR library"
/note="Organ: immature leaf"

ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 570;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGGCTAATC 19
|||||
Db 144 CCCCTGAGTCGAGCTAATC 162

RESULT 57
BE403208
LOCUS BE403208 572 bp mRNA linear EST 21-JUL-2000
DEFINITION WHE0426 F08 K162S Wheat etiolated seedling root cDNA library
Triticum aestivum cDNA clone WHE0426_F08_K16, mRNA sequence.
ACCESSION BE403208
VERSION BE403208.1 GI:9362676
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 572)
REFERENCE
AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.I. and Tong, J.C.
TITLE The structure and function of the expressed portion of the wheat
genomes
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strategene SK primer.
FEATURES
source
1..572
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"

/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0426_F08_K16"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give phluescript
phagemids in the T0 close lab (Choi, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
```

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ORIGIN
Query Match      83.2%; Score 15.8; DB 2; Length 574;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGTAATC 19
|||||
Db 519 CCCCTGAGTCGAGCTAATC 537
|||||

RESULT 59
CX625718/c
LOCUS      CX625718
DEFINITION GAN00611lu GAN Hordeum vulgare cDNA clone GAN006111 3-PRIME, mRNA
EST.
ACCESSION  CX625718.1
VERSION     CX625718.1
KEYWORDS   EST.
SOURCE     Hordeum vulgare
ORGANISM   Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 579)
AUTHORS   Biemelt,S., Jansen,C., Schaefer,P., Hueckelhoven,R., Felk,A.,
Schaefer,W., Scholz,U., Sonnenswald,U. and Kogel,K.H.
Barley ESTs from different tissues challenged with fungal pathogens
Unpublished (2004)
CONTACT:  Sophia Biemelt
Molecular Developmental Physiology, Department Molecular Cell
Biology
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466 Gatersleben, Germany
Tel.: +49 (0)39482-5476
Fax: +49 (0)39482-5515
Email: biemelt@ipk-gatersleben.de
Insert Length: 579 Std Error: 0.00
Plate: 6 row: I column: 11
Seq primer: M13uni.
FEATURES
source
1..579
Location/Qualifiers
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Ingred Wt"
/db_xref="GABI:861142"
/db_xref="taxon:4513"
/clone="GAN00611"
/tissue_type="leaf epidermis"
/lab_host="XLI-Blue"
/clone_lib="GAN"
/note="Vector: PCR blunt (Invitrogen); Site 1: NotI;
Site 2: NotI; seedlings were grown at 18 degr. C, 60 %
rel. humidity, and a photoperiod of 16 h (100 microE * s-1
* m-2). A. 8 days, seedl. were treated with ASM (syn. BTH;
20 ppm soil drench). Leaf epid. was harv. 8, 24, 48, 72
hpt). PolyA-RNA was isolated from leaf epidermis and used
to create a cDNA-library using the Time Saver
cDNA-Synthesis Kit (Amersham). Normalisation was performed
essentially as described by Ko (1990, Nucl. Acid Res. 16,
9877) with some modification of Kohchi et al. (1995, Plant
J. 8, 771-776). Normalised cDNAs were digested with NotI
and cloned into NotI digested pCRblunt vector.
(GABI-Agrotech Project)"

ORIGIN
Query Match      83.2%; Score 15.8; DB 8; Length 579;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGTAATC 19
|||||

ORIGIN
Query Match      83.2%; Score 15.8; DB 7; Length 581;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGTAATC 19
|||||
Db 526 CCCCTGAGTCGAGCTAATC 544
|||||

RESULT 61
CX255155
LOCUS      CX255155
DEFINITION SCEPFL4176B07.9 FL4 Saccharum officinarum cDNA clone SCEPFL4176B07
5', mRNA sequence.
ACCESSION  CA255155
VERSION     CA255155.1
KEYWORDS   EST.
SOURCE     Saccharum officinarum
ORGANISM   Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE  1 (bases 1 to 594)
AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

```

Db 200 CCCCTGAATCGCGTAATC 182

```

RESULT 60
CF954381
LOCUS      CF954381
DEFINITION 5763rsiceb 9633.y1 Oryza sativa cv. PA64s leaf cDNA library Oryza
sativa (indica cultivar-group) cDNA 5', mRNA sequence.
ACCESSION  CF954381
VERSION     CF954381.1
KEYWORDS   EST.
SOURCE     Oryza sativa (indica cultivar-group)
ORGANISM   Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 581)
AUTHORS   Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
The Genomes of Oryza sativa: A History of Duplications
PLOS Biol. 3 (2), e38 (2005)
15685292
CONTACT:  Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel.: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 581
POLYA=NO.
FEATURES
source
1..581
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="PA64s"
/db_xref="taxon:39946"
/tissue_type="leaf"
/dev stage="trefoil"
/clone_lib="Oryza sativa cv. PA64s leaf cDNA library"

ORIGIN
Query Match      83.2%; Score 15.8; DB 7; Length 581;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGTAATC 19
|||||
Db 526 CCCCTGAGTCGAGCTAATC 544
|||||

RESULT 61
CX255155
LOCUS      CX255155
DEFINITION SCEPFL4176B07.9 FL4 Saccharum officinarum cDNA clone SCEPFL4176B07
5', mRNA sequence.
ACCESSION  CA255155
VERSION     CA255155.1
KEYWORDS   EST.
SOURCE     Saccharum officinarum
ORGANISM   Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE  1 (bases 1 to 594)
AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

```

```

TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 176 row: B column: 07
Seq primer: T7 Promoter Primer.

FEATURES
    source
        1..594
            /organism="Saccharum officinarum"
            /mol_type="mRNA"
            /db_xref="taxon:4547"
            /clone="SCEPFL4176B07"
            /lab_host="DH10B"
            /clone_lib="FL4"
            /note="Organ: Developed inflorescence and rachis
            (20cm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI;
            An unidirectional cDNA library generated from [Developed
            inflorescence and rachis (20cm-long)]. cDNA was prepared
            from polyA+ mRNA using SuperScript Plasmid System Kit
            (Invitrogen). The double-strand cDNAs were fractionated
            in a sepharose CL-2B 40cm-columns and fragments sizing
            between 0.8 and 1.5 Kb were directionally cloned into the
            vector. Details of each source of RNA and library
            construction can be obtained at
            http://sucest.lad.ic.unicamp.br/public"

ORIGIN
    Query Match      83.2%; Score 15.8; DB 6; Length 594;
    Best Local Similarity 89.5%; Pred. No. 1.6e+03;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||||| |||||
Db 2 CCCCTGGATGCAGCTAATC 20

RESULT 62
CD876322 597 bp mRNA linear EST 11-JUL-2003
LOCUS AZ03.109F19F011010 AZ03 Triticum aestivum cDNA clone AZ03109F19,
DEFINITION mRNA sequence.
ACCESSION CD876322 GI:32560138
VERSION CD876322
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 597)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
    source
        1..597
            /organism="Triticum aestivum"
            /mol_type="mRNA"

/cultivar="recital"
/db_xref="taxon:4565"
/clone="AZ03109F19"
/tissue_type="leaf"
/clone_lib="AZ03"

ORIGIN
    Query Match      83.2%; Score 15.8; DB 6; Length 597;
    Best Local Similarity 89.5%; Pred. No. 1.6e+03;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||||| |||||
Db 216 CCCCTGATGCAGCTAATC 234

RESULT 63
BM135186 598 bp mRNA linear EST 28-NOV-2001
LOCUS WHE0454_H12_H122S Wheat Fusarium graminearum infected spike cDNA
DEFINITION library Triticum aestivum cDNA clone WHE0454_H12_H12, mRNA
sequence.
ACCESSION BM135186 GI:17143456
VERSION WHE0454_H12_H122S
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 598)
AUTHORS Anderson, O.D., Chao, S., Han, P.S., Heinen, S., Hsia, C.C., Kang, Y.,
Kruger, W.M., Iazov, G.R., Miller, S., Muehlbauer, G.J., Miller, R.,
Pritsch, C., Rausch, C.J., Seaton, C.L., Tong, J.C., Vance, C. and
Wilson, C.F.
The structure and function of the expressed portion of the wheat
genomes - Fusarium graminearum infected spike cDNA library
Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: anders@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20. No effort was taken
to identify ESTs of fungal origin from this library, thus this EST
could be of wheat or fungal origin.
Seq primer: Stratagene SK primer.

FEATURES
    source
        1..598
            /organism="Triticum aestivum"
            /mol_type="mRNA"
            /cultivar="Sumai3"
            /db_xref="taxon:4565"
            /clone="WHE0454_H12_H12"
            /tissue_type="Spike"
            /dev_stage="Adult plant"
            /lab_host="E. coli SOLR"
            /clone_lib="Wheat Fusarium graminearum infected spike cDNA
            library"
            /note="Vector: Lambda Uni-ZAP XR, excised phagemid
            pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Plants were
            grown in the greenhouse. Spikes were sprayed at anthesis
            with Fusarium graminearum. Total RNA, and poly(A) RNA were
            prepared and pooled from infected spike at 0, 6, 12, 24,
            36 and 48 hours after inoculation. A cDNA library was
            made, and the cDNA clones were in vivo excised to give
            pBluescript phagemids in G. Muehlbauer lab at the
            University of Minnesota (Kruger, W.M., Muehlbauer, G.J.,
            Pritsch, C., Vance, C.). The cDNA library should contain
            genes of both wheat and fungal pathogen origin. Plasmid

```

DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 83.2%; Score 15.8; DB 3; Length 598;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
||||| ||| |||||
Db 578 CCCCTGAGTCGAGCTAATC 596

RESULT 64

CB680958

LOCUS OSJNEF06J19.f OSJNEF Oryza sativa (japonica cultivar-group) cDNA linear mRNA 601 bp EST 09-APR-2003
DEFINITION clone OSJNEF06J19 5', mRNA sequence.

ACCESSION CB680958

VERSION CB680958

KEYWORDS EST.

SOURCE CB680958.1 GI:29684683

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS 1 (bases 1 to 601)

Jantassuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R. A., Wing, R. A., Soderlund, C. and Wang, G. L.
Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)

COMMENT 1588683

CONTACT: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: gta aaa cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 06 row: J column: 19

Seq primer: gta aaa cga cgg cca gtc.

FEATURES

source

Location/Qualifiers

1..601

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="OSJNEF06J19"

/tissue_type="leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEF"

/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Uninfected Control"

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 601;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
||||| ||| |||||
Db 495 CCCCTGAGTCGAGCTAATC 513

RESULT 65

DN178545

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Patrick Schweizer

Transcriptome Analysis, Cytogenetics Department

Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, D-06466 Gatersleben, Germany

Tel: 0049 (0)39482-5660

Fax: 0049 (0)39482-5595

Email: schweiz@ipk-gatersleben.de

Insert Length: 602 Std Error: 0.00

Plate: 33 row: C column: 5

Seq primer: SK.

Location/Qualifiers

1..602

/organism="Hordeum vulgare"

/mol_type="mRNA"

/cultivar="Ingrid BC mlo-5"

/db_xref="GABI:1099872"

/db_xref="taxon:4513"

/clone="HO33C05"

/tissue_type="leaf epidermis, 6 h and 24 h post

inoculation with Blumeria graminis"

/dev_stage="7 d after germination"

/lab_host="XL10-Gold"

/clone_lib="HO"

/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of

cDNA); Site_2: XhoI (3'-end of cDNA); Approximately 5 % of

the clones correspond to cDNA from the fungi B. graminis

hordei and tritici, respectively. Due to a cloning

artefact caused by the kit, in most cases the EcoRI site

is NOT present, as well as the EcoRI adapter used for

cloning. To excise the insert, restriction sites upstream

EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also

due to the cloning system used Blue/white selection for

recombinants is not 100% reliable. Average insert size is

1.2 kb"

ORIGIN

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

Qy

1 CCCCTGAATGGCGCTAATC 19

||||| ||| |||||

Db

212 CCCCTGAGTCGAGCTAATC 230

||||| ||| |||||

RESULT 66

AV933787

LOCUS

DEFINITION

AV933787

K. Sato unpublished cDNA library, cv. Haruna Nijo adult,

heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA

clone baal8p11 5', mRNA sequence.

ACCESSION

AV933787

VERSION

AV933787.1

GI:18229584

KEYWORDS

EST.

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

DN178545
HO33C055 HO Hordeum vulgare cDNA clone HO33C05 5-PRIME, mRNA linear EST 24-FEB-2005
sequence.

ACCESSION

DN178545

VERSION

DN178545.1

GI:60273802

KEYWORDS

EST.

SOURCE

Hordeum vulgare

Hordeum vulgare

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Patrick Schweizer

Transcriptome Analysis, Cytogenetics Department

Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, D-06466 Gatersleben, Germany

Tel: 0049 (0)39482-5660

Fax: 0049 (0)39482-5595

Email: schweiz@ipk-gatersleben.de

Insert Length: 602 Std Error: 0.00

Plate: 33 row: C column: 5

Seq primer: SK.

Location/Qualifiers

1..602

/organism="Hordeum vulgare"

/mol_type="mRNA"

/cultivar="Ingrid BC mlo-5"

/db_xref="GABI:1099872"

/db_xref="taxon:4513"

/clone="HO33C05"

/tissue_type="leaf epidermis, 6 h and 24 h post

inoculation with Blumeria graminis"

/dev_stage="7 d after germination"

/lab_host="XL10-Gold"

/clone_lib="HO"

/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of

cDNA); Site_2: XhoI (3'-end of cDNA); Approximately 5 % of

the clones correspond to cDNA from the fungi B. graminis

hordei and tritici, respectively. Due to a cloning

artefact caused by the kit, in most cases the EcoRI site

is NOT present, as well as the EcoRI adapter used for

cloning. To excise the insert, restriction sites upstream

EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also

due to the cloning system used Blue/white selection for

recombinants is not 100% reliable. Average insert size is

1.2 kb"

ORIGIN

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

Qy

1 CCCCTGAATGGCGCTAATC 19

||||| ||| |||||

Db

212 CCCCTGAGTCGAGCTAATC 230

||||| ||| |||||

RESULT 66

AV933787

LOCUS

DEFINITION

AV933787

K. Sato unpublished cDNA library, cv. Haruna Nijo adult,

heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA

clone baal8p11 5', mRNA sequence.

ACCESSION

AV933787

VERSION

AV933787.1

GI:18229584

KEYWORDS

EST.

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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/organism="Sorghum bicolor"
/mol type="genomic DNA"

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DEFINITION OSJNEC10P06.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
ACCESSION CB5656403
VERSION CB5656403.1 GI:29660246
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 636)
AUTHORS Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 15888683
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: p column: 06
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1..636
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC10P06"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS+; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES
source
Query Match 83.2%; Score 15.8; DB 6; Length 636;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 494 CCCCTGAGTCGAGCTAATC 512

RESULT 70
CB5656403
LOCUS OSJNEC10L13.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEC10L13 5', mRNA sequence.
ACCESSION CB5656403
VERSION CB5656403.1 GI:29660128
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 637)
AUTHORS Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in

```

```

rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 15888683
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: l column: 13
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1..637
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC10L13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS+; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES
source
Query Match 83.2%; Score 15.8; DB 6; Length 637;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 495 CCCCTGAGTCGAGCTAATC 513

RESULT 71
CB472488
LOCUS BJ472488 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
clone baal34n08 5', mRNA sequence.
ACCESSION BJ472488
VERSION BJ472488.1 GI:21150991
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 648)
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene.nig.ac.jp.
Location/Qualifiers
1..648
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baal34n08"

```

```

/tissue type="top three leaves"
/dev stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 3; Length 648;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 255 CCCCTGAGTCGAGCTAATC 273

RESULT 72
BJ469669
LOCUS
DEFINITION
  BJ469669 K. Sato unpublished cDNA library, linear EST 23-MAY-2002
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal27n10 5', mRNA sequence.
ACCESSION
  BJ469669
VERSION
  BJ469669.1 GI:21148172
KEYWORDS
  EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  Hordeum vulgare subsp. vulgare
ORGANISM
  Eukaryota; Viridiplantae; Hordeum vulgare subsp. vulgare
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Poideae; Triticeae; Hordeum.
  1 (bases 1 to 654)
REFERENCE
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tehini@genes.nig.ac.jp.
FEATURES
  source
  1. .654
  /organism="Hordeum vulgare subsp. vulgare"
  /mol_type="mRNA"
  /cultivar="Haruna Nijo"
  /sub_species="vulgare"
  /db_xref="taxon:112509"
  /clones="baal27n10"
  /tissue type="top three leaves"
  /dev stage="adult, heading stage"
  /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
  Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 3; Length 654;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 256 CCCCTGAGTCGAGCTAATC 274

RESULT 73
AJ432460
LOCUS
DEFINITION
  AJ432460 S00007 Hordeum vulgare cDNA clone S0000700037F06P1, mRNA
  sequence.
ACCESSION
  AJ432460
VERSION
  AJ432460.1 GI:19520912
KEYWORDS
  EST.
SOURCE
  Hordeum vulgare
  Hordeum vulgare
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Poideae; Triticeae; Hordeum.
  1 (bases 1 to 659)
REFERENCE
  Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
  Barley EST's
  Unpublished (2002)
  Contact: Schulman AH
  Institute of Biotechnology
  University of Helsinki
  P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
  Finland.
FEATURES
  source
  1. .659
  /organism="Hordeum vulgare"
  /mol_type="mRNA"
  /db_xref="taxon:4513"
  /clone="S0000700037F06P1"
  /dev stage="Shoot"
  /clone_lib="S00007"
  /note="2,3-,4-days after germination"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 659;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 161 CCCCTGAGTCGAGCTAATC 179

RESULT 74
AV933115
LOCUS
DEFINITION
  AV933115 K. Sato unpublished cDNA library, linear EST 18-JAN-2002
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal59l8 5', mRNA sequence.
ACCESSION
  AV933115
VERSION
  AV933115.1 GI:18228912
KEYWORDS
  EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  Hordeum vulgare subsp. vulgare
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Poideae; Triticeae; Hordeum.
  1 (bases 1 to 662)
REFERENCE
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tehini@genes.nig.ac.jp.
FEATURES
  source
  1. .662
  /organism="Hordeum vulgare subsp. vulgare"
  /mol_type="mRNA"
  /cultivar="Haruna Nijo"
  /sub_species="vulgare"
  /db_xref="taxon:112509"
  /clone="baal59l8"
  /tissue type="top three leaves"
  /dev stage="adult, heading stage"
  /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
  Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 662;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
  1 (bases 1 to 659)
REFERENCE
  Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
  Barley EST's
  Unpublished (2002)
  Contact: Schulman AH
  Institute of Biotechnology
  University of Helsinki
  P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
  Finland.
FEATURES
  Location/Qualifiers
  1..659
  /organism="Hordeum vulgare"
  /mol_type="mRNA"
  /db_xref="taxon:4513"
  /clone="S0000700037F06P1"
  /dev stage="Shoot"
  /clone_lib="S00007"
  /note="2,3-,4-days after germination"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 659;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 161 CCCCTGAGTCGAGCTAATC 179

RESULT 74
AV933115
LOCUS
DEFINITION
  AV933115 K. Sato unpublished cDNA library, linear EST 18-JAN-2002
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal59l8 5', mRNA sequence.
ACCESSION
  AV933115
VERSION
  AV933115.1 GI:18228912
KEYWORDS
  EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  Hordeum vulgare subsp. vulgare
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Poideae; Triticeae; Hordeum.
  1 (bases 1 to 662)
REFERENCE
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tehini@genes.nig.ac.jp.
FEATURES
  Location/Qualifiers
  1..662
  /organism="Hordeum vulgare subsp. vulgare"
  /mol_type="mRNA"
  /cultivar="Haruna Nijo"
  /sub_species="vulgare"
  /db_xref="taxon:112509"
  /clone="baal59l8"
  /tissue type="top three leaves"
  /dev stage="adult, heading stage"
  /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
  Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 662;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;

```

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||
Db 256 CCCCTGAGTGCAGCTAATC 274

RESULT 75
CA744325 681 bp mRNA linear EST 26-NOV-2002
LOCUS wrils.pk007.018 wrils Triticum aestivum cDNA clone wrils.pk007.018
DEFINITION 5' end, mRNA sequence.

ACCESSION CA744325
VERSION CA744325.1 GI:25560148
KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Poolidae; Triticeae; Triticum.

JOURNAL 1 (bases 1 to 681)
COMMENT Tingley, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.

DiPont Wheat cDNA Sequence

Unpublished (2002)

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: T7.

FEATURES

source

Location/Qualifiers

1..681

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone="wrils.pk007.018"

/tissue_type="leaf"

/lab_host="DH10B"

/clone_lib="wrils"

/note="Vector: pGEM-T Easy; Site1: SmaI; Riband

(susceptible) wheat leaves infected with Septoria tritici

strain A, 24 hours after infection, subtracted w/

comparable uninfected leaves"

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 681;

Best Local Similarity 89.5%; Pred. NO. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||

Db 253 CCCCTGAGTGCAGCTAATC 271
||||| ||| |||||

RESULT 76

CD054348

LOCUS

DEFINITION HO01L09r HO Hordeum vulgare cDNA clone HO01L09 5-PRIME, mRNA

sequence.

ACCESSION CD054348

VERSION CD054348.1 GI:30595183

KEYWORDS EST.

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

TITLE Poolidae; Triticeae; Hordeum.

1 (bases 1 to 686)

Zierold, U. and Schweizer, P.

Transcriptome analysis of mlo-mediated resistance in the epidermis

JOURNAL

COMMENT

of barley

Mol. Plant Pathol. (2005) In press

Contact: Patrick Schweizer

Transcriptome Analysis, Cytogenetics Department

Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, D-06466 Gatersleben, Germany

Tel: 0049 (0)39482-5660

Fax: 0049 (0)39482-5595

Email: schweiz@ipk-gatersleben.de

Insert Length: 686 Std Error: 0.00

Plate: 1 row: L column: 9

Seq primer: M13rev.

Location/Qualifiers

1..686

/organism="Hordeum vulgare"

/mol_type="mRNA"

/cultivar="Ingrid BC mlo-5"

/db_xref="GABI:703932"

/db_xref="taxon:4513"

/clone="HO01L09"

/tissue_type="leaf epidermis, 6 h and 24 h post

inoculation with Blumeria graminis"

/dev_stage="7 d after germination"

/lab_host="XL10-Gold"

/clone_lib="HO"

/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of

cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of

the clones correspond to cDNA from the fungi B. graminis

hordei and tritici, respectively. Due to a cloning

artefact caused by the kit, in most cases the EcoRI site

is NOT present, as well as the EcoRI adapter used for

cloning. To excise the insert, restriction sites upstream

EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also

due to the cloning system used Blue/white selection for

recombinants is not 100% reliable. Average insert size is

1.2 kb"

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 686;

Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||

Db 80 CCCCTGAGTGCAGCTAATC 98
||||| ||| |||||

RESULT 77

BJ471067

LOCUS

DEFINITION

BJ471067 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,

heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA

clone baal30j04 5', mRNA sequence.

ACCESSION BJ471067

VERSION BJ471067.1 GI:21149570

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

TITLE Poolidae; Triticeae; Hordeum.

1 (bases 1 to 695)

Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

FEATURES

```

source
1. .695
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baal30j04"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo adult, heading stage top three leaves"

ORIGIN
Query Match 83.2%; Score 15.8; DB 3; Length 695;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 265 CCCCTGAGTCAGCTAATC 283

RESULT 78
BZ008560 698 bp DNA linear GSS 07-OCT-2002
LOCUS
DEFINITION osf04h07.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.
ACCESSION BZ008560
VERSION BZ008560.1 GI:23556906
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 698)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
JOURNAL Contact: Richard K. Wilson
COMMENT Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: osf04 row: h column: 07
Seq primer: -21UPPOT forward
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 543.
FEATURES
Location/Qualifiers
source
1. .698
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T01000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 83.2%; Score 15.8; DB 9; Length 698;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 177 CCCCTGACGCGGCTAATC 195

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RESULT 79
DN178149
LOCUS
DEFINITION DN178149 HO Hordeum vulgare cdna clone HO34C21 5-PRIME, mRNA
sequence.
ACCESSION DN178149
VERSION DN178149.1 GI:60273406
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 700)
Zierold,U. and Schweizer,P.
Transcriptome analysis of mlo-mediated resistance in the epidermis
of barley
Mol. Plant Pathol. (2005) In press
Contact: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5660
Fax: 0049 (0)39482-5595
Email: schweiz@ipk-gatersleben.de
Insert length: 700 Std Error: 0.00
Plate: 34 row: C column: 21
Seq primer: SK.
FEATURES
Location/Qualifiers
source
1. .700
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Ingrid BC mlo-5"
/db_xref="GABI:1100216"
/db_xref="taxon:4513"
/clone="HO34C21"
/tissue_type="leaf epidermis, 6 h and 24 h post
inoculation with Blumeria graminis"
/dev_stage="7 d after germination"
/lab_host="XL10-Gold"
/clone_lib="HO"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of
the clones correspond to cDNA from the fungi B. graminis
hordel and tritici, respectively. Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is
1.2 kb"

ORIGIN
Query Match 83.2%; Score 15.8; DB 8; Length 700;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 83 CCCCTGAGTCAGCTAATC 101

RESULT 80
BH516786/c
LOCUS
DEFINITION BH516786 BOHG Brassica oleracea genomic clone BOHGR66, genomic
survey sequence.
ACCESSION BH516786
VERSION BH516786.1 GI:17724876
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 713)

REFERENCE
AUTHORS
 Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.

TITLE
 Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis

JOURNAL
PUBLISHED
 Genome Res. 15 (4), 487-495 (2005)

COMMENT
 Other_GSSs: BOHGR66TF
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES

source
 Location/Qualifiers
 1..713

/organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TOL000DH3"
 /db_xref="taxon:3712"
 /clone="BOHGR66"
 /clone_lib="BOHG"
 /note="Vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt1 using BstXI linkers"

ORIGIN

Query Match 83.2%; Score 15.8; DB 9; Length 713;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGATCGGCTAATC 19

Db 348 CCCCTGGACGGCTAATC 330

RESULT 81
CA240024
LOCUS 716 bp mRNA linear EST 25-SEP-2003
DEFINITION SCSBFL4063E11.9 FLA Saccharum officinarum cDNA clone SCSBFL4063E11 5', mRNA sequence.
ACCESSION CA240024
VERSION CA240024.1 GI:35313215
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
 Centro de Biologia Molecular e Engenhariaia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>
 Plate: 063 row: E column: 11
 Seq primer: T7 Promoter Primer.
 Location/Qualifiers
 1..716

FEATURES

source
 Location/Qualifiers
 1..749

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/db_xref="taxon:39947"

/clone="OSJNEd07F03"

/tissue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEd"

/organism="Saccharum officinarum"
 /mol_type="mRNA"
 /db_xref="taxon:4547"
 /clone="SCSBFL4063E11"
 /lab_host="DH10B"
 /clone_lib="FLA"
 /note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>.

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 716;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGATCGGCTAATC 19

Db 684 CCCCTGGATCGAGCTAATC 702

RESULT 82

CE662892

LOCUS

DEFINITION

OSJNEd07F03.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA clone OSJNEd07F03 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: gta aac cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 07 row: F column: 03

Seq primer: gta aac cga cgg cca gtc.

Location/Qualifiers

1..749

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/db_xref="taxon:39947"

/clone="OSJNEd07F03"

/tissue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEd"

CE662892 749 bp mRNA linear EST 09-APR-2003
 OSJNEd07F03.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA clone OSJNEd07F03 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: gta aac cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 07 row: F column: 03

Seq primer: gta aac cga cgg cca gtc.

Location/Qualifiers

1..749

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/db_xref="taxon:39947"

/clone="OSJNEd07F03"

/tissue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEd"

/note="vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 749;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19

Db 501 CCCCTGAGTCAGCTAATC 519

RESULT 83

CO033780/c

LOCUS CO033780 777 bp mRNA linear EST 10-JUN-2004
DEFINITION EST812164 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb Coccidioides posadasii cDNA clone C1FBP43 3' end, mRNA sequence.

ACCESSION CO033780

VERSION CO033780.1 GI:48570202

KEYWORDS EST

SOURCE Coccidioides posadasii

ORGANISM Coccidioides posadasii

REFERENCE 1 (bases 1 to 777)
AUTHORS Gardner, M.J. and Cole, G.T.

TITLE Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags

JOURNAL Unpublished (2003)

COMMENT Other ESTs: EST812165

Contact: Gardner MJ

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 3519

Fax: 301 838 0208

Email: gardner@tigr.org

FEATURES

source

1..777 /organism="Coccidioides posadasii"

/mol_type="mRNA"

/strain="C735"

/db_xref="taxon:199306"

/clone="C1FBP43"

/dev_stage="spherules"

/lab_host="E. coli DH10B, T1 phage resistant"

/clone_lib="Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb"

/note="vector: pExpress 1; Site 1: Not I; Site 2: Eco RV; Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb"

ORIGIN

Query Match 83.2%; Score 15.8; DB 7; Length 777;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19

Db 343 CCCCTGATTCGGCTAATC 325

RESULT 84

CB659097

LOCUS CB659097

DEFINITION OSJNEC15M06.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNEC15M06 5', mRNA sequence.

ACCESSION CB659097

VERSION CB659097.1 GI:29662822

KEYWORDS EST

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 778)

Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,

Soderlund, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,

Soderlund, C., and Wang, G.L.

Large-scale identification of expressed sequence tags involved in

rice and rice blast fungus interaction

Plant Physiol. 138 (1), 105-115 (2005)

15888683

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: gta aaa cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 15 row: M column: 06

Seq primer: gta aaa cga cgg cca gtc.

Location/Qualifiers

1..778

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="OSJNEC15M06"

/tissue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEC"

/note="vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 778;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19

Db 518 CCCCTGAGTCAGCTAATC 536

RESULT 85

CB624346/c

LOCUS CB624346

DEFINITION OSII8a12N18.r OSII8a Oryza sativa (indica cultivar-group) cDNA clone OSII8a12N18 3', mRNA sequence.

ACCESSION CB624346.1 GI:29619334

VERSION CB624346

KEYWORDS EST

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 786)

Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,

Soderlund, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,

Soderlund, C., and Wang, G.L.

Large-scale identification of expressed sequence tags involved in

rice and rice blast fungus interaction

Plant Physiol. 138 (1), 105-115 (2005)

15888683

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

```

Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: N Column: 18
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers
1. .786
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OSJNE12K24"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEa"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Lesion Mimic SPL 11"

ORIGIN
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Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
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Db 782 CCCCTGAGTGCAGCTAATC 764

RESULT 86
CB657398
LOCUS
DEFINITION
OSJNEC12K24.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC12K24 5', mRNA sequence.
ACCESSION
CB657398
VERSION
CB657398
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 790)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
15888683
COMMENT
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: K Column: 24
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1. .790
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC12K24"

FEATURES
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ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 795;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 503 CCCCTGAGTGCAGCTAATC 521

RESULT 87
CB648104
LOCUS
DEFINITION
OSJNEB11F13.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEB11F13 5', mRNA sequence.
ACCESSION
CB648104
VERSION
CB648104
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 795)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F Column: 13
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1. .795
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="OSJNEB11F13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEB"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (Che
86061)"

FEATURES
source
ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 795;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
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/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 790;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 503 CCCCTGAGTGCAGCTAATC 521

RESULT 87
CB648104
LOCUS
DEFINITION
OSJNEB11F13.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEB11F13 5', mRNA sequence.
ACCESSION
CB648104
VERSION
CB648104
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 795)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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15888683
COMMENT
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F Column: 13
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1. .795
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEB11F13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEB"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (Che
86061)"

FEATURES
source
ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 795;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||

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Db 497 CCCTGAGTGCAGCTAATC 515

RESULT 88
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LOCUS
DEFINITION
OSIIEa12N18.f OSIIEa Oryza sativa (indica cultivar-group) cDNA
clone OSIIEa12N18 5', mRNA sequence.
CB624345
ACCESSION
VERSION
CB624345.1 GI:29619333
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 796)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: N column: 18
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1. .796
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/mol_type="mRNA"
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/db_xref="taxon:39946"
/clone="OSIIEa12N18"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIEa"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Lesion Mimic SPL 11"

ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 796;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCTGAGTGCAGCTAATC 19
|||||
Db 629 CCCTGAGTGCAGCTAATC 647

RESULT 89
CL746478/c
LOCUS
DEFINITION
OR_BBa0083P09.r OR_BBa Oryza sativa genomic clone OR_BBa0083P09 3',
genomic survey sequence.
CL746478
ACCESSION
VERSION
CL746478.1 GI:50688734
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 800)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0083 row: P column: 09
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
1. .800
/organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4536"
/clone="OR_BBa0083P09"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/notes="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 83.2%; Score 15.8; DB 10; Length 800;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 644 CCCTTCAATGCGGCTAATC 626

RESULT 90
CB655953
LOCUS
DEFINITION
CB655953
ACCESSION
VERSION
CB655953.1 GI:29659678
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 810)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
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Plant Physiol. 138 (1), 105-115 (2005)
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Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g

Db 497 CCCTGAGTGCAGCTAATC 515

RESULT 88
CB624345
LOCUS
DEFINITION
OSIIEa12N18.f OSIIEa Oryza sativa (indica cultivar-group) cDNA
clone OSIIEa12N18 5', mRNA sequence.
CB624345
ACCESSION
VERSION
CB624345.1 GI:29619333
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 796)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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rice and rice blast fungus interaction
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: N column: 18
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1. .796
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
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/clone="OSIIEa12N18"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
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/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Lesion Mimic SPL 11"

ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 796;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCTGAGTGCAGCTAATC 19
|||||
Db 629 CCCTGAGTGCAGCTAATC 647

RESULT 89
CL746478/c
LOCUS
DEFINITION
OR_BBa0083P09.r OR_BBa Oryza sativa genomic clone OR_BBa0083P09 3',
genomic survey sequence.
CL746478
ACCESSION
VERSION
CL746478.1 GI:50688734
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 800)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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1588683
Contact: Rod Wing
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University of Arizona
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0083 row: P column: 09
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
1. .800
/organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4536"
/clone="OR_BBa0083P09"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/notes="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 83.2%; Score 15.8; DB 10; Length 800;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCCTGAATGCGGCTAATC 19
|||||
Db 644 CCCTTCAATGCGGCTAATC 626

RESULT 90
CB655953
LOCUS
DEFINITION
CB655953
ACCESSION
VERSION
CB655953.1 GI:29659678
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 810)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g

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ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 825;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
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Db 658 CCCCTGAGTGCAGCTAATC 676

RESULT 92
CB657399/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) mRNA
OSJNEc12K24.1 OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEc12K24 3', mRNA sequence.
CB657399
CB657399.1 GI:29661124
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 834)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: K column: 24
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers
1. 834
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEc12K24"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice_Blast (C9240-1)"

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 834;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||| |||||
Db 777 CCCCTGAGTGCAGCTAATC 759

RESULT 93
CB663361/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) mRNA
OSJNEd08d13.1 OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEd08d13 3', mRNA sequence.
CB663361
CB663361.1 GI:29661124
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 834)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: K column: 24
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers
1. 834
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEc12K24"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice_Blast (C9240-1)"

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clone OSJNED08D13 3', mRNA sequence.
ACCESSION CB663361
VERSION CB663361.1 GI:29667086
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 851)
AUTHORS Jantaauriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 1588683
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 08 row: D column: 13
Seq primer: gga aac agc tat gac cat g.
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Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
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/clone="OSJNED08D13"
/tissue_type="Leaf"
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/lab_host="DH10B"
/clone_lib="OSJNED"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"
ORIGIN
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Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCCTGAATCGGCTAATC 19
Db 764 CCCCTGAGTGCAGCTAATC 746
RESULT 94
LOCUS CK156356
DEFINITION FGAS037309 Triticum aestivum FGAS; TaLT4 Triticum aestivum cDNA,
mRNA sequence.
ACCESSION CK156356
VERSION CK156356.1 GI:38979376
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 861)
AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
Genswein,B., Grat,R., Gulick,P., Hrycan,L.D., Laroche,A.,
Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,
Penniket,C., Roach,J.L. and Sarhan,F.
TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
clone OSJNED08D13 3', mRNA sequence.
JOURNAL COMMENT
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_esta@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [122,733].
Plate: TaLT411 row: K column: 10.
FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Wheat line PI 178383"
/db_xref="taxon:4565"
/clone_host="DH5 alpha"
/clone_lib="Triticum aestivum FGAS; TaLT4"
/note="Organ: Crown; Vector: pGEM-T; SSH (suppression
subtractive hybridization) cDNA library from genotype
PI178383 cold hardened at 2 C for 1 day (24 H)(tester) and
subtracted against genotype Norstar cold hardened at 2 C
for 21 days and 49 days (equal amount of cDNA pooled
together before subtraction, driver). Modified Smart cDNA
(Clontech) priming and non-directional cloning."
ORIGIN
Query Match 83.2%; Score 15.8; DB 7; Length 861;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCCTGAATCGGCTAATC 19
Db 346 CCCCTGAGTGCAGCTAATC 364
RESULT 95
LOCUS CF819853/c
DEFINITION EST697235 Coccidioides posadasii saprobic phase cDNA library, 2 to
4 kb Coccidioides posadasii cDNA clone CIDA109 5' end, mRNA
sequence.
ACCESSION CF819853
VERSION CF819853.1 GI:45925894
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 868)
AUTHORS Gardner,M.J. and Cole,G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
spores via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST697234
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
FEATURES
source
Location/Qualifiers
1..868
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"

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/clone="CIDA109"
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 /clone_lib="Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb"
 /note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV; Coccidioides posadasii saprobic phase cDNA library, size fractionated cDNA 2 to 4 kb"

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 868;
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19
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 DB 75 CCCCTGAATCGGCTAATC 57

RESULT 96
 CB680959/c
 LOCUS
 DEFINITION OSJNEF06J19.r OSJNEF Oryza sativa (japonica cultivar-group) cDNA
 clone OSJNEF06J19 3', mRNA sequence.

ACCESSION CB680959
 VERSION
 KEYWORDS
 SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 876)
 AUTHORS Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
 Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
 Soderlund,C. and Wang,G.L.
 TITLE Large-scale identification of expressed sequence tags involved in
 rice and rice blast fungus interaction
 JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
 PUBMED 15888683

COMMENT Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA

Tel: 520 626 3967
 Fax: 520 621 9288
 Email: rwing@genome.arizona.edu
 PCR Primers
 FORWARD: gta aac cga cgg cca gtc
 BACKWARD: gga aac agc tat gac cat g
 Plate: 06 row: J column: 19
 Seq primer: gga aac agc tat gac cat g.

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 /mol_type="mRNA"
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 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_lib="OSJNEF"
 /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
 XhoI; Uninfected Control"

ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 876;
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19

Db 797 CCCCTGAATCGGCTAATC 779
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 |||||

RESULT 97

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..929

/organism="Coccidioides posadasii"

/mol_type="mRNA"

/strain="C735"

/db_xref="taxon:199306"

/clone="CIDAC39"

/dev_stage="saprobic phase (mycelia)"

/lab_host="E. coli DH10B, T1 phage resistant"

/clone_lib="Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb"

/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV; Coccidioides posadasii saprobic phase cDNA library, size fractionated cDNA 2 to 4 kb"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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```

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chi-Bin Chien
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM15253 row: d column: 11
High quality sequence start: 28
High quality sequence stop: 313.

FEATURES
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/organism="Danio rerio"
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/db_xref="taxon:7955"
/clone="IMAGE:7270525"
/tissue_type="neural retina, retinal pigment epithelium,
lens and overlying skin, pooled embryos"
/lab_host="DH10B Tona"
/clone_lib="NIH_ZGC_9"
/notes="Organ: eye; Vector: pME18S-FL3; Site 1: DraIII;
Site 2: DraIII; 1st strand cDNA was primed with an
oligo(dT) primer
[GGCGTGAAGACGGCTATGTGGCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[GGCCUACUGG], digested and directionally cloned into
distinct DraIII sites of the pME18S-FL3. Library was size
selected for 1.0 kb, with a average insert size of ~1.2kb,
and is not amplified. Library constructed by Yutaka Suzuki
(University of Tokyo Institute of Medical Science). Custom
primers recommended for sequencing: 5' end primer
5'-GGATGTGCTTCTACTCTA-3' and 3' end primer
5'-CGACCTGAGCTCGACACA-3'. Note: This is a Zebrafish Gene
Collection (ZGC) library"

ORIGIN
Query Match 83.2%; Score 15.8; DB 7; Length 941;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 449 CCATGAGGCGGCTAATC 467

RESULT 99
CO010346/c
LOCUS
DEFINITION EST798681 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone CIEBH07 3' end, mRNA sequence.
ACCESSION CO010346.1 GI:48517235
VERSION
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 994)
AUTHORS Gardner, M.J. and Cole, G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST798682
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers

FEATURES
Source
1..994
/organism="Coccidioides posadasii"
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/strain="C735"
/db_xref="taxon:199306"
/clone="CIEBH07"
/dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/notes="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

ORIGIN
Query Match 83.2%; Score 15.8; DB 7; Length 994;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 136 CCCTGATCCGGCTAATC 118

RESULT 100
BE743432
LOCUS
DEFINITION 601573680F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3834883 5',
mRNA sequence.
ACCESSION BE743432
VERSION BE743432.1 GI:10157424
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 996)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM515 row: p column: 20
High quality sequence start: 4
High quality sequence stop: 467.
Location/Qualifiers

FEATURES
Source
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/clone="IMAGE:3834883"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 83.2%; Score 15.8; DB 2; Length 996;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
 Db 438 CCCCTGAATGGGCTAATC 456

Search completed: March 9, 2006, 02:45:10
 Job time : 1531.15 secs

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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:09:45 ; Search time 844.272 Seconds
 (without alignments)
 1346.567 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaacacggacacccaa 20

Scoring table:

IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	73	13 AY189930	AY189930 Human ent
C 2	20	100.0	73	13 AY189933	AY189933 Human ent
C 3	20	100.0	103	13 ESU55869	US55869 Enterovirus
C 4	20	100.0	109	13 AY049767	AY049767 Enterovir
C 5	20	100.0	109	13 E7U00872	U00872 Enterovirus
C 6	20	100.0	112	13 AY189929	AY189929 Human ent
C 7	20	100.0	115	13 AY189177	AY189177 Human pol
C 8	20	100.0	115	13 AY189178	AY189178 Human pol
C 9	20	100.0	115	13 AY189210	AY189210 Human ent
C 10	20	100.0	115	13 AY189213	AY189213 Human ent
C 11	20	100.0	115	13 FEN295168	AJ295168 Porcine e
C 12	20	100.0	116	13 AY189158	AY189158 Human ent
C 13	20	100.0	116	13 AY189160	AY189160 Human ent
C 14	20	100.0	116	13 AY189161	AY189161 Human ent
C 15	20	100.0	116	13 AY189162	AY189162 Human ent
C 16	20	100.0	116	13 AY189163	AY189163 Human ent
C 17	20	100.0	116	13 AY189164	AY189164 Human ent
C 18	20	100.0	116	13 AY189165	AY189165 Human ent

C 19	20	100.0	116	13 AY189166	AY189166 Human ent
C 20	20	100.0	116	13 AY189170	AY189170 Human ent
C 21	20	100.0	116	13 AY189171	AY189171 Human ent
C 22	20	100.0	116	13 AY189172	AY189172 Human ent
C 23	20	100.0	116	13 AY189173	AY189173 Human ent
C 24	20	100.0	116	13 AY189175	AY189175 Human ent
C 25	20	100.0	116	13 AY189176	AY189176 Human ent
C 26	20	100.0	116	13 AY189180	AY189180 Human ent
C 27	20	100.0	116	13 AY189181	AY189181 Human ent
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C 32	20	100.0	116	13 AY189187	AY189187 Human ent
C 33	20	100.0	116	13 AY189188	AY189188 Human ent
C 34	20	100.0	116	13 AY189189	AY189189 Human ent
C 35	20	100.0	116	13 AY189190	AY189190 Human ent
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C 37	20	100.0	116	13 AY189194	AY189194 Human ent
C 38	20	100.0	116	13 AY189195	AY189195 Human ent
C 39	20	100.0	116	13 AY189196	AY189196 Human ent
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C 51	20	100.0	116	13 AY189215	AY189215 Human ent
C 52	20	100.0	116	13 AY189216	AY189216 Human ent
C 53	20	100.0	117	13 AB133003	AB133003 Human ent
C 54	20	100.0	119	13 S66302S1	S66302 VP1/2A [5'
C 55	20	100.0	128	13 AJ783777	AJ783777 Human pol
C 56	20	100.0	145	13 HEN312090	AJ312090 Human cox
C 57	20	100.0	145	13 HEN312091	AJ312091 Human cox
C 58	20	100.0	147	13 AF314006	AF314006 Enterovir
C 59	20	100.0	147	13 AF316322	AF316322 Enterovir
C 60	20	100.0	153	13 AF314004	AF314004 Enterovir
C 61	20	100.0	154	13 AF314003	AF314003 Enterovir
C 62	20	100.0	154	13 AF314005	AF314005 Enterovir
C 63	20	100.0	154	13 AF314007	AF314007 Enterovir
C 64	20	100.0	154	13 AY027864	AY027864 Enterovir
C 65	20	100.0	154	13 AY027865	AY027865 Enterovir
C 66	20	100.0	155	13 HEN312089	AJ312089 Human cox
C 67	20	100.0	171	13 HCO295181	AJ295181 Human cox
C 68	20	100.0	172	13 HEN312088	AJ312088 Human ent
C 69	20	100.0	177	13 ESP295207	AJ295207 Echovirus
C 70	20	100.0	184	13 AF521491	AF521491 Human ech
C 71	20	100.0	185	13 AF521433	AF521433 Human ech
C 72	20	100.0	185	13 AF521434	AF521434 Human cox
C 73	20	100.0	185	13 AF521435	AF521435 Human cox
C 74	20	100.0	185	13 AF521436	AF521436 Human ech
C 75	20	100.0	185	13 AF521440	AF521440 Human ech
C 76	20	100.0	185	13 AF521444	AF521444 Human ech
C 77	20	100.0	185	13 AF521445	AF521445 Human ech
C 78	20	100.0	185	13 AF521446	AF521446 Human ech
C 79	20	100.0	185	13 AF521447	AF521447 Human ech
C 80	20	100.0	185	13 AF521448	AF521448 Human cox
C 81	20	100.0	185	13 AF521449	AF521449 Human ech
C 82	20	100.0	185	13 AF521450	AF521450 Human ech
C 83	20	100.0	185	13 AF521451	AF521451 Human ech
C 84	20	100.0	185	13 AF521458	AF521458 Human ech
C 85	20	100.0	185	13 AF521461	AF521461 Human ech
C 86	20	100.0	185	13 AF521464	AF521464 Human ech
C 87	20	100.0	185	13 AF521471	AF521471 Human cox
C 88	20	100.0	185	13 AF521473	AF521473 Human cox
C 89	20	100.0	185	13 AF521474	AF521474 Human cox
C 90	20	100.0	185	13 AF521475	AF521475 Human ech
C 91	20	100.0	185	13 AF521476	AF521476 Human ech

C 92	20	100.0	185	13	AF521477	Human	ech	AF521477	Human	ech	c 165	20	100.0	188	13	AY342841	Human	ech
C 93	20	100.0	185	13	AF521478	Human	ech	AF521478	Human	ech	c 166	20	100.0	188	13	AY342842	Human	ech
C 94	20	100.0	185	13	AF521480	Human	cox	AF521480	Human	cox	c 167	20	100.0	188	13	AY342843	Human	cox
C 95	20	100.0	185	13	AF521481	Human	ech	AF521481	Human	ech	c 168	20	100.0	188	13	AY342844	Human	cox
C 96	20	100.0	185	13	AF521482	Human	ech	AF521482	Human	ech	c 169	20	100.0	188	13	AY342845	Human	ech
C 97	20	100.0	185	13	AF521483	Human	ech	AF521483	Human	ech	c 170	20	100.0	188	13	AY342847	Human	ech
C 98	20	100.0	185	13	AF521484	Human	ech	AF521484	Human	ech	c 171	20	100.0	188	13	AY342848	Human	cox
C 99	20	100.0	185	13	AF521485	Human	ech	AF521485	Human	ech	c 172	20	100.0	188	13	AY342849	Human	cox
C 100	20	100.0	185	13	AF521486	Human	ech	AF521486	Human	ech	c 173	20	100.0	188	13	AY342850	Human	cox
C 101	20	100.0	185	13	AF521487	Human	ech	AF521487	Human	ech	c 174	20	100.0	188	13	AY342853	Human	cox
C 102	20	100.0	185	13	AF521488	Human	ech	AF521488	Human	ech	c 175	20	100.0	188	13	AY342854	Human	ech
C 103	20	100.0	185	13	AF521492	Human	ech	AF521492	Human	ech	c 176	20	100.0	188	13	AY342856	Human	ech
C 104	20	100.0	185	13	AF521493	Human	cox	AF521493	Human	cox	c 177	20	100.0	188	13	AY342857	Human	ech
C 105	20	100.0	185	13	AF521494	Human	cox	AF521494	Human	cox	c 178	20	100.0	188	13	AY342858	Human	ech
C 106	20	100.0	185	13	AF521495	Human	ech	AF521495	Human	ech	c 179	20	100.0	188	13	AY342859	Human	ech
C 107	20	100.0	185	13	AF521496	Human	ech	AF521496	Human	ech	c 180	20	100.0	188	13	AY342860	Human	ech
C 108	20	100.0	185	13	AF521497	Human	ech	AF521497	Human	ech	c 181	20	100.0	188	13	AY342862	Human	ech
C 109	20	100.0	185	13	AF521501	Human	ech	AF521501	Human	ech	c 182	20	100.0	188	13	AY342864	Human	ech
C 110	20	100.0	185	13	AF521502	Human	ech	AF521502	Human	ech	c 183	20	100.0	188	13	AY342865	Human	ech
C 111	20	100.0	185	13	AF521503	Human	ech	AF521503	Human	ech	c 184	20	100.0	188	13	AY342866	Human	ech
C 112	20	100.0	185	13	AF521504	Human	ech	AF521504	Human	ech	c 185	20	100.0	188	13	AY342868	Human	ech
C 113	20	100.0	185	13	AF521505	Human	ech	AF521505	Human	ech	c 186	20	100.0	188	13	AY342869	Human	ech
C 114	20	100.0	185	13	AF521507	Human	ech	AF521507	Human	ech	c 187	20	100.0	188	13	AY342870	Human	ech
C 115	20	100.0	185	13	AF521508	Human	ech	AF521508	Human	ech	c 188	20	100.0	188	13	AY342871	Human	ech
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C 124	20	100.0	185	13	AF521518	Human	ech	AF521518	Human	ech	c 197	20	100.0	188	13	AY342884	Human	ech
C 125	20	100.0	185	13	AF521519	Human	ech	AF521519	Human	ech	c 198	20	100.0	188	13	AY342885	Human	ech
C 126	20	100.0	185	13	AF521520	Human	ech	AF521520	Human	ech	c 199	20	100.0	188	13	AY342886	Human	ech
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C 133	20	100.0	185	13	AF521528	Human	ech	AF521528	Human	ech	c 206	20	100.0	188	13	AY342894	Human	cox
C 134	20	100.0	185	13	AF521529	Human	ech	AF521529	Human	ech	c 207	20	100.0	188	13	AY342895	Human	ech
C 135	20	100.0	185	13	AF521530	Human	ech	AF521530	Human	ech	c 208	20	100.0	188	13	AY342896	Human	ech
C 136	20	100.0	185	13	AF521533	Human	ech	AF521533	Human	ech	c 209	20	100.0	188	13	AY342897	Human	ech
C 137	20	100.0	185	13	AF521534	Human	ech	AF521534	Human	ech	c 210	20	100.0	188	13	AY342898	Human	ech
C 138	20	100.0	185	13	AF521535	Human	ech	AF521535	Human	ech	c 211	20	100.0	188	13	AY342899	Human	ech
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C 143	20	100.0	185	13	AF521543	Human	cox	AF521543	Human	cox	c 216	20	100.0	188	13	AY342905	Human	ech
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C 146	20	100.0	185	13	AF521548	Human	cox	AF521548	Human	cox	c 219	20	100.0	188	13	AY342908	Human	ech
C 147	20	100.0	185	13	AF521549	Human	ech	AF521549	Human	ech	c 220	20	100.0	188	13	AY342909	Human	ech
C 148	20	100.0	185	13	AF521550	Human	ech	AF521550	Human	ech	c 221	20	100.0	188	13	AY342910	Human	ech
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C 150	20	100.0	185	13	AF521552	Human	ech	AF521552	Human	ech	c 223	20	100.0	188	13	AY342912	Human	ech
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C 155	20	100.0	186	13	AF521466	Human	ech	AF521466	Human	ech	c 228	20	100.0	188	13	AY342917	Human	ech
C 156	20	100.0	186	13	AF521470	Human	cox	AF521470	Human	cox	c 229	20	100.0	188	13	AY342918	Human	ech
C 157	20	100.0	186	13	AF521472	Human	cox	AF521472	Human	cox	c 230	20	100.0	188	13	AY342919	Human	ech
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C 163	20	100.0	188	13	AY342838	Human	cox	AY342838	Human	cox	c 236	20	100.0	188	13	AY342927	Human	ech
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C 385	20	100.0	316	13	ECV7335	AJ007335 Echovirus	C 458	20	100.0	629	13	EV4VPGEN	X89534 Echovirus 4
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C 387	20	100.0	316	13	ECV7337	AJ007337 Echovirus	C 460	20	100.0	639	6	Q821453	Q821453 Sequence
C 388	20	100.0	316	13	ECV7338	AJ007338 Echovirus	C 461	20	100.0	641	13	CA22RNAPA	X87603 Coxsackievi
C 389	20	100.0	316	13	ECV7339	AJ007339 Echovirus	C 462	20	100.0	644	13	AY055125	AY055125 Human ent
C 390	20	100.0	316	13	ECV7341	AJ007341 Echovirus	C 463	20	100.0	644	13	AY055126	AY055126 Human ent
C 391	20	100.0	316	13	ECV7342	AJ007342 Echovirus	C 464	20	100.0	644	13	AY055127	AY055127 Human ent
C 392	20	100.0	316	13	ECV7343	AJ007343 Echovirus	C 465	20	100.0	644	13	AY055128	AY055128 Human ent
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C 396	20	100.0	319	13	HEC579639	AJ579639 Human ech	C 469	20	100.0	644	13	AY055132	AY055132 Human ent
C 397	20	100.0	319	13	HEC579640	AJ579640 Human ech	C 470	20	100.0	644	13	AY055133	AY055133 Human ent
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C 400	20	100.0	340	6	Q964031	Q964031 Sequence	C 473	20	100.0	644	13	AY055136	AY055136 Human ent
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C 404	20	100.0	361	13	AJ783787	AJ783787 Human pol	C 477	20	100.0	644	13	AY055140	AY055140 Human ent
C 405	20	100.0	364	13	S76767	S76767 {5' non-tra	C 478	20	100.0	644	13	AY055141	AY055141 Human ent
C 406	20	100.0	379	13	AJ783728	AJ783728 Human pol	C 479	20	100.0	644	13	AY055144	AY055144 Human ent
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C 409	20	100.0	382	13	AJ783778	AJ783778 Human pol	C 482	20	100.0	646	13	AY055146	AY055146 Human ent
C 410	20	100.0	384	13	AJ783723	AJ783723 Human pol	C 483	20	100.0	646	13	AY055166	AY055166 Human ent
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C 412	20	100.0	386	13	AJ783731	AJ783731 Human pol	C 485	20	100.0	648	13	AF117633	AF117633 Enterovir
C 413	20	100.0	388	13	AJ634678	AJ634678 Human pol	C 486	20	100.0	648	13	AF117635	AF117635 Enterovir
C 414	20	100.0	388	13	AY599875	AY599875 Human cox	C 487	20	100.0	648	13	AY055152	AY055152 Human ent
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C 417	20	100.0	389	13	AY599874	AY599874 Human cox	C 490	20	100.0	648	13	AY055155	AY055155 Human ent
C 418	20	100.0	390	13	AJ783730	AJ783730 Human pol	C 491	20	100.0	648	13	AY055156	AY055156 Human ent
C 419	20	100.0	390	13	AJ783773	AJ783773 Human pol	C 492	20	100.0	648	13	AY055157	AY055157 Human ent
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C 422	20	100.0	393	13	E70278125	Z78125 Enterovirus	C 495	20	100.0	648	13	AY055160	AY055160 Human ent
C 423	20	100.0	394	13	E70278127	Z78127 Enterovirus	C 496	20	100.0	648	13	AY055161	AY055161 Human ent
C 424	20	100.0	394	13	E70278133	Z78133 Enterovirus	C 497	20	100.0	648	13	AY055162	AY055162 Human ent
C 425	20	100.0	394	13	E70278137	Z78137 Enterovirus	C 498	20	100.0	648	13	AY055163	AY055163 Human ent
C 426	20	100.0	394	13	E70278139	Z78139 Enterovirus	C 499	20	100.0	648	13	AY055164	AY055164 Human ent
C 427	20	100.0	395	13	AJ783771	AJ783771 Human pol	C 500	20	100.0	648	13	AY055165	AY055165 Human ent
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C 452	20	100.0	617	13	AB059823	AB059823 Enterovir							
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C 454	20	100.0	617	13	AB059826	AB059826 Enterovir							
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C 456	20	100.0	628	6	A37564	A37564 Sequence 5							

ALIGNMENTS

RESULT 1	AY189930/c	AY189930	Human enterovirus B isolate NSW/51/97 5'	RNA	linear	VRL 08-MAY-2003
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ACCESSION	AY189930	Human enterovirus B isolate NSW/51/97 5'	RNA	linear	VRL 08-MAY-2003	
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SOURCE	Human enterovirus B					
ORGANISM	Human enterovirus B					
REFERENCE	1 (bases 1 to 73)					
AUTHORS	Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.					
TITLE	Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA					
JOURNAL	J. Infect. Dis. 187 (10), 1562-1570 (2003)					
PUBMED	12721936					
REFERENCE	2 (bases 1 to 73)					
AUTHORS	Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.					
TITLE	Direct Submission					
JOURNAL	Submitted (03-DEC-2002) Virology Division, University of New South Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia					

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REFERENCE
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AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 73)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Virology Division, University of New South
  Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,
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  ORGANISM Enterovirus sp.
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  Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 103)
AUTHORS Muir, P., Nicholson, F., Spencer, G.T., Ajetunmbi, J.F., Starkey, W.G.,
  Khan, M., Archard, L.C., Cairns, N.J., Anderson, V.E.R., Leigh, P.N.,
  Howard, R.S. and Banatvala, J.E.
  TITLE Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
JOURNAL J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
PUBMED 8757988
REFERENCE 2 (bases 1 to 103)
AUTHORS Muir, P.
TITLE Direct Submission
JOURNAL Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
  Road, London SE1 7EH, UK
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QY 1 AAGGAAACACGGACACCCAA 20
Db 91 AAGGAAACACGGACACCCAA 72
RESULT 4
AY049767/c
LOCUS
  DEFINITION Enterovirus sp. clone Entero-1 5' RNA linear VRL 08-DSC-2001
  sequence.
  ACCESSION AY049767
  VERSION AY049767.1 GI:17426413
  KEYWORDS
  SOURCE Enterovirus sp.
  ORGANISM Enterovirus sp.
  Viruses; ssRNA positive-strand viruses, no DNA stage;
  Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 109)
AUTHORS Kawashima, H., Kasaiwagi, Y. and Mori, T.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Pediatrics, Tokyo Medical University, 6-7-1
  Nishishinjuku, Shinjuku-ku, Tokyo 160-0023, Japan
FEATURES
  source
    Location/Qualifiers
      1..109
      /organism="Enterovirus sp."
      /mol_type="genomic RNA"
      /db_xref="taxon:47681"
      /clones="Entero-1"
      /note="from cerebrospinal fluid"
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5' UTR
ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 30;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAAACACGGACACCCAA 20
Db 97 AAGGAAACACGGACACCCAA 78
RESULT 5
E7U00872/c
LOCUS
  DEFINITION Enterovirus E71 H 5' untranslated region.
  ACCESSION U00872
  VERSION U00872.1 GI:405115
  KEYWORDS
  SOURCE Human enterovirus 71
  ORGANISM Human enterovirus 71

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Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 109)
Zheng,Z.M., He,P.J., Caueffield,D., Neumann,M., Specter,S.,
Baker,C.C. and Bankowski,M.J.
TITLE
Enterovirus 71 isolated from China is serologically similar to the
prototype E71 BrCr strain but differs in the 5'-noncoding region
J. Med. Virol. 47 (2), 161-167 (1995)
JOURNAL
PUBMED
8830120
REFERENCE
2 (bases 1 to 109)
Bankowski,M.J.
AUTHORS
Direct Submission
TITLE
Submitted (17-AUG-1993) Bankowski M.J., Diagnostic Services, Inc.,
JOURNAL
Clinical Virology & Molecular Medicine, 340 Goodlette Road South,
Naples, FL 33940, USA
FEATURES
source
Location/Qualifiers
1. .1109
/organism="Human enterovirus 71"
/mol_type="unassigned DNA"
/strain="E 71 H"
/isolate="H"
/db_xref="taxon:39054"

ORIGIN
Query Match 100.0%; Score 20; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 97 AAGGAAACACGGACACCCAA 78

RESULT 6
AY189929/c
LOCUS
DEFINITION
Human enterovirus B isolate NSW/47/97 5' untranslated region,
partial sequence.
ACCESSION
AY189929
VERSION
AY189929.1 GI:28395428
KEYWORDS
Human enterovirus B
ORGANISM
Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 112)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED
12721936
REFERENCE
2 (bases 1 to 112)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
TITLE
Submitted (03-DEC-2002) Virology Division, University of New South
JOURNAL
Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,
Australia
FEATURES
source
Location/Qualifiers
1. .112
/organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/47/97"
/db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 7
AY189177/c
LOCUS
DEFINITION
Human poliovirus 1 strain Sabin isolate NSW/84/97 5' UTR, partial
sequence.
ACCESSION
AY189177
VERSION
AY189177.1 GI:28274400
KEYWORDS
Human poliovirus 1 strain Sabin
ORGANISM
Human poliovirus 1 strain Sabin
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 115)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED
12721936
REFERENCE
2 (bases 1 to 115)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
TITLE
Submitted (29-NOV-2002) Virology Division, South Eastern Area
JOURNAL
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
source
Location/Qualifiers
1. .115
/organism="Human poliovirus 1 strain Sabin"
/mol_type="genomic RNA"
/isolate="NSW/84/97"
/db_xref="taxon:12082"
/notes="Human poliovirus 1 strain Sabin"
<1. .>115

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 8
AY189178/c
LOCUS
DEFINITION
Human poliovirus 1 strain Sabin isolate NSW/96/97 5' UTR, partial
sequence.
ACCESSION
AY189178
VERSION
AY189178.1 GI:28274401
KEYWORDS
Human poliovirus 1 strain Sabin
ORGANISM
Human poliovirus 1 strain Sabin
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 115)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED
12721936
REFERENCE
2 (bases 1 to 115)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
TITLE
Submitted (29-NOV-2002) Virology Division, South Eastern Area
JOURNAL
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
source
Location/Qualifiers
1. .115
/organism="Human poliovirus 1 strain Sabin"
/mol_type="genomic RNA"

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/isolate="NSW/96/97"
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/notes="Human poliovirus 1 strain Sabin"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 9
AY189210/c
LOCUS
DEFINITION Human enterovirus A isolate NSW/227/99 5' UTR, partial sequence.
ACCESSION AY189210
VERSION AY189210.1 GI:28274433
KEYWORDS
SOURCE Human enterovirus A
ORGANISM Human enterovirus A
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
source
Location/Qualifiers
1..115
/mol_type="genomic RNA"
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/db_xref="taxon:138948"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 10
AY189213/c
LOCUS
DEFINITION Human enterovirus A isolate NSW/255/99 5' UTR, partial sequence.
ACCESSION AY189213
VERSION AY189213.1 GI:28274436
KEYWORDS
SOURCE Human enterovirus A
ORGANISM Human enterovirus A
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936

/isolate="NSW/96/97"
/db_xref="taxon:12082"
/notes="Human poliovirus 1 strain Sabin"
<1..>115

5'UTR
ORIGIN
Query Match 100.0%; Score 20; DB 13; Length 115;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 11
PEN295168/c
LOCUS
DEFINITION Porcine enterovirus 9 genomic RNA for partial 5'UTR, isolate
ITA93-766BE93.
ACCESSION AJ295168
VERSION AJ295168.1 GI:14140111
KEYWORDS
SOURCE Porcine enterovirus 9
ORGANISM Porcine enterovirus 9
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Muscillo,M., La Rosa,G. and Marianelli,C.
JOURNAL Unpublished
REFERENCE
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
00161, Italy
FEATURES
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Location/Qualifiers
1..115
/organism="Porcine enterovirus 9"
/virion
/mol_type="genomic RNA"
/isolate="ITA93-766BE93"
/specific_host="Sus scrofa"
/db_xref="taxon:64141"
/notes="viral particles isolated from serum of swine"
<1..>115

5'UTR
ORIGIN
Query Match 100.0%; Score 20; DB 13; Length 115;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 103 AAGGAAACACGGACACCCAA 84

RESULT 12
AY189158/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/01/97 5' UTR, partial sequence.
ACCESSION AY189158
VERSION AY189158.1 GI:28274381
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936

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SOURCE      Human enterovirus B
ORGANISM     Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
              Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE    2 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
              Laboratory Services, University of New South Wales/Prince of Wales
              Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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               /mol_type="genomic RNA"
               /isolate="NSW/01/97"
               /db_xref="taxon:138949"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 13
AY189160/c
LOCUS        Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.
DEFINITION   Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.
ACCESSION    AY189160
VERSION      AY189160.1 GI:28274383
KEYWORDS     .
SOURCE       Human enterovirus B
ORGANISM     Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
              Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE    2 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
              Laboratory Services, University of New South Wales/Prince of Wales
              Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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               /mol_type="genomic RNA"
               /isolate="NSW/07/97"
               /db_xref="taxon:138949"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAAACACGGACACCCAA 85

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RESULT 14
AY189161/c
LOCUS        Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
DEFINITION   Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
ACCESSION    AY189161
VERSION      AY189161.1 GI:28274384
KEYWORDS     .
SOURCE       Human enterovirus 71
ORGANISM     Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
              Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE    2 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
              Laboratory Services, University of New South Wales/Prince of Wales
              Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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               /mol_type="genomic RNA"
               /isolate="NSW/08/97"
               /db_xref="taxon:39054"
               /note="Human enterovirus 71"
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ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 15
AY189162/c
LOCUS        Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
DEFINITION   Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
ACCESSION    AY189162
VERSION      AY189162.1 GI:28274385
KEYWORDS     .
SOURCE       Human enterovirus B
ORGANISM     Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
              Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE    2 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
              Laboratory Services, University of New South Wales/Prince of Wales
              Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
              1..116
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               /mol_type="genomic RNA"
               /isolate="NSW/14/97"
               /db_xref="taxon:138949"
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ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAAACACGGACACCCAA 85

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5'UTR
ORIGIN
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
    |||||
DB 104 AAGGAAACACGGACACCCAA 85

RESULT 16
AY189163/c
LOCUS AY189163 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/16/97 5' UTR, partial sequence.
ACCESSION AY189163
VERSION AY189163.1 GI:28274386
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
source
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/organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/16/97"
/db_xref="taxon:138949"
<1..>116

5'UTR
ORIGIN

Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
    |||||
DB 104 AAGGAAACACGGACACCCAA 85

RESULT 17
AY189164/c
LOCUS AY189164 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/17/97 5' UTR, partial sequence.
ACCESSION AY189164
VERSION AY189164.1 GI:28274387
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission

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JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
source
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/mol_type="genomic RNA"
/isolate="NSW/17/97"
/db_xref="taxon:138949"
<1..>116

5'UTR
ORIGIN

Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
    |||||
DB 104 AAGGAAACACGGACACCCAA 85

RESULT 18
AY189165/c
LOCUS AY189165 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/19/97 5' UTR, partial sequence.
ACCESSION AY189165
VERSION AY189165.1 GI:28274388
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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/organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/19/97"
/db_xref="taxon:138949"
<1..>116

5'UTR
ORIGIN

Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
    |||||
DB 104 AAGGAAACACGGACACCCAA 85

RESULT 19
AY189166/c
LOCUS AY189166 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus NSW/23/97 5' UTR, partial sequence.
ACCESSION AY189166
VERSION AY189166.1 GI:28274389
KEYWORDS
SOURCE Human enterovirus NSW/23/97
ORGANISM Human enterovirus NSW/23/97
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

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REFERENCE
AUTHORS      1 (bases 1 to 116)
TITLE        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
JOURNAL      Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
PUBMED       Diabetes Associated with Enterovirus RNA
PUBMED       J. Infect. Dis. 187 (10), 1562-1570 (2003)
REFERENCE    12721936
AUTHORS      2 (bases 1 to 116)
TITLE        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
JOURNAL      Direct Submission
SUBMITTED    (29-NOV-2002) Virology Division, South Eastern Area
LABORATORY   Laboratory Services, University of New South Wales/Prince of Wales
HOSPITAL     Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
  source     Location/Qualifiers
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            /mol_type="genomic RNA"
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            /db_xref="taxon:220228"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
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Db      104 AAGGAACACGGACACCCAA 85

RESULT 20
AY189170/c
LOCUS      AY189170      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/48/97 5' UTR, partial sequence.
ACCESSION  AY189170
VERSION     AY189170.1 GI:28274393
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL      Diabetes Associated with Enterovirus RNA
PUBMED       J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
AUTHORS      2 (bases 1 to 116)
TITLE        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
JOURNAL      Direct Submission
SUBMITTED    (29-NOV-2002) Virology Division, South Eastern Area
LABORATORY   Laboratory Services, University of New South Wales/Prince of Wales
HOSPITAL     Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
  source     Location/Qualifiers
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            /organism="Human enterovirus B"
            /mol_type="genomic RNA"
            /isolate="NSW/48/97"
            /db_xref="taxon:138949"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
        |||||||
Db      104 AAGGAACACGGACACCCAA 85

RESULT 21
AY189171/c
LOCUS      AY189171      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/60/97 5' UTR, partial sequence.
ACCESSION  AY189171
VERSION     AY189171.1 GI:28274394
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL      Diabetes Associated with Enterovirus RNA
PUBMED       J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
AUTHORS      2 (bases 1 to 116)
TITLE        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
JOURNAL      Direct Submission
SUBMITTED    (29-NOV-2002) Virology Division, South Eastern Area
LABORATORY   Laboratory Services, University of New South Wales/Prince of Wales
HOSPITAL     Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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            /db_xref="taxon:138949"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
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Db      104 AAGGAACACGGACACCCAA 85

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LOCUS      AY189171      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/60/97 5' UTR, partial sequence.
ACCESSION  AY189171
VERSION     AY189171.1 GI:28274394
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL      Diabetes Associated with Enterovirus RNA
PUBMED       J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
AUTHORS      2 (bases 1 to 116)
TITLE        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
JOURNAL      Direct Submission
SUBMITTED    (29-NOV-2002) Virology Division, South Eastern Area
LABORATORY   Laboratory Services, University of New South Wales/Prince of Wales
HOSPITAL     Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
        |||||||
Db      104 AAGGAACACGGACACCCAA 85

RESULT 22
AY189172/c
LOCUS      AY189172      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus C isolate NSW/68/97 5' UTR, partial sequence.
ACCESSION  AY189172
VERSION     AY189172.1 GI:28274395
KEYWORDS
SOURCE      Human enterovirus C
ORGANISM    Human enterovirus C
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL      Diabetes Associated with Enterovirus RNA
PUBMED       J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
AUTHORS      2 (bases 1 to 116)
TITLE        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
JOURNAL      Direct Submission
SUBMITTED    (29-NOV-2002) Virology Division, South Eastern Area
LABORATORY   Laboratory Services, University of New South Wales/Prince of Wales
HOSPITAL     Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 30;

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QY 1 AAGGAAACACGACACCCAA 20
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DB 104 AAGGAAACACGACACCCAA 85

RESULT 23
AY189173/c
LOCUS AY189173 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/73/97 5' UTR, partial sequence.
ACCESSION AY189173
VERSION AY189173.1 GI:28274396
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
    |||||
DB 104 AAGGAAACACGACACCCAA 85

RESULT 24
AY189175/c
LOCUS AY189175 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/82/97 5' UTR, partial sequence.
ACCESSION AY189175
VERSION AY189175.1 GI:28274398
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
    |||||
DB 104 AAGGAAACACGACACCCAA 85

RESULT 25
AY189176/c
LOCUS AY189176 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/83/97 5' UTR, partial sequence.
ACCESSION AY189176
VERSION AY189176.1 GI:28274399
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
    |||||
DB 104 AAGGAAACACGACACCCAA 85

RESULT 26
AY189180/c
LOCUS AY189180 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/111/98 5' UTR, partial sequence.
ACCESSION AY189180
VERSION AY189180.1 GI:28274403
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
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/organism="Human enterovirus B"
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/db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
    |||||
DB 104 AAGGAAACACGACACCCAA 85

RESULT 25
AY189176/c
LOCUS AY189176 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/83/97 5' UTR, partial sequence.
ACCESSION AY189176
VERSION AY189176.1 GI:28274399
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
    |||||
DB 104 AAGGAAACACGACACCCAA 85

RESULT 26
AY189180/c
LOCUS AY189180 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/111/98 5' UTR, partial sequence.
ACCESSION AY189180
VERSION AY189180.1 GI:28274403
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
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12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 27
AY189181/c
LOCUS AY189181 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/135/98 5' UTR, partial sequence.
ACCESSION AY189181
VERSION AY189181.1 GI:28274404
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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        /isolate="NSW/135/98"
        /db_xref="taxon:138949"
        <1..>116
5'UTR
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Query Match 100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 28
AY189182/c
LOCUS AY189182 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 70 NSW/140/98 5' UTR, partial sequence.
ACCESSION AY189182
VERSION AY189182.1 GI:28274405
KEYWORDS

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Human enterovirus 70
ORGANISM Human enterovirus 70
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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        /isolate="NSW/140/98"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
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Db 104 AAGGAAACACGGACACCCAA 85

RESULT 29
AY189183/c
LOCUS AY189183 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/141/98 5' UTR, partial sequence.
ACCESSION AY189183
VERSION AY189183.1 GI:28274406
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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        /organism="Human enterovirus B"
        /mol_type="genomic RNA"
        /isolate="NSW/141/98"
        /db_xref="taxon:138949"
        <1..>116
5'UTR
ORIGIN
Query Match 100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

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RESULT 30
AY189184/c
LOCUS      AY189184      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/143/98 5' UTR, partial sequence.
ACCESSION  AY189184
VERSION     AY189184.1  GI:28274407
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    source
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               /organism="Human enterovirus B"
               /mol_type="genomic RNA"
               /isolate="NSW/143/98"
               /db_xref="taxon:138949"
               <1..>116
5'UTR
ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAAACACGACACCCAA 20
        ||||||||||||||||||
Db      104 AAGGAAACACGACACCCAA 85

RESULT 31
AY189186/c
LOCUS      AY189186      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/147/98 5' UTR, partial sequence.
ACCESSION  AY189186
VERSION     AY189186.1  GI:28274409
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    source
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ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAAACACGACACCCAA 20
        ||||||||||||||||||
Db      104 AAGGAAACACGACACCCAA 85

RESULT 32
AY189187/c
LOCUS      AY189187      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/149/98 5' UTR, partial sequence.
ACCESSION  AY189187
VERSION     AY189187.1  GI:28274410
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    source
            1..116
               /organism="Human enterovirus B"
               /mol_type="genomic RNA"
               /isolate="NSW/149/98"
               /db_xref="taxon:138949"
               <1..>116
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ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAAACACGACACCCAA 20
        ||||||||||||||||||
Db      104 AAGGAAACACGACACCCAA 85

RESULT 33
AY189188/c
LOCUS      AY189188      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/151/98 5' UTR, partial sequence.
ACCESSION  AY189188
VERSION     AY189188.1  GI:28274411
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
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Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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              /isolate="NSW/151/98"
              /db_xref="taxon:138949"
              <1..>116
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ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 34
AY189189/c
LOCUS      AY189189      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/153/98 5' UTR, partial sequence.
ACCESSION  AY189189
VERSION     AY189189.1 GI:28274412
KEYWORDS    Human enterovirus 71
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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              /mol_type="genomic RNA"
              /isolate="NSW/153/98"
              /db_xref="taxon:39054"
              /note="Human enterovirus 71"
              <1..>116
5'UTR
ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 35
AY189190/c
LOCUS      AY189190      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus NSW/154/98 5' UTR, partial sequence.
ACCESSION  AY189190
VERSION     AY189190.1 GI:28274413
KEYWORDS    Human enterovirus NSW/154/98
SOURCE      Human enterovirus NSW/154/98
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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              /db_xref="taxon:138949"
              <1..>116
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 36
AY189192/c
LOCUS      AY189192      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/157/98 5' UTR, partial sequence.
ACCESSION  AY189192
VERSION     AY189192.1 GI:28274415
KEYWORDS    Human enterovirus 71
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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              /note="Human enterovirus 71"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 37
AY189192/c
LOCUS      AY189192      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/157/98 5' UTR, partial sequence.
ACCESSION  AY189192
VERSION     AY189192.1 GI:28274415
KEYWORDS    Human enterovirus 71
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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              /mol_type="genomic RNA"
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              /db_xref="taxon:39054"
              /note="Human enterovirus 71"
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    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 37
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1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
  source      1..116
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 36
AY189192/c
LOCUS      AY189192      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/157/98 5' UTR, partial sequence.
ACCESSION  AY189192
VERSION     AY189192.1 GI:28274415
KEYWORDS    Human enterovirus 71
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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              /mol_type="genomic RNA"
              /isolate="NSW/157/98"
              /db_xref="taxon:39054"
              /note="Human enterovirus 71"
              <1..>116
5'UTR
ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
    ||||||||||||||||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 37
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AY189194/c
LOCUS      AY189194              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus NSW/161/98 5' UTR, partial sequence.
ACCESSION  AY189194
VERSION     AY189194.1  GI:28274417
KEYWORDS
SOURCE      Human enterovirus NSW/161/98
            Human enterovirus NSW/161/98
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   source
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            /organism="Human enterovirus NSW/161/98"
            /mol_type="genomic RNA"
            /isolate="NSW/161/98"
            /db_xref="taxon:220410"
            <1..>116

5'UTR
ORIGIN

Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||
Db      104 AAGGAACACGACACCCAA 85

RESULT 38
LOCUS      AY189195/c
DEFINITION Human enterovirus 71 isolate NSW/166/98 5' UTR, partial sequence.
ACCESSION  AY189195
VERSION     AY189195.1  GI:28274418
KEYWORDS
SOURCE      Human enterovirus 71
            Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   source
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            /organism="Human enterovirus 71"
            /mol_type="genomic RNA"
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            /note="Human enterovirus 71"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||
Db      104 AAGGAACACGACACCCAA 85

RESULT 39
LOCUS      AY189196/c
DEFINITION Human enterovirus 71 isolate NSW/169/98 5' UTR, partial sequence.
ACCESSION  AY189196
VERSION     AY189196.1  GI:28274419
KEYWORDS
SOURCE      Human enterovirus 71
            Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   source
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            /organism="Human enterovirus 71"
            /mol_type="genomic RNA"
            /isolate="NSW/169/98"
            /db_xref="taxon:39054"
            /note="Human enterovirus 71"
            <1..>116

5'UTR
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||
Db      104 AAGGAACACGACACCCAA 85

RESULT 40
LOCUS      AY189197/c
DEFINITION Human enterovirus NSW/173/98
ACCESSION  AY189197
VERSION     AY189197.1  GI:28274420
KEYWORDS
SOURCE      Human enterovirus NSW/173/98
            Human enterovirus NSW/173/98
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   source
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            /note="Human enterovirus 71"
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FEATURES
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                /mol_type="genomic RNA"
                /isolate="NSW/173/98"
                /db_xref="taxon:220411"
                <1..>116

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ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 41
AY189198/c
LOCUS AY189198 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/180/98 5' UTR, partial sequence.
ACCESSION AY189198
VERSION AY189198.1 GI:28274421
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
  source      Hospital, High Street, Randwick, NSW 2031, Australia
              Location/Qualifiers
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                /mol_type="genomic RNA"
                /isolate="NSW/180/98"
                /db_xref="taxon:39054"
                /note="Human enterovirus 71"
                <1..>116

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ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 42
AY189199/c
LOCUS AY189199 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/182/98 5' UTR, partial sequence.
ACCESSION AY189199
VERSION AY189199.1 GI:28274422
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
  source      Hospital, High Street, Randwick, NSW 2031, Australia
              Location/Qualifiers
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                /mol_type="genomic RNA"
                /isolate="NSW/180/98"
                /db_xref="taxon:39054"
                /note="Human enterovirus 71"
                <1..>116

5'UTR
ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 43
AY189200/c
LOCUS AY189200 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/189/99 5' UTR, partial sequence.
ACCESSION AY189200
VERSION AY189200.1 GI:28274423
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
  source      Hospital, High Street, Randwick, NSW 2031, Australia
              Location/Qualifiers
                1..116
                /organism="Human enterovirus B"
                /mol_type="genomic RNA"
                /isolate="NSW/189/99"
                /db_xref="taxon:138949"
                <1..>116

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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 44
AY189202/c

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AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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              Location/Qualifiers
                1..116
                /organism="Human enterovirus 71"
                /mol_type="genomic RNA"
                /isolate="NSW/182/98"
                /db_xref="taxon:39054"
                /note="Human enterovirus 71"
                <1..>116

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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 43
AY189200/c
LOCUS AY189200 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/189/99 5' UTR, partial sequence.
ACCESSION AY189200
VERSION AY189200.1 GI:28274423
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
  source      Hospital, High Street, Randwick, NSW 2031, Australia
              Location/Qualifiers
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                /organism="Human enterovirus B"
                /mol_type="genomic RNA"
                /isolate="NSW/189/99"
                /db_xref="taxon:138949"
                <1..>116

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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
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Db 104 AAGGAACACGGACACCCAA 85

RESULT 44
AY189202/c

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LOCUS      AY189202              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/196/99 5' UTR, partial sequence.
ACCESSION  AY189202
VERSION     AY189202.1  GI:28274425
KEYWORDS   Human enterovirus 71
SOURCE      Human enterovirus 71
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
             Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
           Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
           Laboratory Services, University of New South Wales/Prince of Wales
           Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    Location/Qualifiers
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             /mol_type="genomic RNA"
             /isolate="NSW/196/99"
             /db_xref="taxon:39054"
             /note="Human enterovirus 71"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||||
Db      104 AAGGAACACGACACCCAA 85

RESULT 45
AY189203/c
LOCUS      AY189203              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/197/99 5' UTR, partial sequence.
ACCESSION  AY189203
VERSION     AY189203.1  GI:28274426
KEYWORDS   Human enterovirus B
SOURCE      Human enterovirus B
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
             Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
           Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
           Laboratory Services, University of New South Wales/Prince of Wales
           Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    Location/Qualifiers
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             /organism="Human enterovirus B"
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             /isolate="NSW/197/99"
             /db_xref="taxon:138949"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||||
Db      104 AAGGAACACGACACCCAA 85

RESULT 46
AY189204/c
LOCUS      AY189204              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/198/99 5' UTR, partial sequence.
ACCESSION  AY189204
VERSION     AY189204.1  GI:28274427
KEYWORDS   Human enterovirus B
SOURCE      Human enterovirus B
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
             Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
           Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
           Laboratory Services, University of New South Wales/Prince of Wales
           Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    Location/Qualifiers
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             /organism="Human enterovirus B"
             /mol_type="genomic RNA"
             /isolate="NSW/198/99"
             /db_xref="taxon:138949"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||||
Db      104 AAGGAACACGACACCCAA 85

RESULT 47
AY189206/c
LOCUS      AY189206              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/208/99 5' UTR, partial sequence.
ACCESSION  AY189206
VERSION     AY189206.1  GI:28274429
KEYWORDS   Human enterovirus B
SOURCE      Human enterovirus B
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
             Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
           Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
           Laboratory Services, University of New South Wales/Prince of Wales
           Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    Location/Qualifiers
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             /organism="Human enterovirus B"
             /mol_type="genomic RNA"
             /isolate="NSW/197/99"
             /db_xref="taxon:138949"
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Query Match      100.0%; Score 20; DB 13; Length 116;

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||||
Db      104 AAGGAACACGACACCCAA 85

RESULT 46
AY189204/c
LOCUS      AY189204              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/198/99 5' UTR, partial sequence.
ACCESSION  AY189204
VERSION     AY189204.1  GI:28274427
KEYWORDS   Human enterovirus B
SOURCE      Human enterovirus B
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
             Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
           Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
           Laboratory Services, University of New South Wales/Prince of Wales
           Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    Location/Qualifiers
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             /mol_type="genomic RNA"
             /isolate="NSW/198/99"
             /db_xref="taxon:138949"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||||
Db      104 AAGGAACACGACACCCAA 85

RESULT 47
AY189206/c
LOCUS      AY189206              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/208/99 5' UTR, partial sequence.
ACCESSION  AY189206
VERSION     AY189206.1  GI:28274429
KEYWORDS   Human enterovirus B
SOURCE      Human enterovirus B
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
             Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
           Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
           Laboratory Services, University of New South Wales/Prince of Wales
           Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    Location/Qualifiers
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             /isolate="NSW/197/99"
             /db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 48
AY189208/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/214/99 5' UTR, partial sequence.
ACCESSION AY189208
VERSION AY189208.1 GI:28274431
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
PUBMED
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
J. Infect. Dis. 187 (10), 1562-1570 (2003)
116 bp RNA linear VRL 08-MAY-2003
/mol_type="genomic RNA"
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/db_xref="taxon:138949"
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5'UTR
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 49
AY189211/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/230/99 5' UTR, partial sequence.
ACCESSION AY189211
VERSION AY189211.1 GI:28274434
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
PUBMED
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
J. Infect. Dis. 187 (10), 1562-1570 (2003)
116 bp RNA linear VRL 08-MAY-2003
/mol_type="genomic RNA"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 50
AY189214/c
LOCUS
DEFINITION Human enterovirus A isolate NSW/277/99 5' UTR, partial sequence.
ACCESSION AY189214
VERSION AY189214.1 GI:28274437
KEYWORDS
SOURCE Human enterovirus A
ORGANISM Human enterovirus A
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
PUBMED
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
J. Infect. Dis. 187 (10), 1562-1570 (2003)
116 bp RNA linear VRL 08-MAY-2003
/mol_type="genomic RNA"
/isolate="NSW/277/99"
/db_xref="taxon:138949"
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Query Match 100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 51
AY189215/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/338/99 5' UTR, partial sequence.
ACCESSION AY189215
VERSION AY189215.1 GI:28274438

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J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
PUBMED
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
J. Infect. Dis. 187 (10), 1562-1570 (2003)
116 bp RNA linear VRL 08-MAY-2003
/mol_type="genomic RNA"
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/db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 50
AY189214/c
LOCUS
DEFINITION Human enterovirus A isolate NSW/277/99 5' UTR, partial sequence.
ACCESSION AY189214
VERSION AY189214.1 GI:28274437
KEYWORDS
SOURCE Human enterovirus A
ORGANISM Human enterovirus A
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
PUBMED
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
J. Infect. Dis. 187 (10), 1562-1570 (2003)
116 bp RNA linear VRL 08-MAY-2003
/mol_type="genomic RNA"
/isolate="NSW/277/99"
/db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 51
AY189215/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/338/99 5' UTR, partial sequence.
ACCESSION AY189215
VERSION AY189215.1 GI:28274438

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KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Sillink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Sillink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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/organism="Human enterovirus B"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
Db 104 AAGGAAACACGGACACCCAA 85
RESULT 52
AY189216/c
LOCUS Human enterovirus 71 isolate NSW/E71/99 5' UTR, partial sequence. VRL 08-MAY-2003
DEFINITION
ACCESSION AY189216
VERSION AY189216.1 GI:28274439
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Sillink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Sillink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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/organism="Human enterovirus 71"
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/note="Human enterovirus 71"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
Db 104 AAGGAAACACGGACACCCAA 85
RESULT 54
S66302S1/c
LOCUS Human poliovirus 3
DEFINITION Human poliovirus 3
ACCESSION S66302
VERSION S66302.1 GI:435703
KEYWORDS
SEGMENT 1 of 2
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 119)
AUTHORS LCDC (Canadian Govt)
TITLE Genomic analysis of type 3 wild poliovirus isolates in southern
Alberta
JOURNAL Can. Commun. Dis. Rep. 19 (13), 96-99 (1993)
PUBMED 8395279
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 138833] from the original journal article.

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Db 104 AAGGAAACACGGACACCCAA 85
RESULT 53
AB183003/c
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DEFINITION
ACCESSION AB183003
VERSION AB183003.1 GI:49614920
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 Fujimoto, T., Yoshida, S., Munemura, T., Yoshida, H., Chikahira, M. and
Nishio, O.
TITLE Enterovirus 71 sequence detected from cerebrospinal fluid
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 117)
AUTHORS Fujimoto, T., Munemura, T. and Chikahira, M.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-2004) Teugoto Fujimoto, Hyogo Prefectural
Institute of Public Health and Environmental Sciences, Infectious
Disease Research Division; 2-1-29, Arata-cho, Hyogo-Ku, Kobe, Hyogo
652-0032, Japan (E-mail: Teugoto.Fujimoto@pref.hyogo.jp,
URL: http://www.iphes.pref.hyogo.jp/, Tel: 81-78-511-6640 (ex.236),
Fax: 81-78-531-7080)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 105 AAGGAAACACGGACACCCAA 86
RESULT 54
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LOCUS Human poliovirus 3
DEFINITION Human poliovirus 3
ACCESSION S66302
VERSION S66302.1 GI:435703
KEYWORDS
SEGMENT 1 of 2
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 119)
AUTHORS LCDC (Canadian Govt)
TITLE Genomic analysis of type 3 wild poliovirus isolates in southern
Alberta
JOURNAL Can. Commun. Dis. Rep. 19 (13), 96-99 (1993)
PUBMED 8395279
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 138833] from the original journal article.

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        /organism="Human poliovirus 3"
        /mol_type="genomic RNA"
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Qy 1 AAGGAAACACGGACACCCAA 20
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Db 101 AAGGAAACACGGACACCCAA 82

RESULT 55
AJ783777/c
LOCUS
DEFINITION Human poliovirus 1, partial 5'UTR, genomic RNA, isolate P20.
ACCESSION AJ783777
VERSION AJ783777.1 GI:72534022
KEYWORDS
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1 Pavlov,D.N.
  Genomic mutations in oral poliovirus vaccine strains:Implications
  for the eradication of poliovirus
  Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 128)
AUTHORS Pavlov,D.N.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2004) Pavlov D.N., Medical Virology, University
of Pretoria, P.O.Box 2034, Pretoria, Gauteng, 0001, SOUTH AFRICA
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        /mol_type="genomic RNA"
        /isolate="P20"
        /isolation_source="stool specimen from immunodeficient
        infant"
        /specific_host="Homo sapiens"
        /db_xref="taxon:12080"
        /country="South Africa:Gauteng"
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  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
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Db 118 AAGGAAACACGGACACCCAA 99

RESULT 56
HEN312090/c
LOCUS
DEFINITION Human coxsackievirus B2 partial 5'UTR, strain /ra/Roma99.
ACCESSION AJ312090
VERSION AJ312090.1 GI:16555708
KEYWORDS
SOURCE Human coxsackievirus B2
ORGANISM Human coxsackievirus B2
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1
  Manzara,S., Muscillo,M., La Rosa,G., Marianelli,C., Cattani,P. and
  Fadda,G.
  Molecular identification and typing of enteroviruses isolated from
  clinical specimens
  J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
  12454151
  2 (bases 1 to 145)
  Muscillo,M.
  Direct Submission
  Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
  Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
  00161, Italy
  Location/Qualifiers
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      /mol_type="genomic RNA"
      /strain="/ra/Roma99"
      /isolate="IT99-5108"
      /db_xref="taxon:82639"
      /lab_host="LLC-MK2 cell culture"
      /note="throat swab from child with aseptic meningitis,
      identified by immunofluorescence assay"
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  Best Local Similarity 100.0%; Pred. No. 30;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
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Db 121 AAGGAAACACGGACACCCAA 102

RESULT 57
HEN312091/c
LOCUS
DEFINITION Human coxsackievirus B2 partial 5'UTR, strain /ro/Roma98.
ACCESSION AJ312091
VERSION AJ312091.1 GI:16555709
KEYWORDS
SOURCE Human coxsackievirus B2
ORGANISM Human coxsackievirus B2
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1
  Manzara,S., Muscillo,M., La Rosa,G., Marianelli,C., Cattani,P. and
  Fadda,G.
  Molecular identification and typing of enteroviruses isolated from
  clinical specimens
  J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
  12454151
  2 (bases 1 to 145)
  Muscillo,M.
  Direct Submission
  Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
  Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
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RESULT 58
AF314006/c
LOCUS AF314006 147 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 5506/SIN/001309 5' UTR, partial sequence.
ACCESSION AF314006
VERSION AF314006.1 GI:12667229
KEYWORDS
SOURCE
ORGANISM Enterovirus 5506/SIN/001309
Enterovirus 5506/SIN/001309
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 147)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
JOURNAL PUBLISHED 12149336
REFERENCE 2 (bases 1 to 107)
Singh, S., Chow, V.T.K. and Poh, C.L.
AUTHORS Direct Submission
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
LOCATION/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:150715"
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5'UTR
ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 122 AAGGAAACACGGACACCCAA 103

RESULT 59
AF316322/c
LOCUS AF316322 147 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 71 isolate 5855/sin/000009 5'UTR, partial sequence.
ACCESSION AF316322
VERSION AF316322.1 GI:12744302
KEYWORDS
SOURCE
ORGANISM Human enterovirus 71
Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 147)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
JOURNAL PUBLISHED 12149336
REFERENCE 2 (bases 1 to 147)
Singh, S., Chow, V.T.K. and Poh, C.L.
AUTHORS Direct Submission
TITLE Direct Submission

JOURNAL Submitted (24-OCT-2000) Department of Microbiology, National
University of Singapore, 5, Science Drive 2, Singapore 117597,
Singapore
FEATURES Location/Qualifiers
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/organism="Human enterovirus 71"
/mol_type="mRNA"
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/db_xref="taxon:39054"
/note="Human enterovirus 71
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saliva, lung, heart, brain, rectal swab, tonsils, spleen,
foot swab, throat swab, intestine, and oral mucosa."
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5'UTR
ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
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Db 122 AAGGAAACACGGACACCCAA 103

RESULT 60
AF314004/c
LOCUS AF314004 153 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 5589/SIN/001809 5' UTR, partial sequence.
ACCESSION AF314004
VERSION AF314004.2 GI:13111667
KEYWORDS
SOURCE
ORGANISM Enterovirus 5589/SIN/001809
Enterovirus 5589/SIN/001809
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 153)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
JOURNAL PUBLISHED 12149336
REFERENCE 2 (bases 1 to 153)
Singh, S., Chow, V.T.K. and Poh, C.L.
AUTHORS Direct Submission
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
LOCATION/Qualifiers
FEATURES source
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/mol_type="mRNA"
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/db_xref="taxon:150718"
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Query Match 100.0%; Score 20; DB 13; Length 153;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
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Db 122 AAGGAAACACGGACACCCAA 103

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RESULT 61
AF314003/c
LOCUS AF314003 154 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 5627/SIN/002009 5' UTR, partial sequence.
ACCESSION AF314003
VERSION AF314003.2 GI:13111666
KEYWORDS
SOURCE Enterovirus 5627/SIN/002009
ORGANISM Enterovirus 5627/SIN/002009
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
JOURNAL
PUBMED 12149336
REFERENCE
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
REFERENCE
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
REMARK Sequence update by submitter
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667226.
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Db 122 AAGGAAACACGGACACCCAA 103

RESULT 62
AF314005/c
LOCUS AF314005 154 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 5656/SIN/002209 5' UTR, partial sequence.
ACCESSION AF314005
VERSION AF314005.2 GI:13111668
KEYWORDS
SOURCE Enterovirus 5656/SIN/002209
ORGANISM Enterovirus 5656/SIN/002209
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
JOURNAL
PUBMED 12149336
REFERENCE
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of
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Singapore, 5 Science Drive 2, Singapore 117597, Singapore
3 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (23-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Sequence update by submitter
On Feb 23, 2001 this sequence version replaced gi:12667228.
FEATURES
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/db_xref="taxon:150720"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AAGGAAACACGGACACCCAA 20
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Db 122 AAGGAAACACGGACACCCAA 103

RESULT 63
AF314007/c
LOCUS AF314007 154 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 5536/SIN/001409 5' UTR, partial sequence.
ACCESSION AF314007
VERSION AF314007.2 GI:13111669
KEYWORDS
SOURCE Enterovirus 5536/SIN/001409
ORGANISM Enterovirus 5536/SIN/001409
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
JOURNAL
PUBMED 12149336
REFERENCE
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
REFERENCE
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
REMARK Sequence update by submitter
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667230.
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Cy 1 AAGGAAACACGGACACCCAA 20
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Db 122 AAGGAAACACGGACACCCAA 103
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RESULT 64
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DEFINITION Enterovirus TS/SIN/001002 5'UTR, partial sequence.
ACCESSION  AY027864
VERSION     AY027864.1  GI:13591397
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SOURCE
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    Enterovirus TS/SIN/001002
    Enterovirus TS/SIN/001002
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
  1 (bases 1 to 154)
    Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
    Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
    from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
    Reverse Transcription-PCR with Universal Enterovirus and
    EV71-Specific Primers
  J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
  12149336
  2 (bases 1 to 154)
    Singh, S., Chow, V.T.K. and Poh, C.L.
    Direct Submission
  Submitted (22-FEB-2001) Microbiology, National University of
  Singapore, 5 Science Drive 2, Singapore 117597, Singapore
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RESULT 65
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ACCESSION  AY027865
VERSION     AY027865.1  GI:13591398
KEYWORDS
SOURCE
  ORGANISM
    Enterovirus TF/SIN/000704
    Enterovirus TF/SIN/000704
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
  1 (bases 1 to 154)
    Singh, S., Chow, V.T.K. and Poh, C.L.
    Enterovirus strains from an outbreak of Hand, Foot and Mouth
    disease in Singapore (2000)
    Unpublished
  2 (bases 1 to 154)
    Singh, S., Chow, V.T.K. and Poh, C.L.
    Direct Submission
  Submitted (22-FEB-2001) Microbiology, National University of
  Singapore, 5 Science Drive 2, Singapore 117597, Singapore
  Location/Qualifiers
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      /note="isolated from tissue fluid"

5'UTR
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Db  122 AAGGAACACGACACCCAA 103

RESULT 66
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LOCUS      155 bp      RNA      linear      VRL 02-JUL-2003
DEFINITION Human coxsackievirus B2 partial 5'UTR, strain /ia/Roma9.
ACCESSION  AJ312089
VERSION     AJ312089.1  GI:16555707
KEYWORDS
SOURCE
  ORGANISM
    Human coxsackievirus B2
    Human coxsackievirus B2
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
  1
    Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and
    Fadda, G.
    Molecular identification and typing of enteroviruses isolated from
    clinical specimens
  J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
  12454151
  2 (bases 1 to 155)
    Muscillo, M.
    Direct Submission
  Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
  Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
  00161, Italy
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      identified by immunofluorescence assay"
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5'UTR
ORIGIN
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Qy  1 AAGGAACACGACACCCAA 20
    ||||||||||||||||
Db  122 AAGGAACACGACACCCAA 103

RESULT 67
HCO295181
LOCUS      171 bp      RNA      linear      VRL 15-MAY-2001
DEFINITION Human coxsackievirus B5 genomic RNA for partial 5'UTR, isolate
  ITA99-21.
ACCESSION  AJ295181
VERSION     AJ295181.1  GI:14139958
KEYWORDS
SOURCE
  ORGANISM
    Human coxsackievirus B5
    Human coxsackievirus B5
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
  1
    Muscillo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,

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<1..>154

5'UTR
ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 154;
 Best Local Similarity 100.0%; Pred. No. 30;
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Qy 1 AAGGAACACGACACCCAA 20
 ||||||||||||||||
 Db 122 AAGGAACACGACACCCAA 103

RESULT 66
 HEN312089/c

LOCUS 155 bp RNA linear VRL 02-JUL-2003
 DEFINITION Human coxsackievirus B2 partial 5'UTR, strain /ia/Roma9.
 ACCESSION AJ312089
 VERSION AJ312089.1 GI:16555707
 KEYWORDS
 SOURCE
 ORGANISM

Human coxsackievirus B2
 Human coxsackievirus B2
 Viruses; ssRNA positive-strand viruses, no DNA stage;
 Picornaviridae; Enterovirus.

REFERENCE 1
 AUTHORS Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and
 Fadda, G.
 TITLE Molecular identification and typing of enteroviruses isolated from
 clinical specimens
 J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
 12454151
 REFERENCE 2 (bases 1 to 155)
 AUTHORS Muscillo, M.
 TITLE Direct Submission
 JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
 Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
 00161, Italy
 FEATURES Location/Qualifiers

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 identified by immunofluorescence assay"
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5'UTR

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
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 Db 122 AAGGAACACGACACCCAA 103

RESULT 67
 HCO295181

LOCUS 171 bp RNA linear VRL 15-MAY-2001
 DEFINITION Human coxsackievirus B5 genomic RNA for partial 5'UTR, isolate
 ITA99-21.
 ACCESSION AJ295181
 VERSION AJ295181.1 GI:14139958
 KEYWORDS
 SOURCE
 ORGANISM

Human coxsackievirus B5
 Human coxsackievirus B5
 Viruses; ssRNA positive-strand viruses, no DNA stage;
 Picornaviridae; Enterovirus.

REFERENCE 1
 AUTHORS Muscillo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,

Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and Ticca,F.

A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated with swimming pools

JOURNAL
REFERENCE 2 (bases 1 to 171)

AUTHORS Muscillo,M.

TITLE Direct Submission

JOURNAL Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy

FEATURES Location/Qualifiers

1. .171
/organism="Human coxsackievirus B5"
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/strain="F/Roma99"
/isolate="ITA99-21"
/specific_host="Homo sapiens"
/db_xref="taxon:12074"
/note="sporadic case of aseptic meningitis; BGM cell culture of stools from a four years old child"
<1. .>171

5'UTR

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 171;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 41 AAGGAACACGGACACCCAA 60

RESULT 68

HEN312088/c

LOCUS HEN312088 172 bp RNA linear VRL 02-JUL-2003

DEFINITION Human enterovirus 71 partial 5'UTR, strain /di/Roma98.

ACCESSION AJ312088

VERSION AJ312088.1 GI:16555706

KEYWORDS Human enterovirus 71

SOURCE Human enterovirus 71

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1

AUTHORS Manzara,S., Muscillo,M., La Rosa,G., Marianelli,C., Cattani,P. and Fadda,G.

TITLE Molecular identification and typing of enteroviruses isolated from clinical specimens

JOURNAL J. Clin. Microbiol. 40 (12), 4554-4560 (2002)

PUBMED 12454151

REFERENCE 2 (bases 1 to 172)

AUTHORS Muscillo,M.

TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy

FEATURES Location/Qualifiers

1. .172
/organism="Human enterovirus 71"
/viralion
/mol_type="genomic RNA"
/strain="di/Roma98"
/isolate="IT98-5114"
/db_xref="taxon:39054"
/lab_host="vero cell cultures"
/note="throat swab from child with aseptic meningitis, identified by immunofluorescence assay"
<1. .>172

5'UTR

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 172;

Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 120 AAGGAACACGGACACCCAA 101

RESULT 69

ESP295207

LOCUS ESP295207

DEFINITION Echovirus sp. genomic RNA for partial 5'UTR, linear VRL 15-MAY-2001

ACCESSION AJ295207

VERSION AJ295207.1 GI:14140008

KEYWORDS Echovirus sp.

SOURCE Echovirus sp.

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1

AUTHORS Muscillo,M., La Rosa,G., Marianelli,C., Capobianchi,M.R., Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and Ticca,F.

TITLE A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated with swimming pools

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 177)

AUTHORS Muscillo,M.

TITLE Direct Submission

JOURNAL Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy

FEATURES Location/Qualifiers

1. .177
/organism="Echovirus sp."
/viralion
/mol_type="genomic RNA"
/strain="Bastiani"
/isolate="ATCC VR-322"
/db_xref="taxon:145390"
/note="isolated from fecal specimen of 10-year-old boy with symptoms of headache, stiff neck, fever"
<1. .>177

5'UTR

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 177;

Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 58 AAGGAACACGGACACCCAA 77

RESULT 70

AF521491/c

LOCUS AF521491/c

DEFINITION Human echovirus 13 isolate BR00-82 5' UTR, partial sequence.

ACCESSION AF521491

VERSION AF521491.1 GI:31790833

KEYWORDS Human echovirus 13

SOURCE Human echovirus 13

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 184)

AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K., Lindberg,A.M. and Van Raust,M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

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PUBMED
REFERENCE 12767006
AUTHORS 2 (bases 1 to 184)
        Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES Location/Qualifiers
        source 1..184
        /organism="Human echovirus 13"
        /vifion
        /mol_type="genomic RNA"
        /isolate="BE00-82"
        /isolation_source="patient 82 - zipcode Belgium 8560"
        /db_xref="taxon:47501"
        <1..>184
5'UTR
ORIGIN
Query Match 100.0%; Score 20; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACCCCAA 20
Db 128 AAGGAACACGACCCCAA 109

RESULT 71
AF521433/c
LOCUS AF521433 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-14 5' UTR, partial sequence.
ACCESSION AF521433
VERSION AF521433.1 GI:31790775
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
AUTHORS 2 (bases 1 to 185)
        Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES Location/Qualifiers
        source 1..185
        /organism="Human echovirus 30"
        /vifion
        /mol_type="genomic RNA"
        /isolate="BE00-14"
        /isolation_source="patient 14 - zipcode Belgium 9310"
        /db_xref="taxon:41846"
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5'UTR
ORIGIN
Query Match 100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACCCCAA 20

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Db 128 AAGGAACACGACCCCAA 109

RESULT 72
AF521434/c
LOCUS AF521434 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-15 5' UTR, partial sequence.
ACCESSION AF521434
VERSION AF521434.1 GI:31790776
KEYWORDS
SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
REFERENCE 1 (bases 1 to 185)
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
AUTHORS 2 (bases 1 to 185)
        Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES Location/Qualifiers
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        /organism="Human coxsackievirus B5"
        /vifion
        /mol_type="genomic RNA"
        /isolate="BE00-15"
        /isolation_source="patient 15 - zipcode Belgium 9820"
        /db_xref="taxon:12074"
        <1..>185
5'UTR
ORIGIN
Query Match 100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACCCCAA 20
Db 128 AAGGAACACGACCCCAA 109

RESULT 73
AF521435/c
LOCUS AF521435 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-1 5' UTR, partial sequence.
ACCESSION AF521435
VERSION AF521435.1 GI:31790777
KEYWORDS
SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
REFERENCE 1 (bases 1 to 185)
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
AUTHORS 2 (bases 1 to 185)
        Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission

```

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES

source
1. .185
Location/Qualifiers
/organism="Human coxsackievirus B5"
/virion
/mol type="genomic RNA"
/isolate="BE00-1"
/isolation source="patient 1 - zipcode Belgium 9840"
/db_xref="taxon:12074"
<1..>185

5'UTR

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 128 AAGGAACACGGACACCCAA 109

RESULT 74

AF521436/c AF521436 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-2 5' UTR, partial sequence.
DEFINITION AF521436
ACCESSION AF521436
VERSION AF521436.1 GI:31790778

SOURCE

Human echovirus 30
Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.

Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES

source
1. .185
Location/Qualifiers
/organism="Human echovirus 30"
/virion
/mol type="genomic RNA"
/isolate="BE00-2"
/isolation source="patient 2 - zipcode Belgium 3001"
/db_xref="taxon:41846"
<1..>185

5'UTR

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 128 AAGGAACACGGACACCCAA 109

RESULT 75

AF521440/c

LOCUS AF521440 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-6 5' UTR, partial sequence.
ACCESSION AF521440
VERSION AF521440.1 GI:31790782

KEYWORDS

source
Human echovirus 30

ORGANISM

Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE

AUTHORS

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.

Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers

1. .185

/organism="Human echovirus 30"

/virion

/mol type="genomic RNA"

/isolate="BE00-6"

/isolation source="patient 6 - zipcode Belgium 9400"

/db_xref="taxon:41846"

<1..>185

5'UTR

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 128 AAGGAACACGGACACCCAA 109

RESULT 76

AF521444/c

LOCUS AF521444 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-11 5' UTR, partial sequence.
ACCESSION AF521444
VERSION AF521444.1 GI:31790786

KEYWORDS

source
Human echovirus 30

ORGANISM

Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE

AUTHORS

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.

Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers

1. .185

/organism="Human echovirus 30"

/virion

/mol type="genomic RNA"

/isolate="BE00-11"

/isolation source="patient 11 - zipcode Belgium 9400"

/db_xref="taxon:41846"

<1..>185

5'UTR

ORIGIN

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source
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/organism="Human echovirus 30"
/virion
/mol_type="genomic RNA"
/isolate="BE00-11"
/isolation_source="patient 11 - zipcode Belgium 9400"
/db_xref="taxon:41846"
<1. .>185

5'UTR
ORIGIN
Query Match 100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 128 AAGGAAACACGGACACCCAA 109

RESULT 77
AF521445/c 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-12 5' UTR, partial sequence.
DEFINITION
ACCESSION AF521445
VERSION AF521445.1 GI:31790787
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
109
1 AAGGAAACACGGACACCCAA 20
|||||
128 AAGGAAACACGGACACCCAA 109

RESULT 78
AF521446/c 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 16 isolate BE00-13 5' UTR, partial sequence.
DEFINITION
ACCESSION AF521446
VERSION AF521446.1 GI:31790788
KEYWORDS
SOURCE Human echovirus 16
ORGANISM Human echovirus 16
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
109
1 AAGGAAACACGGACACCCAA 20
|||||
128 AAGGAAACACGGACACCCAA 109

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SOURCE Human echovirus 16
ORGANISM Human echovirus 16
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
109
1 AAGGAAACACGGACACCCAA 20
|||||
128 AAGGAAACACGGACACCCAA 109

Query Match 100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 128 AAGGAAACACGGACACCCAA 109

RESULT 79
AF521447/c 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-30 5' UTR, partial sequence.
DEFINITION
ACCESSION AF521447
VERSION AF521447.1 GI:31790789
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
109
1 AAGGAAACACGGACACCCAA 20
|||||
128 AAGGAAACACGGACACCCAA 109

Query Match 100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 128 AAGGAAACACGGACACCCAA 109

RESULT 79
AF521447/c 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-30 5' UTR, partial sequence.
DEFINITION
ACCESSION AF521447
VERSION AF521447.1 GI:31790789
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
109
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|||||
128 AAGGAAACACGGACACCCAA 109

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5'UTR
ORIGIN
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Query Match      100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 128 AAGGAAACACGGACACCCAA 109

RESULT 80
AF521448/c
LOCUS AF521448 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-31 5' UTR, partial sequence.
ACCESSION AF521448
VERSION AF521448.1 GI:31790790
KEYWORDS Human coxsackievirus B5
SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
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    1..185
    /organism="Human coxsackievirus B5"
    /mol_type="genomic RNA"
    /isolate="BE00-31"
    /isolation_source="patient 31 - zipcode Belgium 9320"
    /db_xref="taxon:12074"
    <1..>185

5'UTR
ORIGIN
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    /db_xref="taxon:12074"
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Query Match      100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 128 AAGGAAACACGGACACCCAA 109

RESULT 81
AF521449/c
LOCUS AF521449 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-32 5' UTR, partial sequence.
ACCESSION AF521449
VERSION AF521449.1 GI:31790791
KEYWORDS Human echovirus 30
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)

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AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
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Db 128 AAGGAAACACGGACACCCAA 109

RESULT 82
AF521450/c
LOCUS AF521450 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-33 5' UTR, partial sequence.
ACCESSION AF521450
VERSION AF521450.1 GI:31790792
KEYWORDS Human echovirus 30
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
    Viruses; ssRNA positive-strand viruses, no DNA stage;
    Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
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Db 128 AAGGAAACACGGACACCCAA 109

RESULT 83
AF521451/c
LOCUS      185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-34 5' UTR, partial sequence.
ACCESSION  AF521451
VERSION     AF521451.1 GI:31790793
KEYWORDS
SOURCE
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE  2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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Best Local Similarity 100.0%; Pred. No. 30;
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Db 128 AAGGAAACACGGACACCCAA 109

RESULT 84
AF521458/c
LOCUS      185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-43 5' UTR, partial sequence.
ACCESSION  AF521458
VERSION     AF521458.1 GI:31790800
KEYWORDS
SOURCE
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE  2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 128 AAGGAAACACGGACACCCAA 109

RESULT 85
AF521461/c
LOCUS      185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-48 5' UTR, partial sequence.
ACCESSION  AF521461
VERSION     AF521461.1 GI:31790803
KEYWORDS
SOURCE
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE  2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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Qy 1 AAGGAAACACGGACACCCAA 20
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J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 128 AAGGAAACACGGACACCCAA 109

RESULT 85
AF521461/c
LOCUS      185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-48 5' UTR, partial sequence.
ACCESSION  AF521461
VERSION     AF521461.1 GI:31790803
KEYWORDS
SOURCE
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE  2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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Qy 1 AAGGAAACACGGACACCCAA 20
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Db 128 AAGGAAACACGGACACCCAA 109

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AF521474/c
LOCUS       AF521474               185 bp    RNA        linear    VRL 17-JUN-2003
DEFINITION   Human echovirus 30 isolate BE00-16 5' UTR, partial sequence.
ACCESSION   AF521474
VERSION     AF521474.1  GI:31790816
KEYWORDS    .
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
            Lindberg, A.M. and Van Ranst, M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
            Lindberg, M.A. and Van Ranst, M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
FEATURES    Location/Qualifiers
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DB 128 AAGGAAACACGGACACCCAA 109

RESULT 90
AF521475/c
LOCUS       AF521475               185 bp    RNA        linear    VRL 17-JUN-2003
DEFINITION   Human echovirus 30 isolate BE00-17 5' UTR, partial sequence.
ACCESSION   AF521475
VERSION     AF521475.1  GI:31790817
KEYWORDS    .
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
            Lindberg, A.M. and Van Ranst, M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
            Lindberg, M.A. and Van Ranst, M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium

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DB 128 AAGGAAACACGGACACCCAA 109

RESULT 91
AF521476/c
LOCUS       AF521476               185 bp    RNA        linear    VRL 17-JUN-2003
DEFINITION   Human echovirus 30 isolate BE00-18 5' UTR, partial sequence.
ACCESSION   AF521476
VERSION     AF521476.1  GI:31790818
KEYWORDS    .
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
            Lindberg, A.M. and Van Ranst, M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
            Lindberg, M.A. and Van Ranst, M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 128 AAGGAAACACGGACACCCAA 109

RESULT 92
AF521477/c
LOCUS       AF521477               185 bp    RNA        linear    VRL 17-JUN-2003
DEFINITION   Human echovirus 30 isolate BE00-19 5' UTR, partial sequence.
ACCESSION   AF521477
VERSION     AF521477.1  GI:31790819

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KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE
AUTHORS     1 (bases 1 to 185)
            Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE       Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL     J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS     Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
FEATURES    Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 AAGGAAACACGGACACCCAA 20
      128 AAGGAAACACGGACACCCAA 109
Db
RESULT 93
AF521478/c
LOCUS      AF521478      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-20 5' UTR, partial sequence.
ACCESSION  AF521478
VERSION     AF521478.1 GI:31790820
KEYWORDS    Human echovirus 30
SOURCE      Human echovirus 30
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS     Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE       Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL     J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS     Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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      128 AAGGAAACACGGACACCCAA 109
Db
RESULT 94
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LOCUS      AF521480      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-27 5' UTR, partial sequence.
ACCESSION  AF521480
VERSION     AF521480.1 GI:31790822
KEYWORDS    Human coxsackievirus B5
SOURCE      Human coxsackievirus B5
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS     Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE       Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL     J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS     Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
FEATURES    Location/Qualifiers
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      128 AAGGAAACACGGACACCCAA 109
Db
RESULT 95
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LOCUS      AF521481      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 16 isolate BE00-72 5' UTR, partial sequence.
ACCESSION  AF521481
VERSION     AF521481.1 GI:31790823
KEYWORDS    Human echovirus 16
SOURCE      Human echovirus 16
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.

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REFERENCE
AUTHORS      1 (bases 1 to 185)
              Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
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TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED       12767006
REFERENCE    2 (bases 1 to 185)
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              Lindberg,M.A. and Van Ranst,M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium
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QY 1 AAGGAACACGGACACCCAA 20
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Db 128 AAGGAACACGGACACCCAA 109

RESULT 96
AF521482/c
LOCUS      Human echovirus 13 isolate BE00-73 5' UTR, partial sequence.
DEFINITION
ACCESSION  AF521482
VERSION     AF521482.1 GI:31790824
KEYWORDS
SOURCE      Human echovirus 13
ORGANISM    Human echovirus 13
REFERENCE    1 (bases 1 to 185)
              Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
              Lindberg,A.M. and Van Ranst,M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED       12767006
REFERENCE    2 (bases 1 to 185)
              Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
              Lindberg,M.A. and Van Ranst,M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium
FEATURES     Location/Qualifiers
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DEFINITION
ACCESSION  AF521483
VERSION     AF521483.1 GI:31790825
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
REFERENCE    1 (bases 1 to 185)
              Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
              Lindberg,A.M. and Van Ranst,M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED       12767006
REFERENCE    2 (bases 1 to 185)
              Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
              Lindberg,M.A. and Van Ranst,M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium
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RESULT 98
AF521484/c
LOCUS      Human echovirus 16 isolate BE00-75 5' UTR, partial sequence.
DEFINITION
ACCESSION  AF521484
VERSION     AF521484.1 GI:31790826
KEYWORDS
SOURCE      Human echovirus 16
ORGANISM    Human echovirus 16
REFERENCE    1 (bases 1 to 185)
              Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
              Lindberg,A.M. and Van Ranst,M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000

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2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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DEFINITION Human echovirus 30 isolate BE00-76 5' UTR, partial sequence.
ACCESSION AF521485
VERSION AF521485.1 GI:31790827.
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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DEFINITION Human echovirus 30 isolate BE00-77 5' UTR, partial sequence.
ACCESSION AF521486
VERSION AF521486.1 GI:31790828
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 20:59:06 ; Search time 75.9223 Seconds
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468.258 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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SUMMARIES

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C 10	20	100.0	7441	3	US-09-284-349B-1
C 11	19.2	100.0	28	3	US-09-724-678D-11
C 12	18.4	92.0	1560	3	US-09-724-678D-16
C 13	17	85.0	33	3	US-09-129-686-20
C 14	17	85.0	33	3	US-09-566-581-20
C 15	17	85.0	39	3	US-09-061-273-8
C 16	17	85.0	627	2	US-08-221-816B-31
C 17	17	85.0	627	3	US-10-112-547-31
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C 19	17	85.0	627	3	US-10-104-241-31
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27	16	80.0	601	3	US-09-949-016-194126	Sequence 194126, A
C 28	16	80.0	18568	3	US-09-949-016-16963	Sequence 16963, A
C 29	16	80.0	137949	3	US-09-949-016-12196	Sequence 12196, A
C 30	16	80.0	137956	3	US-09-949-016-17260	Sequence 17260, A
C 31	15.8	79.0	601	3	US-09-949-016-56995	Sequence 56995, A
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C 33	15.8	79.0	1817	2	US-08-743-637B-1	Sequence 1, Appli
C 34	15.8	79.0	1817	2	US-08-536-840B-1	Sequence 1, Appli
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C 38	15.4	77.0	2053	3	US-09-270-767-247	Sequence 247, App
C 39	15.4	77.0	2053	3	US-09-270-767-15529	Sequence 15529, A
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C 41	15.4	77.0	2690	3	US-10-020-445A-514	Sequence 514, App
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c 156	14.4	72.0	72504	3	US-09-949-016-14855	Sequence 14855, A	229	14.2	71.0	2272	3	US-08-949-004-1	Sequence 51, Appl
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c 160	14.2	71.0	158	3	US-09-270-767-2490	Sequence 2490, App	233	14.2	71.0	2622	3	US-10-104-047-1005	Sequence 1005, App
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; LOCATION: 610
; OTHER INFORMATION: /note= "non-authentic sequence
; OTHER INFORMATION: due to a base pair substitution from C to G
; OTHER INFORMATION: at position 610"
; PUBLICATION INFORMATION:
; AUTHORS: Sarnow, P.
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-387-845-5

Query Match 100.0%; Score 20; DB 2; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 565 AAGGAACACGACACCCAA 546

RESULT 2
US-08-778-275-5/c
; Sequence 5, Application US/08778275
; Patent No. 5935819
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; TITLE OF INVENTION: bicistronic vector system in mammalian cells
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,275
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,845
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 628 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
; IMMEDIATE SOURCE:
; CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..628
; OTHER INFORMATION: /note= "shown are the first
; OTHER INFORMATION: 628 nt of the 5' non-translated region of
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
; FEATURE:
; NAME/KEY: -
; LOCATION: 610
; OTHER INFORMATION: /note= "non-authentic sequence
; OTHER INFORMATION: due to a base pair substitution from C to G
; OTHER INFORMATION: at position 610"
; PUBLICATION INFORMATION:
; AUTHORS: Sarnow, P.
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-867-352-5

Query Match 100.0%; Score 20; DB 3; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 565 AAGGAACACGACACCCAA 546
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; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-778-275-5

Query Match 100.0%; Score 20; DB 2; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 565 AAGGAACACGACACCCAA 546

RESULT 3
US-08-867-352-5/c
; Sequence 5, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multicistronic expression units and their use
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,847
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 628 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
; IMMEDIATE SOURCE:
; CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..628
; OTHER INFORMATION: /note= "shown are the first
; OTHER INFORMATION: 628 nt of the 5' non-translated region of
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
; FEATURE:
; NAME/KEY: -
; LOCATION: 610
; OTHER INFORMATION: /note= "non-authentic sequence
; OTHER INFORMATION: due to a base pair substitution from C to G
; OTHER INFORMATION: at Location 610"
; PUBLICATION INFORMATION:
; AUTHORS: Sarnow, P.
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-867-352-5

Query Match 100.0%; Score 20; DB 3; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 565 AAGGAACACGACACCCAA 546
```

RESULT 4

US-09-116-032-2/c

; Sequence 2, Application US/09116032

; Patent No. 6200576

; GENERAL INFORMATION:

; APPLICANT: HWONG, CHING LONG

; APPLICANT: LO, CHENG-KAI

; APPLICANT: YANG, YING-CHUAN

; APPLICANT: JENG, KING-SONG

; APPLICANT: CHANG, EDWARD L.

; APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY

; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND

; FILE REFERENCE: 9751.79US01

; CURRENT APPLICATION NUMBER: US/09/116.032

; CURRENT FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: CHINA 86105814

; EARLIER FILING DATE: 1997-05-01

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 1220

; TYPE: DNA

; ORGANISM: SWINE VESICULAR DISEASE VIRUS

US-09-116-032-2

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 1220;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 AAGGAACACGACGCCAACCA 20

Db

568 AAGGAACACGACGCCAACCA 549

RESULT 5

US-09-202-904A-10/c

; Sequence 10, Application US/09202904A

; Patent No. 6395471

; GENERAL INFORMATION:

; APPLICANT: Kang, Sung Key

; APPLICANT: Hahn, Bumsuk

; TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing

; TITLE OF INVENTION: the Activity of Hepatitis C Virus Protease, a Recombinant

; FILE REFERENCE: A32210-PCT-USA 072944.0104

; CURRENT APPLICATION NUMBER: US/09/202.904A

; CURRENT FILING DATE: 2001-01-22

; PRIOR APPLICATION NUMBER: PCT/KR97/00120

; PRIOR FILING DATE: 1997-06-25

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Genetically engineered virus derived from

; OTHER INFORMATION: poliovirus and hepatitis C virus

US-09-202-904A-10

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 2320;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 AAGGAACACGACGCCAACCA 20

Db

565 AAGGAACACGACGCCAACCA 546

RESULT 6

US-09-116-032-1/c

; Sequence 1, Application US/09116032

; Patent No. 6200576

; GENERAL INFORMATION:

; APPLICANT: HWONG, CHING LONG

; APPLICANT: LO, CHENG-KAI

; APPLICANT: YANG, YING-CHUAN

; APPLICANT: JENG, KING-SONG

; APPLICANT: CHANG, EDWARD L.

; APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY

; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND

; FILE REFERENCE: 9751.79US01

; CURRENT APPLICATION NUMBER: US/09/116.032

; CURRENT FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: CHINA 86105814

; EARLIER FILING DATE: 1997-05-01

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 7400

; TYPE: DNA

; ORGANISM: SWINE VESICULAR DISEASE VIRUS

US-09-116-032-1

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 7400;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 AAGGAACACGACGCCAACCA 20

Db

568 AAGGAACACGACGCCAACCA 549

RESULT 7

US-07-852-260-1/c

; Sequence 1, Application US/07852260

; Patent No. 5525715

; GENERAL INFORMATION:

; APPLICANT: Racaniello, Vincent

; APPLICANT: Tatem, Joanne M.

; APPLICANT: Weeks-Levy, Carolyn L.

; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM

; TITLE OF INVENTION: CDNA

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; APPLICATION NUMBER: US/07/852.260

; FILING DATE: 19920619

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 36607-B-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 977-9550

; TELEX: 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7432 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 743..7361
US-07-852-260-1

Query Match 100.0%; Score 20; DB 2; Length 7432;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 568 AAGGAAACACGGACACCCAA 549

RESULT 8

US-08-461-503-1/c
Sequence 1, Application US/08461503
Patent No. 5834302
GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
TITLE OF INVENTION: FROM CDNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,503
FILING DATE: 5-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 743..7361
US-08-461-503-1

Query Match 100.0%; Score 20; DB 2; Length 7432;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 568 AAGGAAACACGGACACCCAA 549

RESULT 9

US-08-465-250-1/c
Sequence 1, Application US/08465250
Patent No. 6136570
GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,250
FILING DATE: 6-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36607-E-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 743..7361
US-08-465-250-1

Query Match 100.0%; Score 20; DB 3; Length 7432;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 568 AAGGAAACACGGACACCCAA 549

RESULT 10

US-09-284-349B-1/c
Sequence 1, Application US/09284349B
Patent No. 6696289
GENERAL INFORMATION:
APPLICANT: Yong Soo, Bae
APPLICANT: Jung, Hye Rhan
TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain
FILE REFERENCE: Docket No. 6696289; 4220-109 US
CURRENT APPLICATION NUMBER: US/09/284,349B
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: PCT/KR98/00242
PRIOR FILING DATE: 1998-07-08

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; PRIOR APPLICATION NUMBER: KR 97/37812
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7441
; TYPE: DNA
; ORGANISM: Human poliovirus 1
US-09-284-349B-1

Query Match      100.0%; Score 20; DB 3; Length 7441;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 565 AAGGAAACACGGACACCCAA 546

RESULT 11
US-09-724-678D-11/c
; Sequence 11, Application US/09724678D
; Patent No. 6818397
; GENERAL INFORMATION:
; APPLICANT: Lee, Kang-Hung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Tseng, Yang-Yuan
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Wang, Shing-Hwan
; TITLE OF INVENTION: Methods for Detecting and Probes Therefor
; FILE REFERENCE: TAI 316
; CURRENT APPLICATION NUMBER: US/09/724,678D
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Sequence is Synthesized
; Patent No. 6818397
US-09-724-678D-11

Query Match      100.0%; Score 20; DB 3; Length 28;
Best Local Similarity 95.0%; Pred. No. 4.7;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 24 AAGGAAACACGGACACCCAA 5

RESULT 12
US-09-724-678D-16/c
; Sequence 16, Application US/09724678D
; Patent No. 6818397
; GENERAL INFORMATION:
; APPLICANT: Lee, Kang-Hung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Tseng, Yang-Yuan
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Wang, Shing-Hwan
; TITLE OF INVENTION: Methods for Detecting and Probes Therefor
; FILE REFERENCE: TAI 316
; CURRENT APPLICATION NUMBER: US/09/724,678D
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-09-724-678D-16

Query Match      92.0%; Score 18.4; DB 3; Length 1560;
Best Local Similarity 95.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 570 AAGGAAACACGGACACCCAA 551

RESULT 13
US-09-129-686-20
; Sequence 20, Application US/09129686A
; Patent No. 6264940
; GENERAL INFORMATION:
; APPLICANT: Gromeier PhD, Matthias
; APPLICANT: Wimmer Prof, Eckard
; TITLE OF INVENTION: Recombinant Poliovirus For The Treatment of Cancer
; FILE REFERENCE: Recomb Poliovirus for Cancer Treatment
; CURRENT APPLICATION NUMBER: US/09/129,686A
; CURRENT FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Human rhinovirus 2
US-09-129-686-20

Query Match      85.0%; Score 17; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACC 17
Db 17 AAGGAAACACGGACACC 33

RESULT 14
US-09-566-581-20
; Sequence 20, Application US/09566581
; Patent No. 6464972
; GENERAL INFORMATION:
; APPLICANT: Matthias Gromeier and Eckard Wimmer
; TITLE OF INVENTION: RECOMBINANT POLIOVIRUS FOR THE TREATMENT OF CANCER
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/566,581
; FILING DATE: May 8, 2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/129,686
; FILING DATE: August 5, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C. H. Lin
; REGISTRATION NUMBER: 29,323
```

REFERENCE/DOCKET NUMBER: 3927-4135US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: nucleotides
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human Rhinovirus
STRAIN: Type 2
POSITION IN GENOME:
CHROMOSOME/SEGMENT: IRES
US-09-566-581-20

Query Match 85.0%; Score 17; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACC 17
Db 17 AAGGAACACGGACACC 33

RESULT 15
US-09-061-273-8
Sequence 8, Application US/09061273
Patent No. 6258570
GENERAL INFORMATION:
APPLICANT: Glustein, Joseph Z.
APPLICANT: Ehrlich, Garth D.
APPLICANT: Zhang, Yingze
TITLE OF INVENTION: PCR Assay For Bacterial and
TITLE OF INVENTION: Viral Meningitis
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Pittsburgh
STREET: Office of Technology Transfer
CITY: Pittsburgh
STATE: Pennsylvania
COUNTRY: USA
ZIP: 15260
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" high density diskette
COMPUTER: IBM PC or compatibles
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,273
FILING DATE: 17-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6258570 applicable
FILING DATE: No. 6258570 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Mary-Elizabeth Buckles
REGISTRATION NUMBER: 31,907
REFERENCE/DOCKET NUMBER: 017917/20132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/414-9267
TELEFAX: 202/414/9299
TELEX: 64711
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA
US-09-061-273-8

Query Match 85.0%; Score 17; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
Db 1 GAAACACGGACACCCAA 17

RESULT 16
US-08-221-816B-31/c
Sequence 31, Application US/08221816B
Patent No. 5738985
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
APPLICANT: Mathews, Michael B.
APPLICANT: Katze, Michael G.
APPLICANT: Witherell, Gary
APPLICANT: Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
TITLE OF INVENTION: OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-221-816B-31

Query Match 85.0%; Score 17; DB 2; Length 627;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
Db 568 GAAACACGGACACCCAA 552

RESULT 17
US-10-112-547-31/c
Sequence 31, Application US/10112547
Patent No. 6579674
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.

Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,547
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-112-547-31
Query Match 85.0%; Score 17; DB 3; Length 627;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 GAAACACGACACCCAA 20
|||||
Db 568 GAAACACGACACCCAA 552
RESULT 18
US-10-112-241-31/c
Sequence 31, Application US/10112241
Patent No. 6623961
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,241
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-112-241-31
Query Match 85.0%; Score 17; DB 3; Length 627;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 GAAACACGACACCCAA 20
|||||
Db 568 GAAACACGACACCCAA 552
RESULT 19
US-10-104-611-31/c
Sequence 31, Application US/10104611
Patent No. 6667152
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,611
FILING DATE: 22-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31

Query Match 85.0%; Score 17; DB 3; Length 627;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAAACACGGACACCCAA 20
DB 568 GAAACACGGACACCCAA 552

RESULT 20
US-10-109-368-31/c
; Sequence 31, Application US/10109368
; Patent No. 677179
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-10-109-368-31

Query Match 85.0%; Score 17; DB 3; Length 627;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAAACACGGACACCCAA 20
DB 568 GAAACACGGACACCCAA 552

RESULT 21
US-09-724-380-31/c
; Sequence 31, Application US/09724380
; Patent No. 6824976
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,380
; FILING DATE: 01-APR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,816
; FILING DATE: 01-APR-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-09-724-380-31

Query Match 85.0%; Score 17; DB 3; Length 627;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAAACACGGACACCCAA 20
DB 568 GAAACACGGACACCCAA 552

RESULT 22
US-09-949-016-78843
; Sequence 78843, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78843
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-78843

Query Match 84.0%; Score 16.8; DB 3; Length 601;
Best Local Similarity 90.0%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||||| ||| |||||
Db 162 AAGGAAGACGACACCCAA 181

RESULT 23
US-09-949-016-78844
; Sequence 78844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78844
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-78844

Query Match 84.0%; Score 16.8; DB 3; Length 601;
Best Local Similarity 90.0%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||||| ||| |||||
Db 51 AAGGAAGACGACACCCAA 70

RESULT 24
US-09-949-016-14033
; Sequence 14033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14033
; LENGTH: 784019
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(784019)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033

Query Match 84.0%; Score 16.8; DB 3; Length 784019;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||||| ||| |||||
Db 362237 AAGGAAGACGACACCCAA 362256

RESULT 25
US-09-949-016-12777
; Sequence 12777, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12777
; LENGTH: 828152
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(828152)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12777

Query Match 84.0%; Score 16.8; DB 3; Length 828152;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||||| ||| |||||
Db 358370 AAGGAAGACGACACCCAA 358389

RESULT 26
US-09-949-016-78842
; Sequence 78842, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78842
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-78842

Query Match      82.0%; Score 16.4; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACCCCAA 20
Db 288 AAGGAAACACGGACCCCAA 307

RESULT 27
US-09-949-016-194126
; Sequence 194126, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194126
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-194126

Query Match      80.0%; Score 16; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAAACACGGACACC 17
Db 450 AGGAAACACGGACACC 465

RESULT 28
US-09-949-016-16963/c
; Sequence 16963, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16963
; LENGTH: 18568
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16963

Query Match      80.0%; Score 16; DB 3; Length 18568;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACAC 16
Db 17024 AAGGAAACACGGACAC 17009

RESULT 29
US-09-949-016-12196/c
; Sequence 12196, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12196
; LENGTH: 137949
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(137949)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12196

Query Match      80.0%; Score 16; DB 3; Length 137949;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAAACACGGACACC 17
Db 90635 AGGAAACACGGACACC 90620

RESULT 30
US-09-949-016-17260/c
; Sequence 17260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13390
; LENGTH: 46626
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13390

Query Match 79.0%; Score 15.8; DB 3; Length 46626;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCCA 19
|||||
DB 32280 AAGGAACACGGACACCCA 32262

RESULT 38

US-09-270-767-247/c
; Sequence 247, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 247
; LENGTH: 2053
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-247

Query Match 77.0%; Score 15.4; DB 3; Length 2053;
Best Local Similarity 94.1%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAAACACGGACACCCA 19
|||||
DB 1036 GGAAACACGGACACCCA 1020

RESULT 39

US-09-270-767-15529/c
; Sequence 15529, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15529
; LENGTH: 2053
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-15529

Query Match 77.0%; Score 15.4; DB 3; Length 2053;
Best Local Similarity 94.1%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAAACACGGACACCCA 19
|||||
DB 1036 GGAAACACGGACACCCA 1020

RESULT 40

US-09-999-833A-514/c
; Sequence 514, Application US/09999833A
; Patent No. 6916648
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664

; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
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; PRIOR APPLICATION NUMBER: 60/079923
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; PRIOR APPLICATION NUMBER: 60/080328
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; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
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; PRIOR APPLICATION NUMBER: 60/085338
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; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
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; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 77.0%; Score 15.4; DB 3; Length 2690;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GAACACGGACCCCAA 20
|||||
Db 169 GAACACGGACCCCAA 153

RESULT 41
US-10-020-445A-514/c
; Sequence 514, Application US/10020445A
; Patent No. 6962797
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C74
CURRENT APPLICATION NUMBER: US/10/020,445A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
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; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 77.0%; Score 15.4; DB 3; Length 2690;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAAACACGACACCCAA 20
Db 169 GAAACACGACACCCAA 153

RESULT 42
US-09-949-016-11868/c
; Sequence 11868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11868
; LENGTH: 300598
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(300598)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868

Query Match 77.0%; Score 15.4; DB 3; Length 300598;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACC 17
Db 105906 AAGGAACACGACACC 105890

RESULT 43
US-09-949-016-14588/c
; Sequence 14588, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14588
; LENGTH: 302604
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(302604)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588

Query Match 77.0%; Score 15.4; DB 3; Length 302604;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACC 17
Db 155912 AAGGAACACGACACC 155896

RESULT 44
US-09-949-016-14589/c
; Sequence 14589, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-10-20

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14589
; LENGTH: 302604
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(302604)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589

Query Match 77.0%; Score 15.4; DB 3; Length 302604;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACC 17
Db 155912 AAGGAAACACGGACAC 155896

RESULT 45
US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17119
; LENGTH: 308362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(308362)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119

Query Match 77.0%; Score 15.4; DB 3; Length 308362;
Best Local Similarity 94.1%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACC 17
Db 155728 AAGGAAACACGGACAC 155712

RESULT 46
US-09-107-532A-826
; Sequence 826, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 826:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...507
; SEQUENCE DESCRIPTION: SEQ ID NO: 826:
US-09-107-532A-826

Query Match 76.0%; Score 15.2; DB 3; Length 507;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACCCAA 20
Db 332 AAGGACACACGGAAACGAA 351

RESULT 47
US-09-949-016-26382/c
; Sequence 26382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26382
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26382

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
|||||
DB 333 AAGGAAACACACACACAA 314
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RESULT 48

US-09-949-016-26383/c
; Sequence 26383, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26383
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26383

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
|||||
DB 594 AAGGAAACACACACACAA 575
|||||

RESULT 49

US-09-949-016-58446/c
; Sequence 58446, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58446
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-58446

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
|||||
DB 257 AAGGAGACACAGACACCAA 238
|||||

RESULT 50

US-09-949-016-58447/c
; Sequence 58447, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58447
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58447

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
|||||
DB 396 AAGGAGACACAGACACCAA 377
|||||

RESULT 51

US-09-949-016-58448/c
; Sequence 58448, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58448
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58448

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 412 AAGGAGACACAGACACCA 393

RESULT 52
US-09-949-016-58449/c
; Sequence 58449, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58449
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58449

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 508 AAGGAGACACAGACACCA 489

RESULT 53
US-09-949-016-58450/c
; Sequence 58450, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58450
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58450

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 538 AAGGAGACACAGACACCA 519

RESULT 54
US-09-949-016-110157
; Sequence 110157, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110157
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-110157

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 93 AAGGAAACACAGTACCCAA 112

RESULT 55
US-09-949-016-110158
; Sequence 110158, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110158
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-110158

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 258 AAGGAAACACAGTACCCAA 277

RESULT 56
US-09-949-016-110159
; Sequence 110159, Application US/09949016
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110159
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-110159

Query Match          76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   |||||
Db 536 AGGGAACACGATCATCCCA 555

RESULT 57
US-09-949-016-138287/c
; Sequence 138287, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138287
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-138287

Query Match          76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   |||||
Db 333 AAGGAAACACACACACAA 314

RESULT 58
US-09-949-016-138288/c
; Sequence 138288, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138288
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-138288

Query Match          76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   |||||
Db 594 AAGGAAACACACACACAA 575

RESULT 59
US-09-949-016-149759
; Sequence 149759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149759
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-149759

Query Match          76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   |||||
Db 328 AAGGAAACACGTGACACAA 347

RESULT 60
US-09-533-559-6526
; Sequence 6526, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
```

```
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6526
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-6526

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 675;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 370 ACGGAATAAGGACACCCAA 389

RESULT 61
US-09-248-796A-4726/c
; Sequence 4726, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4726
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-4726

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 1455;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 287 AACGAATATGGACACCCAA 268

RESULT 62
US-08-631-200-13/c
; Sequence 13, Application US/08631200
; Patent No. 5646040
; GENERAL INFORMATION:
; APPLICANT: Kievn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,200
; FILING DATE: 12-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/631,200
; FILING DATE: 12-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; MEDIUM TYPE: DNA (genomic)
US-08-631-200-13

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 2; Length 1622;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 1180 AAGGATAGACAGACCCAA 1161

RESULT 63
US-08-829-553-13/c
; Sequence 13, Application US/08829553
; Patent No. 5817762
; GENERAL INFORMATION:
; APPLICANT: Kievn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,553
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/631,200
; FILING DATE: 12-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; MEDIUM TYPE: DNA (genomic)
US-08-829-553-13/c
```

```

; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-829-553-13

Query Match          76.0%; Score 15.2; DB 2; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
DB 1180 AAGGATAGACAGACACCCAA 1161

RESULT 64
US-08-922-267A-13/c
; Sequence 13, Application US/08922267A
; Patent No. 5861239
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,267A
; FILING DATE: 2-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US 08/829,553
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/631,200
; FILING DATE: 12-APR-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-085
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-922-267A-13

Query Match          76.0%; Score 15.2; DB 2; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
DB 1180 AAGGATAGACAGACACCCAA 1161

RESULT 65
US-08-936-707A-13/c
; Sequence 13, Application US/08936707A
; Patent No. 5871931
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,707A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-936-707A-13

Query Match          76.0%; Score 15.2; DB 2; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
DB 1180 AAGGATAGACAGACACCCAA 1161

RESULT 66
US-08-936-706A-13/c
; Sequence 13, Application US/08936706A
; Patent No. 5876919
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,706A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-099
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-936-706A-13

Query Match 76.0%; Score 15.2; DB 2; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 1180 AAGGATAGACAGACACCCAA 1161

RESULT 67
US-09-248-203-13/c
; Sequence 13, Application US/09248203
; Patent No. 6043346
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/248,203
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/936,707
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-248-203-13

Query Match 76.0%; Score 15.2; DB 3; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 1180 AAGGATAGACAGACACCCAA 1161

RESULT 68
US-09-406-071-13/c
; Sequence 13, Application US/09406071
; Patent No. 6207386
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,071
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/936,707
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-406-071-13

Query Match 76.0%; Score 15.2; DB 3; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 1180 AAGGATAGACAGACACCCAA 1161

RESULT 69
US-09-814-986-13/c
; Sequence 13, Application US/09814986
; Patent No. 6605437
; GENERAL INFORMATION:
```

APPLICANT: Kleya, Patrick W.
Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/814,986
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/936,707
FILING DATE: 24-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1622 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-814-986-13

Query Match 76.0%; Score 15.2; DB 3; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||
Db 1180 AAGGATAGACAGACCCAA 1161

RESULT 70
US-08-990-379-1/c
; Sequence 1, Application US/08990379
; Patent No. 5998188
; GENERAL INFORMATION:
; APPLICANT: Stork, Philip J
; APPLICANT: Misra-Press, Anita
; TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
; TITLE OF INVENTION: Their Biologically Active Expression Products
; FILE REFERENCE: 4104-000322USA
; CURRENT APPLICATION NUMBER: US/08/990,379
; CURRENT FILING DATE: 1997-12-15
; EARLIER APPLICATION NUMBER: PCT/US96/10402
; EARLIER FILING DATE: 1996-06-14
; EARLIER APPLICATION NUMBER: 60/000,263
; EARLIER FILING DATE: 1995-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-08-990-379-1

Query Match 76.0%; Score 15.2; DB 2; Length 1987;
Best Local Similarity 85.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||
Db 1826 AAGGAACACGACACCCAA 1807

RESULT 71

US-08-990-379-2/c
; Sequence 2, Application US/08990379
; Patent No. 5998188
; GENERAL INFORMATION:
; APPLICANT: Stork, Philip J
; APPLICANT: Misra-Press, Anita
; TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
; TITLE OF INVENTION: Their Biologically Active Expression Products
; FILE REFERENCE: 4104-000322USA
; CURRENT APPLICATION NUMBER: US/08/990,379
; CURRENT FILING DATE: 1997-12-15
; EARLIER APPLICATION NUMBER: PCT/US96/10402
; EARLIER FILING DATE: 1996-06-14
; EARLIER APPLICATION NUMBER: 60/000,263
; EARLIER FILING DATE: 1995-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1993
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-08-990-379-2

Query Match 76.0%; Score 15.2; DB 2; Length 1993;
Best Local Similarity 85.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||
Db 1832 AAGGAACACGACACCCAA 1813

RESULT 72

US-09-555-820A-1
; Sequence 1, Application US/09555820A
; Patent No. 6680429
; GENERAL INFORMATION:
; APPLICANT: Webster, David
; APPLICANT: Burgess, Diane
; TITLE OF INVENTION: A Starchless Variety of Pisum Sativum Having Elevated Levels of S
; FILE REFERENCE: SVS3801P0302US
; CURRENT APPLICATION NUMBER: US/09/555,820A
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2391
; TYPE: DNA
; ORGANISM: Pisum sativum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1274)..(1350)
; OTHER INFORMATION: N=A or C or G or T/U
US-09-555-820A-1

Query Match 76.0%; Score 15.2; DB 3; Length 2391;
Best Local Similarity 85.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||

Db 1947 ACGGAGACACGGACACCAAA 1966

RESULT 73

US-09-555-820A-2
; Sequence 2, Application US/09555820A
; Patent No. 6680429
; GENERAL INFORMATION:
; APPLICANT: Webster, David
; APPLICANT: Burgess, Diane
; TITLE OF INVENTION: A Starchless Variety of Pisum Sativum Having Elevated Levels of Starch
; FILE REFERENCE: SVS3801P0302US
; CURRENT APPLICATION NUMBER: US/09/555.820A
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2391
; TYPE: DNA
; ORGANISM: Pisum sativum
US-09-555-820A-2

Query Match 76.0%; Score 15.2; DB 3; Length 2391;
Best Local Similarity 85.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCAAA 20

Db 1947 ACGGAGACACGGACACCAAA 1966

RESULT 74

US-09-270-767-12587
; Sequence 12587, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12587
; LENGTH: 4983
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12587

Query Match 76.0%; Score 15.2; DB 3; Length 4983;
Best Local Similarity 85.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCAAA 20

Db 1762 AGGGAACACGGACACCAAA 1781

RESULT 75

US-09-949-016-13437
; Sequence 13437, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13437

; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13437
; LENGTH: 17353
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13437

Query Match 76.0%; Score 15.2; DB 3; Length 17353;
Best Local Similarity 85.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCAAA 20

Db 4679 AAGGAGACACGACCAAA 4698

RESULT 76

US-09-949-016-14781/c
; Sequence 14781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14781
; LENGTH: 54463
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14781

Query Match 76.0%; Score 15.2; DB 3; Length 54463;
Best Local Similarity 85.0%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCAAA 20

Db 14853 AGGGAACACGATCACCACAA 14834

RESULT 77

US-09-949-016-12838/c
; Sequence 12838, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838

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; LENGTH: 57178
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12838

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 57178;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| |||||
DB 9713 AAGGAAACACACATACACAA 9694

RESULT 78
US-09-949-016-17458/c
; Sequence 17458, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17458
; LENGTH: 57178
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17458

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 57178;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| |||||
DB 9713 AAGGAAACACACATACACAA 9694

RESULT 79
US-09-949-016-15543
; Sequence 15543, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15543
; LENGTH: 75929
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(75929)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15543

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 75929;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| |||||
DB 47908 AAGGAAACACAGACACCTA 47927

RESULT 80
US-09-949-016-15544
; Sequence 15544, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15544
; LENGTH: 75929
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(75929)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15544

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 75929;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| |||||
DB 47908 AAGGAAACACAGACACCTA 47927

RESULT 81
US-09-949-016-13597/c
; Sequence 13597, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13597
; LENGTH: 98439
; TYPE: DNA
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(98439)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13597

Query Match          76.0%; Score 15.2; DB 3; Length 98439;
Best Local Similarity 85.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCCAA 20
Db      94040 AGGAAACACGACACCCCA 94021

RESULT 82
US-09-949-016-15953
; Sequence 15953, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15953
; LENGTH: 105050
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15953

Query Match          76.0%; Score 15.2; DB 3; Length 105050;
Best Local Similarity 85.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCCAA 20
Db      93225 AAGGACACACAGACACACAA 93244

RESULT 83
US-09-949-016-12080/c
; Sequence 12080, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12080
; LENGTH: 119594
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-12080

Query Match          76.0%; Score 15.2; DB 3; Length 119594;
Best Local Similarity 85.0%; Pred. No. 9.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCCAA 20
Db      13996 AAGAAACACTGACACCCAA 13977

RESULT 84
US-09-949-016-15952/c
; Sequence 15952, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15952
; LENGTH: 119601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15952

Query Match          76.0%; Score 15.2; DB 3; Length 119601;
Best Local Similarity 85.0%; Pred. No. 9.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCCAA 20
Db      13996 AAGAAACACTGACACCCAA 13977

RESULT 85
US-09-949-016-12174
; Sequence 12174, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12174
; LENGTH: 153642
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(153642)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12174
```

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Query Match          76.0%; Score 15.2; DB 3; Length 153642;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
Db 121010 AAGGAAACACACACACAA 121029

RESULT 86
US-09-949-016-15635
; Sequence 15635, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15635
; LENGTH: 153643
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(153643)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15635

Query Match          76.0%; Score 15.2; DB 3; Length 153643;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
Db 121010 AAGGAAACACACACACAA 121029

RESULT 87
US-09-949-016-14157/c
; Sequence 14157, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14157
; LENGTH: 455726
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1)....(455726)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14157

Query Match          76.0%; Score 15.2; DB 3; Length 455726;
Best Local Similarity 85.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
Db 416568 AAGGAAACACACACACAA 416549

RESULT 88
US-09-949-016-11940/c
; Sequence 11940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11940
; LENGTH: 481115
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(481115)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11940

Query Match          76.0%; Score 15.2; DB 3; Length 481115;
Best Local Similarity 85.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
Db 393957 AAGGAAACACACACACAA 393938

RESULT 89
US-08-361-337-12
; Sequence 12, Application US/08361337
; Patent No. 5728519
; GENERAL INFORMATION:
; APPLICANT: Levenbook, Inessa S.
; APPLICANT: Chumakov, Konstantin M.
; APPLICANT: No. 5728519wood, Laurie P.
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,337
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414,634
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-361-337-12

Query Match 75.0%; Score 15; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AACACGGACACCCAA 20
Db 1 AACACGGACACCCAA 15

RESULT 90
US-09-396-149-1/c
; Sequence 1, Application US/09396149
; Patent No. 6538176
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVENTION: Maize Replication Protein A and Use
; FILE REFERENCE: 5718-59
; CURRENT APPLICATION NUMBER: US/09/396,149
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Zea Mays
; FEATURE:
; NAME/KEY: (157)...(2025)
; LOCATION: (157)...(2025)
; OTHER INFORMATION: Coding sequence for the Maize RPA Large Subunit
; OTHER INFORMATION: Homologue-1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Maize RPA Large subunit Homologue-1
US-09-396-149-1

Query Match 75.0%; Score 15; DB 3; Length 2497;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AACACGGACACCCAA 20
Db 1769 AACACGGACACCCAA 1755

RESULT 91
US-09-949-016-12147
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match 75.0%; Score 15; DB 3; Length 767677;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACA 15
Db 407477 AAGGAACACGGACA 407491

RESULT 92
US-09-949-016-17361
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match 75.0%; Score 15; DB 3; Length 767677;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACA 15
Db 407477 AAGGAACACGGACA 407491

RESULT 93
US-09-621-976-1696/c
; Sequence 1696, Application US/09621976
```

```
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1696
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 139..378
; NAME/KEY: sig_peptide
; LOCATION: 139..198
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5
; OTHER INFORMATION: seq HLLAGCVMVVLG/WV
US-09-621-976-1696

Query Match          74.0%; Score 14.8; DB 3; Length 577;
Best Local Similarity 88.9%; Pred. No. 8.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AGGAACACGGACACCCA 19
      ||||| ||||| ||||| |||||
DB      59 AGGAGACAGGACACCCA 42

RESULT 94
US-09-270-767-8728/c
; Sequence 8728, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8728
; LENGTH: 751
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8728

Query Match          74.0%; Score 14.8; DB 3; Length 751;
Best Local Similarity 88.9%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AGGAACACGGACACCCA 19
      ||||| ||||| ||||| |||||
DB      383 AGGAACACGGACACCCA 366

RESULT 95
US-09-270-767-24010/c
; Sequence 24010, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver.. 2.0
US-09-270-767-24010

; SEQ ID NO 24010
; LENGTH: 751
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-24010

Query Match          74.0%; Score 14.8; DB 3; Length 751;
Best Local Similarity 88.9%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AGGAACACGGACACCCA 19
      ||||| ||||| ||||| |||||
DB      383 AGGAACACGGACACCCA 366

RESULT 96
US-09-023-655-195
; Sequence 195, Application US/09023655
; Patent No. 6807879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1049 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIEB01
; CLONE: 073345
US-09-023-655-195

Query Match          74.0%; Score 14.8; DB 3; Length 1049;
Best Local Similarity 88.9%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGAAACACGGACACCCA 20
      ||||| ||||| ||||| |||||
DB      335 GGACACACGGAAACCCA 352
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RESULT 97

US-09-107-532A-3518
Sequence 3518, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3518:

SEQUENCE CHARACTERISTICS:

LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:

NAME/KEY: misc feature
LOCATION: (8) LOCATION 1...1281
SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

US-09-107-532A-3518

Query Match 74.0%; Score 14.8; DB 3; Length 1281;
Best Local Similarity 88.9%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACAGTACACCC 861

RESULT 98

US-09-722-377-12/c
Sequence 12, Application US/09722377
Patent No. 6791007
GENERAL INFORMATION:

APPLICANT: Panstruga, Ralph
APPLICANT: Schulze-Lefert, Paul MJ
TITLE OF INVENTION: Buschges, Rainer
TITLE OF INVENTION: Polynucleotide and its use for modulating a defence
TITLE OF INVENTION: response in plants
FILE REFERENCE: 620-58

CURRENT APPLICATION NUMBER: US/09/722,377
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/GB97/02046
PRIOR FILING DATE: 1997-07-29
PRIOR APPLICATION NUMBER: GB 9615879.5
PRIOR FILING DATE: 1996-07-29
PRIOR APPLICATION NUMBER: GB 9622626.1
PRIOR FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: GB 9704789.8
PRIOR FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 1635
TYPE: DNA
ORGANISM: Hordeum vulgare
US-09-722-377-12

Query Match

Best Local Similarity 88.9%; Pred. No. 9.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCA 19

Db 930 AGGAACACGACATCCA 913

RESULT 99

US-09-599-360B-38/c

Sequence 38, Application US/09599360B
Patent No. 6548633
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bougueret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 38
LENGTH: 1888
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:

NAME/KEY: CDS
LOCATION: 139..1389
NAME/KEY: sig_peptide
LOCATION: 139..198
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.00
OTHER INFORMATION: seq HLLAGFCVWVVLG/WV
NAME/KEY: polyA signal
LOCATION: 1854..1859
NAME/KEY: polyA_site
LOCATION: 1873..1888
US-09-599-360B-38

Query Match 74.0%; Score 14.8; DB 3; Length 1888;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCA 19

Db 59 AGGAGACAAGGACACCCA 42

Search completed: March 8, 2006, 21:07:05
Job time : 91.9223 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:29:05 ; Search time 435.728 Seconds
(without alignments)
105.905 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaacacggacaccaa 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications NA New:*

- 1: /cgm2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 2: /cgm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /cgm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 5: /cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 6: /cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 8: /cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 9: /cgm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 10: /cgm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 11: /cgm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 12: /cgm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 13: /cgm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.4	92.0	810	12	US-11-155-478A-137
C 2	17	85.0	415	7	US-10-886-517A-21
C 3	17	85.0	627	12	US-11-195-109-31
C 4	17	85.0	681	12	US-11-155-478A-138
C 5	16.8	84.0	585	6	US-09-925-065A-156382
C 6	16.8	84.0	585	6	US-09-925-065A-156383
C 7	16.8	84.0	147700	8	US-10-857-780-3
C 8	16.6	83.0	25	12	US-11-119-231-48
C 9	16.6	83.0	25	12	US-11-119-231-96
C 10	16.4	82.0	201	8	US-10-995-561-41106
C 11	16.4	82.0	201	12	US-11-124-367A-13200
C 12	16.4	82.0	201	12	US-11-124-367A-33200
C 13	16.4	82.0	578	6	US-09-925-065A-139374
C 14	16.4	82.0	778	8	US-10-750-185-62571
C 15	16.4	82.0	778	8	US-10-750-623-31642
C 16	16.4	82.0	42060	12	US-11-124-367A-5040
C 17	16.4	82.0	1125000	8	US-10-995-561-13286
C 18	15.8	79.0	169	6	US-09-925-065A-187976
C 19	15.8	79.0	449	6	US-09-925-065A-527437
C 20	15.8	79.0	449	6	US-09-925-065A-527438
C 21	15.8	79.0	449	6	US-09-925-065A-527438
C 22	15.8	79.0	449	6	US-09-925-065A-527438
C 23	15.8	79.0	449	6	US-09-925-065A-527438
C 24	15.8	79.0	449	6	US-09-925-065A-527438
C 25	15.8	79.0	449	6	US-09-925-065A-527438
C 26	15.8	79.0	449	6	US-09-925-065A-527438
C 27	15.8	79.0	449	6	US-09-925-065A-527438
C 28	15.8	79.0	449	6	US-09-925-065A-527438
C 29	15.8	79.0	449	6	US-09-925-065A-527438
C 30	15.8	79.0	449	6	US-09-925-065A-527438
C 31	15.8	79.0	449	6	US-09-925-065A-527438
C 32	15.8	79.0	449	6	US-09-925-065A-527438
C 33	15.8	79.0	449	6	US-09-925-065A-527438
C 34	15.4	77.0	50	12	US-11-175-859-2211
C 35	15.4	77.0	537	6	US-09-925-065A-366331
C 36	15.4	77.0	537	6	US-09-925-065A-366333
C 37	15.4	77.0	620	6	US-09-925-065A-544937
C 38	15.4	77.0	4562	12	US-11-136-527-1862
C 39	15.4	77.0	94035	12	US-11-124-368A-2902
C 40	15.4	77.0	121736	9	US-11-114-798-49
C 41	15.4	77.0	318488	9	US-11-114-780-58
C 42	15.2	76.0	30	8	US-10-857-780-1527
C 43	15.2	76.0	55	8	US-10-500-831-360
C 44	15.2	76.0	61	8	US-10-310-914A-143
C 45	15.2	76.0	81	8	US-10-775-169-361
C 46	15.2	76.0	201	8	US-10-995-561-35611
C 47	15.2	76.0	201	8	US-10-995-561-69264
C 48	15.2	76.0	440	6	US-09-925-065A-102175
C 49	15.2	76.0	542	6	US-09-925-065A-192787
C 50	15.2	76.0	550	6	US-09-925-065A-20386
C 51	15.2	76.0	550	6	US-09-925-065A-482407
C 52	15.2	76.0	550	6	US-09-925-065A-482408
C 53	15.2	76.0	560	6	US-09-925-065A-138729
C 54	15.2	76.0	580	6	US-09-925-065A-99970
C 55	15.2	76.0	580	6	US-09-925-065A-412774
C 56	15.2	76.0	585	6	US-09-925-065A-794043
C 57	15.2	76.0	597	6	US-09-925-065A-436621
C 58	15.2	76.0	614	6	US-09-925-065A-436622
C 59	15.2	76.0	614	6	US-09-925-065A-919663
C 60	15.2	76.0	614	6	US-09-925-065A-919664
C 61	15.2	76.0	623	6	US-09-925-065A-692481
C 62	15.2	76.0	625	6	US-09-925-065A-820980
C 63	15.2	76.0	633	6	US-09-925-065A-783213
C 64	15.2	76.0	650	6	US-09-925-065A-214200
C 65	15.2	76.0	654	6	US-09-925-065A-529196
C 66	15.2	76.0	654	6	US-09-925-065A-529197
C 67	15.2	76.0	674	6	US-09-925-065A-192788
C 68	15.2	76.0	674	6	US-09-925-065A-192789
C 69	15.2	76.0	766	6	US-09-925-065A-6885
C 70	15.2	76.0	877	8	US-10-750-185-27789
C 71	15.2	76.0	877	8	US-10-750-623-27789
C 72	15.2	76.0	878	8	US-10-750-185-61482
C 73	15.2	76.0	878	8	US-10-750-623-61482
C 74	15.2	76.0	925	6	US-09-925-065A-710787
C 75	15.2	76.0	925	6	US-09-925-065A-710788
C 76	15.2	76.0	925	6	US-09-925-065A-710789
C 77	15.2	76.0	1125	6	US-09-925-065A-717601
C 78	15.2	76.0	1125	6	US-09-925-065A-717602
C 79	15.2	76.0	1139	8	US-10-750-185-59220
C 80	15.2	76.0	1139	8	US-10-750-623-59220
C 81	15.2	76.0	1371	7	US-10-932-182A-76110
C 82	15.2	76.0	1371	7	US-10-932-182A-76110
C 83	15.2	76.0	1619	8	US-10-750-185-25747
C 84	15.2	76.0	1619	8	US-10-750-623-25747
C 85	15.2	76.0	1816	8	US-10-750-185-33198
C 86	15.2	76.0	1816	8	US-10-750-623-33198
C 87	15.2	76.0	2168	8	US-10-750-185-31642
C 88	15.2	76.0	2168	8	US-10-750-623-31642
C 89	15.2	76.0	2406	7	US-10-932-182A-1309
C 90	15.2	76.0	2406	7	US-10-932-182A-1309
C 91	15.2	76.0	2590	6	US-09-925-065A-697075
C 92	15.2	76.0	2590	6	US-09-925-065A-697076
C 93	15.2	76.0	2828	8	US-10-750-185-54418

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c 94	15.2	76.0	2828	8	US-10-750-623-54418	Sequence 54418, A	167	14.4	72.0	641	6	US-09-925-065A-481968	Sequence 481968,
c 95	15.2	76.0	23367	7	US-10-330-773-916	Sequence 916, App	c 168	14.4	72.0	654	8	US-10-467-657-8509	Sequence 8509, Ap
c 96	15.2	76.0	123331	7	US-10-330-773-829	Sequence 829, App	c 169	14.4	72.0	658	6	US-09-925-065A-313953	Sequence 313953,
c 97	15.2	76.0	161874	12	US-11-121-086-75	Sequence 75, Appl	c 170	14.4	72.0	664	6	US-09-925-065A-518152	Sequence 518152,
c 98	15.2	76.0	171423	12	US-11-121-086-85	Sequence 85, Appl	c 171	14.4	72.0	784	6	US-09-925-065A-953534	Sequence 953534,
c 99	15.2	76.0	1691140	12	US-11-091-018-1	Sequence 1, Appl	c 172	14.4	72.0	784	6	US-09-925-065A-953535	Sequence 953535,
c 100	15	75.0	201	8	US-10-995-561-51045	Sequence 51045, A	c 173	14.4	72.0	838	6	US-09-925-065A-57538	Sequence 57538, A
c 101	15	75.0	537	6	US-09-925-065A-366332	Sequence 366332, A	c 174	14.4	72.0	942	8	US-10-750-185-43041	Sequence 43041, A
c 102	15	75.0	50353	8	US-10-995-561-13305	Sequence 13305, A	c 175	14.4	72.0	942	8	US-10-750-623-43041	Sequence 43041, A
c 103	15	75.0	180531	9	US-11-114-798-57	Sequence 57, Appl	c 176	14.4	72.0	1219	8	US-10-750-185-61348	Sequence 61348, A
c 104	14.8	74.0	20	8	US-10-310-914A-1088291	Sequence 1088291, A	c 177	14.4	72.0	1219	8	US-10-750-623-61348	Sequence 61348, A
c 105	14.8	74.0	25	12	US-11-121-849-93014	Sequence 93014, A	c 178	14.4	72.0	2243	6	US-09-925-065A-548770	Sequence 548770, A
c 106	14.8	74.0	201	8	US-10-995-561-35609	Sequence 35609, A	c 179	14.4	72.0	2595	7	US-10-932-182A-1628	Sequence 1628, Ap
c 107	14.8	74.0	201	8	US-10-995-561-69262	Sequence 69262, A	c 180	14.4	72.0	2595	7	US-10-932-182A-1628	Sequence 1628, Ap
c 108	14.8	74.0	323	6	US-09-925-065A-481041	Sequence 481041, A	c 181	14.4	72.0	27553	7	US-10-922-2328-54	Sequence 54, Appl
c 109	14.8	74.0	491	6	US-09-925-065A-523226	Sequence 523226, A	c 182	14.4	72.0	103665	7	US-10-330-773-680	Sequence 680, App
c 110	14.8	74.0	491	6	US-09-925-065A-523227	Sequence 523227, A	c 183	14.4	72.0	127722	7	US-10-330-773-278	Sequence 278, App
c 111	14.8	74.0	491	6	US-09-925-065A-523228	Sequence 523228, A	c 184	14.4	72.0	171423	12	US-11-121-086-85	Sequence 85, Appl
c 112	14.8	74.0	491	6	US-09-925-065A-429072	Sequence 429072, A	c 185	14.4	72.0	181172	12	US-11-121-086-41	Sequence 41, Appl
c 113	14.8	74.0	551	6	US-09-925-065A-183625	Sequence 183625, A	c 186	14.4	72.0	201309	9	US-11-114-798-51	Sequence 51, Appl
c 114	14.8	74.0	575	6	US-09-925-065A-183625	Sequence 183625, A	c 187	14.4	72.0	201309	9	US-11-114-798-51	Sequence 51, Appl
c 115	14.8	74.0	577	6	US-09-925-065A-462434	Sequence 462434, A	c 188	14.4	72.0	21	8	US-10-750-185-11072	Sequence 11072, A
c 116	14.8	74.0	599	6	US-09-925-065A-954034	Sequence 954034, A	c 189	14.2	71.0	21	8	US-10-750-623-11072	Sequence 11072, A
c 117	14.8	74.0	603	6	US-09-925-065A-954559	Sequence 954559, A	c 190	14.2	71.0	21	8	US-10-310-914A-892075	Sequence 892075, A
c 118	14.8	74.0	606	6	US-09-925-065A-324037	Sequence 324037, A	c 191	14.2	71.0	21	8	US-10-310-914A-1006288	Sequence 1006288, A
c 119	14.8	74.0	643	6	US-09-925-065A-312506	Sequence 312506, A	c 192	14.2	71.0	25	7	US-10-932-182A-13878	Sequence 13878, A
c 120	14.8	74.0	647	6	US-09-925-065A-453189	Sequence 453189, A	c 193	14.2	71.0	33	8	US-10-310-914A-891835	Sequence 891835, A
c 121	14.8	74.0	753	8	US-10-750-185-45627	Sequence 45627, A	c 194	14.2	71.0	201	8	US-10-995-561-18661	Sequence 18661, A
c 122	14.8	74.0	886	6	US-10-750-623-45627	Sequence 45627, A	c 195	14.2	71.0	201	8	US-10-995-561-19907	Sequence 19907, A
c 123	14.8	74.0	886	6	US-09-925-065A-804	Sequence 804, App	c 196	14.2	71.0	201	8	US-10-995-561-30110	Sequence 30110, A
c 124	14.8	74.0	1176	8	US-10-750-185-34939	Sequence 34939, A	c 197	14.2	71.0	201	8	US-10-995-561-30127	Sequence 30127, A
c 125	14.8	74.0	1233	7	US-10-524-972-123	Sequence 123, App	c 198	14.2	71.0	201	12	US-11-124-368A-18918	Sequence 18918, A
c 126	14.8	74.0	1233	8	US-10-524-972-123	Sequence 123, App	c 199	14.2	71.0	201	12	US-11-124-368A-18919	Sequence 18919, A
c 127	14.8	74.0	1343	6	US-09-925-065A-94518	Sequence 94518, A	c 200	14.2	71.0	201	12	US-11-124-368A-18920	Sequence 18920, A
c 128	14.8	74.0	1343	6	US-09-925-065A-94519	Sequence 94519, A	c 201	14.2	71.0	201	12	US-11-124-368A-18921	Sequence 18921, A
c 129	14.8	74.0	1343	6	US-09-925-065A-94519	Sequence 94519, A	c 202	14.2	71.0	201	12	US-11-124-367A-11450	Sequence 11450, A
c 130	14.8	74.0	1721	9	US-11-096-568A-25406	Sequence 25406, A	c 203	14.2	71.0	201	12	US-11-124-367A-26724	Sequence 26724, A
c 131	14.8	74.0	1872	8	US-10-750-185-38275	Sequence 38275, A	c 204	14.2	71.0	266	6	US-09-925-065A-528026	Sequence 528026, A
c 132	14.8	74.0	1872	8	US-10-750-623-38275	Sequence 38275, A	c 205	14.2	71.0	266	6	US-09-925-065A-567190	Sequence 567190, A
c 133	14.8	74.0	1888	5	US-09-978-360A-15	Sequence 15, Appl	c 206	14.2	71.0	287	6	US-09-925-065A-471636	Sequence 471636, A
c 134	14.8	74.0	1896	6	US-09-925-065A-704574	Sequence 704574, A	c 207	14.2	71.0	300	6	US-09-925-065A-521676	Sequence 521676, A
c 135	14.8	74.0	2332	9	US-11-096-568A-33708	Sequence 33708, A	c 208	14.2	71.0	323	6	US-09-925-065A-581746	Sequence 581746, A
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c 138	14.8	74.0	5510	12	US-11-150-406-1	Sequence 1, Appl	c 211	14.2	71.0	436	6	US-09-925-065A-208786	Sequence 208786, A
c 139	14.8	74.0	13816	8	US-10-995-561-13409	Sequence 13409, A	c 212	14.2	71.0	436	6	US-09-925-065A-208787	Sequence 208787, A
c 140	14.8	74.0	21728	7	US-10-330-773-362	Sequence 362, App	c 213	14.2	71.0	465	6	US-09-925-065A-763835	Sequence 763835, A
c 141	14.8	74.0	142303	12	US-11-121-086-42	Sequence 42, Appl	c 214	14.2	71.0	469	6	US-09-925-065A-752751	Sequence 752751, A
c 142	14.8	74.0	149382	8	US-10-995-561-13272	Sequence 13272, A	c 215	14.2	71.0	490	6	US-09-925-065A-512113	Sequence 512113, A
c 143	14.8	74.0	149419	12	US-11-112-908-49	Sequence 49, Appl	c 216	14.2	71.0	490	6	US-09-925-065A-512114	Sequence 512114, A
c 144	14.8	74.0	161726	12	US-11-112-908-48	Sequence 48, Appl	c 217	14.2	71.0	490	6	US-09-925-065A-512115	Sequence 512115, A
c 145	14.8	74.0	161726	12	US-11-112-908-52	Sequence 52, Appl	c 218	14.2	71.0	490	6	US-09-925-065A-818203	Sequence 818203, A
c 146	14.8	74.0	166111	12	US-11-112-908-47	Sequence 47, Appl	c 219	14.2	71.0	496	6	US-09-925-065A-342392	Sequence 342392, A
c 147	14.4	72.0	21	8	US-10-310-914A-346286	Sequence 346286, A	c 220	14.2	71.0	509	6	US-09-925-065A-400679	Sequence 400679, A
c 148	14.4	72.0	22	8	US-10-310-914A-346423	Sequence 346423, A	c 221	14.2	71.0	509	6	US-09-925-065A-400680	Sequence 400680, A
c 149	14.4	72.0	23	8	US-10-310-914A-346287	Sequence 346287, A	c 222	14.2	71.0	509	6	US-09-925-065A-400681	Sequence 400681, A
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ALIGNMENTS

RESULT 1

US-11-155-478A-137/c

; Sequence 137, Application US/11155478A

; Publication No. US2006001410A1

; GENERAL INFORMATION:

; APPLICANT: Boivin, Guy

; APPLICANT: UNIVERSITE LAVAL

; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING

; TITLE OF INVENTION: RESPIRATORY VIRUSES

; FILE REFERENCE: 6013-148US

; CURRENT APPLICATION NUMBER: US/11/155,478A

; CURRENT FILING DATE: 2005-06-20

; PRIOR FILING DATE: 2005-06-20

; PRIOR FILING DATE: 2002-12-19

; PRIOR FILING DATE: 2002-12-19

; PRIOR APPLICATION NUMBER: CA 2,418,004

; PRIOR APPLICATION NUMBER: PCT/CA2003/001994

; PRIOR FILING DATE: 2003-01-24

; PRIOR FILING DATE: 2003-12-19

; NUMBER OF SEQ ID NOS: 174

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 137

; LENGTH: 810

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; ORGANISM: human Enterovirus

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US-11-155-478A-137

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
US-10-886-517A-21/c
; Sequence 21, Application US/10886517A
; Publication No. US2006000810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: F003-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 23, 24, 25, 26, 27, 28, 29, 31, 32, 33, 34, 35, 44, 60,
; LOCATION: 61, 135, 136, 137, 138, 139, 167, 203, 224, 225, 231, 232,
; LOCATION: 284, 346, 390
; OTHER INFORMATION: n = A,T,C or G
US-10-886-517A-21

Query Match          85.0%; Score 17; DB 7; Length 415;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
   |||||
Db 415 GAAACACGGACACCCAA 399

RESULT 3
US-11-195-109-31/c
; Sequence 31, Application US/11195109
; Publication No. US20050265975A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

Query Match          85.0%; Score 17; DB 12; Length 681;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
   |||||
Db 568 GAAACACGGACACCCAA 552

RESULT 4
US-11-155-478A-138/c
; Sequence 138, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 681
; TYPE: DNA
; ORGANISM: human Rhinovirus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(681)
; OTHER INFORMATION: human Rhinovirus
; OTHER INFORMATION: strain 14
; OTHER INFORMATION: accession number k02121
US-11-155-478A-138
```

Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AAGAACGGACACCCAA 20
Db 92 AAGAACGGACACCCAA 76

RESULT 5

US-09-925-065A-156382
; Sequence 156382, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156382
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-156382

Query Match 84.0%; Score 16.8; DB 6; Length 585;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGAACGGACACCCAA 20
Db 85 AAGAACGGACACCCAA 104

RESULT 6

US-09-925-065A-156383
; Sequence 156383, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156383
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-156383

Query Match 84.0%; Score 16.8; DB 6; Length 585;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGAACGGACACCCAA 20
Db 85 AAGAACGGACACCCAA 104

RESULT 7

US-10-857-780-3/c
; Sequence 3, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 147700
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51510)..(51510)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51526)..(51526)
; OTHER INFORMATION: n is a, c, g, or t
US-10-857-780-3

Query Match 84.0%; Score 16.8; DB 8; Length 147700;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGAACGGACACCCAA 20
Db 50345 ATGGAACACGGACACCCAA 50326

RESULT 8

US-11-119-231-48
; Sequence 48, Application US/11119231
; Publication No. US20060003352A1
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. Ian
; APPLICANT: Jingyue, Ju
; APPLICANT: Thomas, Briese
; TITLE OF INVENTION: Mass Tag PCR for Multiplex Diagnostics
; FILE REFERENCE: 0575/71310-A
; CURRENT APPLICATION NUMBER: US/11/119,231
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: REVERSE PRIMER FOR ENTEROVIRUS
US-11-119-231-48

Query Match      83.0%; Score 16.6; DB 12; Length 25;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAAACACGGACGCCCAA 20
DB      1 GAAACACGGACGCCCAA 17

RESULT 9
US-11-119-231-96
; Sequence 96, Application US/11119231
; Publication No. US20060003352A1
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. Ian
; APPLICANT: Jingyue, Ju
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
; FILE REFERENCE: 0575/71310-A
; CURRENT APPLICATION NUMBER: US/11/119,231
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 96
; LENGTH: 25
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: REVERSE PRIMER FOR ENTEROVIRUS
US-11-119-231-96

Query Match      83.0%; Score 16.6; DB 12; Length 25;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAAACACGGACGCCCAA 20
DB      1 GAAACACGGACGCCCAA 17

RESULT 10
US-10-995-561-41106
; Sequence 41106, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41106
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-41106

Query Match      82.0%; Score 16.4; DB 8; Length 201;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AAGGAACACGGACGCCCAA 20
DB      1 AAGGAACACGGACGCCCAA 20
```

```
DB      88 AAGGAACACGGACGCCCAA 107

RESULT 11
US-11-124-367A-15797/c
; Sequence 15797, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15797
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-15797

Query Match      82.0%; Score 16.4; DB 12; Length 201;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AGGAACACGGACGCCCAA 19
DB      185 AGGAACACGGACGCCCAA 168

RESULT 12
US-11-124-367A-33200
; Sequence 33200, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33200
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-33200

Query Match      82.0%; Score 16.4; DB 12; Length 201;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AAGGAACACGGACGCCCAA 20
DB      88 AAGGAACACGGACGCCCAA 107
```

RESULT 13
US-09-925-065A-319374
; Sequence 319374, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319374
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-319374

Query Match 82.0%; Score 16.4; DB 6; Length 578;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAACACGGACACCCAA 20
|||||
Db 89 GGAACACGGACACCCAA 106

RESULT 14
US-10-750-185-62571
; Sequence 62571, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62571
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Bovine 19866881638593
US-10-750-185-62571

Query Match 82.0%; Score 16.4; DB 8; Length 778;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGAAACACGGACACCC 18
|||||
Db 300 AAGAAACACGTACACCC 317

RESULT 15
US-10-750-623-62571
; Sequence 62571, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62571
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Bovine 19866881638593
US-10-750-623-62571

Query Match 82.0%; Score 16.4; DB 8; Length 778;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGAAACACGGACACCC 18
|||||
Db 300 AAGAAACACGTACACCC 317

RESULT 16
US-11-124-367A-5040/c
; Sequence 5040, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5040
; LENGTH: 42060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5040

Query Match 82.0%; Score 16.4; DB 12; Length 42060;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGAACACGGACACCCA 19
|||||
Db 28555 AGGAACACGGACACCCA 28538

RESULT 17
US-10-995-561-13286
; Sequence 13286, Application US/10995561

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; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13286
; LENGTH: 1125000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1125000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13286

Query Match      82.0%; Score 16.4; DB 8; Length 1125000;
Best Local Similarity 85.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
Db 699287 AAGGAAACACGACACCCAA 699306

RESULT 18
US-09-925-065A-187976
; Sequence 187976, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187976
; LENGTH: 169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-187976

Query Match      79.0%; Score 15.8; DB 6; Length 169;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCCA 19
Db 34 AAGGAAACACGACACCCCA 52

RESULT 19
US-09-925-065A-527437/c
; Sequence 527437, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 527437
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-527437

Query Match      79.0%; Score 15.8; DB 6; Length 449;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAAACACGACACCCCA 20
Db 383 AGGAAACACGACACCCCTA 365

RESULT 20
US-09-925-065A-527438/c
; Sequence 527438, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 527438
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-527438

Query Match      79.0%; Score 15.8; DB 6; Length 449;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAAACACGACACCCCA 20
Db 383 AGGAAACACGACACCCCTA 365

RESULT 21
US-09-925-065A-287845/c

```

; Sequence 287845, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 287845
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-287845

Query Match 79.0%; Score 15.8; DB 6; Length 500;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCCA 19
||| ||||| ||||| ||||| |||||
Db 26 AAGCAACACGACACCCCA 8

RESULT 22
US-09-925-065A-216395/c
; Sequence 216395, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216395
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-216395

Query Match 79.0%; Score 15.8; DB 6; Length 532;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCCA 20
||||| ||||| ||||| ||||| |||||
Db 299 AGGAACACGACACCCCA 281

RESULT 23
US-09-925-065A-187867
; Sequence 187867, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187867
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-187867

Query Match 79.0%; Score 15.8; DB 6; Length 560;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCCA 20
||||| ||||| ||||| ||||| |||||
Db 273 AGGAACGTCGACACCCCA 291

RESULT 24
US-09-925-065A-708503
; Sequence 708503, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 708503
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-708503

Query Match 79.0%; Score 15.8; DB 6; Length 632;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCCA 19

```
Db      85 AAGGAAACACGGCTCACCCA 103
|||||
RESULT 25
US-09-925-065A-136278
; Sequence 136278, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136278
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-136278

Query Match      79.0%; Score 15.8; DB 6; Length 634;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AGGAAACACGACACCCAA 20
|||||
Db      155 AGGGAACACGAGGACACCCAA 173

RESULT 26
US-09-925-065A-879054
; Sequence 879054, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 879054
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-879054

Query Match      79.0%; Score 15.8; DB 6; Length 647;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      85 AAGGAAACACGGCTCACCCA 103
|||||
RESULT 25
US-09-925-065A-136278
; Sequence 136278, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136278
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-136278

Query Match      79.0%; Score 15.8; DB 6; Length 634;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AGGAAACACGACACCCAA 20
|||||
Db      155 AGGGAACACGAGGACACCCAA 173

RESULT 26
US-09-925-065A-879054
; Sequence 879054, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 879054
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-879054

Query Match      79.0%; Score 15.8; DB 6; Length 647;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCA 19
|||||
Db      553 AAGTAAACACGACACCCA 571

RESULT 27
US-09-925-065A-722637/c
; Sequence 722637, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 722637
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-722637

Query Match      79.0%; Score 15.8; DB 6; Length 963;
Best Local Similarity 89.5%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AGGAAACACGACACCCAA 20
|||||
Db      482 AGGAAACACGACACCCA 464

RESULT 28
US-09-925-065A-65977/c
; Sequence 65977, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65977
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-65977
```

Query Match 79.0%; Score 15.8; DB 6; Length 1463;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCA 19
Db 246 AAGGAACACGGACACTCA 228

RESULT 29
US-10-750-185-47447/c
; Sequence 47447, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47447
; LENGTH: 3908
; TYPE: DNA
; ORGANISM: Bovine 19866880584558
US-10-750-185-47447

Query Match 79.0%; Score 15.8; DB 8; Length 3908;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCA 19
Db 2887 AAGGACACAGGACACCCA 2869

RESULT 30
US-10-623-47447/c
; Sequence 47447, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47447
; LENGTH: 3908
; TYPE: DNA
; ORGANISM: Bovine 19866880584558
US-10-750-623-47447

Query Match 79.0%; Score 15.8; DB 8; Length 3908;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAACACGGACACCCA 19
Db 2887 AAGGACACAGGACACCCA 2869

RESULT 31
US-10-330-773-896
; Sequence 896, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 98638
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(98638)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-896

Query Match 79.0%; Score 15.8; DB 7; Length 98638;
Best Local Similarity 89.5%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCA 19
Db 59276 AAGGAGTCACGGACACCCA 59294

RESULT 32
US-10-330-773-365/c
; Sequence 365, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 137454
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-330-773-365

Query Match 79.0%; Score 15.8; DB 7; Length 137454;
Best Local Similarity 89.5%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAACACGGACACCCA 20
Db 34447 AGGAAGCCCGACACCCA 34429

RESULT 33
US-10-330-773-937/c
; Sequence 937, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris

```
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 937
; LENGTH: 390183
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...((390183))
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-937

Query Match          79.0%; Score 15.8; DB 7; Length 390183;
Best Local Similarity 89.5%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 AGGAAACACGGACACCCAA 20
Db  228440 AGGAAACCGGACACTCAA 228422

RESULT 34
US-11-175-859-2211
; Sequence 2211, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2211
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-2211

Query Match          77.0%; Score 15.4; DB 12; Length 50;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 AGGAAACACGGACACCC 18
Db  33 AGGAAACACGGACACCC 49

RESULT 35
US-09-925-065A-366331/c
; Sequence 366331, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
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; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366331
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-366331

Query Match          77.0%; Score 15.4; DB 6; Length 537;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 AAGGAACACGGACACC 17
Db  345 AAGGAACACGGACACC 329

RESULT 36
US-09-925-065A-366333/c
; Sequence 366333, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366333
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-366333

Query Match          77.0%; Score 15.4; DB 6; Length 537;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 AAGGAACACGGACACC 17
Db  345 AAGGAACACGGACACC 329

RESULT 37
US-09-925-065A-544937/c
; Sequence 544937, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
```


; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-58

Query Match 77.0%; Score 15.4; DB 9; Length 318488;
Best Local Similarity 94.1%; Pred. No. 9.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAAACACGACGCCAA 20
|||||
Db 33125 GAAACACACGCCAA 33109

RESULT 42

US-10-857-780-1527/c
; Sequence 1527, Application US/10857780
; Publication No. US20050272043A1

; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1527
; LENGTH: 30
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-10-857-780-1527

Query Match 76.0%; Score 15.2; DB 8; Length 30;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
|||||
Db 23 AAGCAACACGACATCAA 4

RESULT 43

US-10-500-831-260
; Sequence 260, Application US/10500831
; Publication No. US20050244813A1

; GENERAL INFORMATION:
; APPLICANT: Frank KARSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052U800
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 260
; LENGTH: 55

; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
US-10-500-831-260

Query Match 76.0%; Score 15.2; DB 8; Length 55;
Best Local Similarity 85.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
|||||
Db 28 AAGCACCACGACACAA 47

RESULT 44

US-10-310-914A-143
; Sequence 143, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 143
; LENGTH: 61
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-143

Query Match 76.0%; Score 15.2; DB 8; Length 61;
Best Local Similarity 85.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
|||||
Db 26 AAGGAUACACAGACCUAA 45

RESULT 45

US-10-775-169-361/c
; Sequence 361, Application US/10775169
; Publication No. US20050287532A9

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 361
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-361

Query Match 76.0%; Score 15.2; DB 8; Length 81;
Best Local Similarity 85.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
|||||
Db 66 AAGGAAGACAGACTCCAA 47

```
RESULT 46
US-10-995-561-35611/c
; Sequence 35611, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995.561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35611
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-35611

Query Match          76.0%; Score 15.2; DB 8; Length 201;
Best Local Similarity 85.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      122 AAGGAGCAGCGACACGCTA 103

RESULT 47
US-10-995-561-69264/c
; Sequence 69264, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995.561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69264
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-69264

Query Match          76.0%; Score 15.2; DB 8; Length 201;
Best Local Similarity 85.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      122 AAGGAGCAGCGACACGCTA 103

RESULT 48
US-10-995-561-102175
; Sequence 102175, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243.096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252.147
; PRIOR FILING DATE: 2000-11-20
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; PRIOR APPLICATION NUMBER: US 60/250.092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261.766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289.846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102175
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-102175

Query Match          76.0%; Score 15.2; DB 6; Length 440;
Best Local Similarity 85.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      201 AAGCAATATACAGACCCCAA 220

RESULT 49
US-09-925-065A-192787
; Sequence 192787, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243.096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252.147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250.092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261.766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289.846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192787
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-192787

Query Match          76.0%; Score 15.2; DB 6; Length 542;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      406 AAGGAAACACGGACACTGAA 425

RESULT 50
US-09-925-065A-20386
; Sequence 20386, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243.096
```

```
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20386
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-20386

Query Match          76.0%; Score 15.2; DB 6; Length 550;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
Db 130 AAGGAAACACGACGACCTAA 149
```

```
RESULT 51
US-09-925-065A-482407
; Sequence 482407, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 482407
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-482407
```

```
Query Match          76.0%; Score 15.2; DB 6; Length 550;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
Db 136 AAGGAAACACTGTCTACCCAA 155
```

```
RESULT 52
US-09-925-065A-482408
; Sequence 482408, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 482408
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-482408
```

```
Query Match          76.0%; Score 15.2; DB 6; Length 550;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
Db 136 AAGGAAACACTGTCTACCCAA 155
```

```
RESULT 53
US-09-925-065A-138729
; Sequence 138729, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138729
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-138729
```

```
Query Match          76.0%; Score 15.2; DB 6; Length 560;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
Db 487 AAGGAAACACTGTCTACCCAA 506
```

```
RESULT 54
US-09-925-065A-99970/c
; Sequence 99970, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99970
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-99970

Query Match 76.0%; Score 15.2; DB 6; Length 580;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 256 AAGGAAACACGTCGACCCAA 237

RESULT 55

US-09-925-065A-412774
; Sequence 412774, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412774
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-412774

Query Match 76.0%; Score 15.2; DB 6; Length 580;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 11 AAGGAAACACACACACAA 30

RESULT 56

US-09-925-065A-794043/c
; Sequence 794043, Application US/09925065A

; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 794043
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-794043

Query Match 76.0%; Score 15.2; DB 6; Length 585;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 221 AAGGAGACAGGACACCGAA 202

RESULT 57

US-09-925-065A-436621
; Sequence 436621, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436621
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-436621

Query Match 76.0%; Score 15.2; DB 6; Length 597;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 564 AAGGAAACAGGGACACCCCA 583

QY 1 AAGGAAACACGGACACCCAA 20

```
Query Match          76.0%; Score 15.2; DB 6; Length 623;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 1 AAGGAAACACGGACACCCAA 20
 |||||
 Db 423 AAGGAAACACATACACAA 442

RESULT 62
 US-09-925-065A-820980
 ; Sequence 820980, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 820980
 ; LENGTH: 625
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-820980

Query Match 76.0%; Score 15.2; DB 6; Length 625;
 Best Local Similarity 85.0%; Pred. No. 5.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
 |||||
 Db 300 AAGAAACACACGGACACAA 319

RESULT 63
 US-09-925-065A-783213/c
 ; Sequence 783213, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 783213
 ; LENGTH: 633
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-783213

Query Match 76.0%; Score 15.2; DB 6; Length 633;
 Best Local Similarity 85.0%; Pred. No. 5.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
 |||||
 Db 365 AAGAAACACGGACACCA 346

RESULT 64
 US-09-925-065A-214200/c
 ; Sequence 214200, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 214200
 ; LENGTH: 650
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-214200

Query Match 76.0%; Score 15.2; DB 6; Length 650;
 Best Local Similarity 85.0%; Pred. No. 5.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
 |||||
 Db 641 AAGGAAAGACGACACCA 622

RESULT 65
 US-09-925-065A-529196
 ; Sequence 529196, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 529196
 ; LENGTH: 654
 ; TYPE: DNA

```
! ORGANISM: Homo sapiens
! US-09-925-065A-529196

Query Match      76.0%; Score 15.2; DB 6; Length 654;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 133 AAGGAGACACGGAAACTCAA 152

RESULT 66
US-09-925-065A-529197
! Sequence 529197, Application US/09925065A
! Publication No. US20040181048A1
! GENERAL INFORMATION:
! APPLICANT: Wang, David G.
! TITLE OF INVENTION: Identification and Mapping of Single
! TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
! FILE REFERENCE: 108827.135
! CURRENT APPLICATION NUMBER: US/09/925,065A
! CURRENT FILING DATE: 2001-08-08
! PRIOR APPLICATION NUMBER: US 60/243,096
! PRIOR FILING DATE: 2000-10-24
! PRIOR APPLICATION NUMBER: US 60/252,147
! PRIOR FILING DATE: 2000-11-20
! PRIOR APPLICATION NUMBER: US 60/250,092
! PRIOR FILING DATE: 2000-11-30
! PRIOR APPLICATION NUMBER: US 60/261,766
! PRIOR FILING DATE: 2001-01-16
! PRIOR APPLICATION NUMBER: US 60/289,846
! PRIOR FILING DATE: 2001-05-09
! NUMBER OF SEQ ID NOS: 957086
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 529197
! LENGTH: 654
! TYPE: DNA
! ORGANISM: Homo sapiens
! US-09-925-065A-529197

Query Match      76.0%; Score 15.2; DB 6; Length 654;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 133 AAGGAGACACGGAAACTCAA 152

RESULT 67
US-09-925-065A-192788
! Sequence 192788, Application US/09925065A
! Publication No. US20040181048A1
! GENERAL INFORMATION:
! APPLICANT: Wang, David G.
! TITLE OF INVENTION: Identification and Mapping of Single
! TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
! FILE REFERENCE: 108827.135
! CURRENT APPLICATION NUMBER: US/09/925,065A
! CURRENT FILING DATE: 2001-08-08
! PRIOR APPLICATION NUMBER: US 60/243,096
! PRIOR FILING DATE: 2000-10-24
! PRIOR APPLICATION NUMBER: US 60/252,147
! PRIOR FILING DATE: 2000-11-20
! PRIOR APPLICATION NUMBER: US 60/250,092
! PRIOR FILING DATE: 2000-11-30
! PRIOR APPLICATION NUMBER: US 60/261,766
! PRIOR FILING DATE: 2001-01-16
! PRIOR APPLICATION NUMBER: US 60/289,846
! PRIOR FILING DATE: 2001-05-09
! NUMBER OF SEQ ID NOS: 957086
! SOFTWARE: FastSeq for Windows Version 4.0

! SEQ ID NO 192788
! LENGTH: 674
! TYPE: DNA
! ORGANISM: Homo sapiens
! US-09-925-065A-192788

Query Match      76.0%; Score 15.2; DB 6; Length 674;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 186 AAGGAAACACGGACACTGAA 205

RESULT 68
US-09-925-065A-192789
! Sequence 192789, Application US/09925065A
! Publication No. US20040181048A1
! GENERAL INFORMATION:
! APPLICANT: Wang, David G.
! TITLE OF INVENTION: Identification and Mapping of Single
! TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
! FILE REFERENCE: 108827.135
! CURRENT APPLICATION NUMBER: US/09/925,065A
! CURRENT FILING DATE: 2001-08-08
! PRIOR APPLICATION NUMBER: US 60/243,096
! PRIOR FILING DATE: 2000-10-24
! PRIOR APPLICATION NUMBER: US 60/252,147
! PRIOR FILING DATE: 2000-11-20
! PRIOR APPLICATION NUMBER: US 60/250,092
! PRIOR FILING DATE: 2000-11-30
! PRIOR APPLICATION NUMBER: US 60/261,766
! PRIOR FILING DATE: 2001-01-16
! PRIOR APPLICATION NUMBER: US 60/289,846
! PRIOR FILING DATE: 2001-05-09
! NUMBER OF SEQ ID NOS: 957086
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 192789
! LENGTH: 674
! TYPE: DNA
! ORGANISM: Homo sapiens
! US-09-925-065A-192789

Query Match      76.0%; Score 15.2; DB 6; Length 674;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 186 AAGGAAACACGGACACTGAA 205

RESULT 69
US-09-925-065A-6885
! Sequence 6885, Application US/09925065A
! Publication No. US20040181048A1
! GENERAL INFORMATION:
! APPLICANT: Wang, David G.
! TITLE OF INVENTION: Identification and Mapping of Single
! TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
! FILE REFERENCE: 108827.135
! CURRENT APPLICATION NUMBER: US/09/925,065A
! CURRENT FILING DATE: 2001-08-08
! PRIOR APPLICATION NUMBER: US 60/243,096
! PRIOR FILING DATE: 2000-10-24
! PRIOR APPLICATION NUMBER: US 60/252,147
! PRIOR FILING DATE: 2000-11-20
! PRIOR APPLICATION NUMBER: US 60/250,092
! PRIOR FILING DATE: 2000-11-30
! PRIOR APPLICATION NUMBER: US 60/261,766
! PRIOR FILING DATE: 2001-01-16
! PRIOR APPLICATION NUMBER: US 60/289,846
! PRIOR FILING DATE: 2001-05-09
! NUMBER OF SEQ ID NOS: 957086
! SOFTWARE: FastSeq for Windows Version 4.0
```

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; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6885
; LENGTH: 766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-6885

Query Match          76.0%; Score 15.2; DB 6; Length 766;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
    ||||| ||||| ||||| |||||
Db 222 AAGGAACACTCACCCAA 241

RESULT 70
US-10-750-185-27789/c
; Sequence 27789, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27789
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866881436091
US-10-750-185-27789

Query Match          76.0%; Score 15.2; DB 8; Length 877;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
    ||||| ||||| ||||| |||||
Db 258 AAGGAACAGTTACCCAA 239

RESULT 71
US-10-750-623-27789/c
; Sequence 27789, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27789
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866881436091
US-10-750-623-27789

Query Match          76.0%; Score 15.2; DB 8; Length 877;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
    ||||| ||||| ||||| |||||
Db 258 AAGGAACAGTTACCCAA 239

RESULT 72
US-10-750-185-61482/c
; Sequence 61482, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61482
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Bovine 19866880980307
US-10-750-185-61482

Query Match          76.0%; Score 15.2; DB 8; Length 878;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
    ||||| ||||| ||||| |||||
Db 658 AGGAGACACGCGACTCCAA 639

RESULT 73
US-10-750-623-61482/c
; Sequence 61482, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61482
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Bovine 19866880980307
US-10-750-623-61482
```

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; ORGANISM: Bovine 19866880980307
US-10-750-623-61482

Query Match          76.0%; Score 15.2; DB 8; Length 878;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
Db 658 AGGGAGACACGGACTCCCAA 639

RESULT 74
US-09-925-065A-710787/c
; Sequence 710787, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 710787
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-710787

Query Match          76.0%; Score 15.2; DB 6; Length 925;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
Db 229 AAGGACACACACACCCAA 210

RESULT 75
US-09-925-065A-710788/c
; Sequence 710788, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 710788
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-710788

Query Match          76.0%; Score 15.2; DB 6; Length 925;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
Db 229 AAGGACACACACACCCAA 210

RESULT 76
US-09-925-065A-710789/c
; Sequence 710789, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 710789
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-710789

Query Match          76.0%; Score 15.2; DB 6; Length 925;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
Db 229 AAGGACACACACACCCAA 210

RESULT 77
US-09-925-065A-717601/c
; Sequence 717601, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
```

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; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717601
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-717601

Query Match          76.0%; Score 15.2; DB 6; Length 1125;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 619 AAGGAAACATTACCCAA 600

RESULT 78
US-09-925-065A-717602/c
; Sequence 717602, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717602
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-717602

Query Match          76.0%; Score 15.2; DB 6; Length 1125;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 619 AAGGAAACATTACCCAA 600

RESULT 79
US-10-750-185-59220/c
; Sequence 59220, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
```

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; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59220
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Bovine 19866881082830
US-10-750-185-59220

Query Match          76.0%; Score 15.2; DB 8; Length 1139;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 966 AAGGAAACAGACACACAA 947

RESULT 80
US-10-750-623-59220/c
; Sequence 59220, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59220
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Bovine 19866881082830
US-10-750-623-59220

Query Match          76.0%; Score 15.2; DB 8; Length 1139;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 966 AAGGAAACAGACACACAA 947

RESULT 81
US-10-932-182A-76110
; Sequence 76110, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76110
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
```

US-10-932-182A-76110

Query Match 76.0%; Score 15.2; DB 7; Length 1371;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 154 AATGAATACGGACACCTAA 173

RESULT 82

US-10-932-182A-76110
; Sequence 76110, Application US/10932182A
; Publication No. US20050046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 76110
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus

US-10-932-182A-76110

Query Match 76.0%; Score 15.2; DB 7; Length 1371;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 154 AATGAATACGGACACCTAA 173

RESULT 83

US-10-185-25747
; Sequence 25747, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25747
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Bovine 19866880936728

US-10-185-25747

Query Match 76.0%; Score 15.2; DB 8; Length 1619;
Best Local Similarity 85.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

Db 702 AAGAAACTCTGACACCCAA 721

RESULT 84

US-10-750-623-25747
; Sequence 25747, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25747
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Bovine 19866880936728

US-10-750-623-25747

Query Match 76.0%; Score 15.2; DB 8; Length 1619;
Best Local Similarity 85.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 702 AAGAAACTCTGACACCCAA 721

RESULT 85

US-10-185-33198/C
; Sequence 33198, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 33198
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Bovine 19866880641575

US-10-185-33198

Query Match 76.0%; Score 15.2; DB 8; Length 1816;
Best Local Similarity 85.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 1497 AAGGAAACACGGACACCCAA 1478

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RESULT 86
US-10-750-623-33198/c
; Sequence 33198, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33198
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Bovine 19866880775685
US-10-750-623-33198

Query Match      76.0%; Score 15.2; DB 8; Length 1816;
Best Local Similarity 85.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACCGGACACCCAA 20
      ||||| ||||| ||||| |||||
Db      1497 AAGGAAACCGGACACCCAA 1478

RESULT 87
US-10-750-185-31642
; Sequence 31642, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31642
; LENGTH: 2168
; TYPE: DNA
; ORGANISM: Bovine 19866880775685
US-10-750-185-31642

Query Match      76.0%; Score 15.2; DB 8; Length 2168;
Best Local Similarity 85.0%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACCGGACACCCAA 20
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Db      265 AAGGAAACCGGACACCCAA 284

RESULT 88
US-10-750-623-31642
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; Sequence 31642, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31642
; LENGTH: 2168
; TYPE: DNA
; ORGANISM: Bovine 19866880775685
US-10-750-623-31642

Query Match      76.0%; Score 15.2; DB 8; Length 2168;
Best Local Similarity 85.0%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACCGGACACCCAA 20
      ||||| ||||| ||||| |||||
Db      265 AAGGAAACCGGACACCCAA 284

RESULT 89
US-10-932-182A-1309/c
; Sequence 1309, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1309
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1309

Query Match      76.0%; Score 15.2; DB 7; Length 2406;
Best Local Similarity 85.0%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACCGGACACCCAA 20
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Db      892 AAGGAAACCGGACACCCAA 873

RESULT 90
US-10-932-182A-1309/c
; Sequence 1309, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
```

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; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1309
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1309

Query Match          76.0%; Score 15.2; DB 7; Length 2406;
Best Local Similarity 85.0%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 892 AAGGAAACCGGACCCAA 873

RESULT 91
US-09-925-065A-697075/c
; Sequence 697075, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697075
; LENGTH: 2590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-697075

Query Match          76.0%; Score 15.2; DB 6; Length 2590;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 2581 AAGGAAACACGACATTCAA 2562

RESULT 92
US-09-925-065A-697076/c
; Sequence 697076, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697076
; LENGTH: 2590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-697076

Query Match          76.0%; Score 15.2; DB 6; Length 2590;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 2581 AAGGAAACACGACATTCAA 2562

RESULT 93
US-10-750-185-54418/c
; Sequence 54418, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54418
; LENGTH: 2828
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-54418

Query Match          76.0%; Score 15.2; DB 8; Length 2828;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 245 AAGGAAACATGCGACCCAA 226

RESULT 94
US-10-750-623-54418/c
; Sequence 54418, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
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; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54418
; LENGTH: 2828
; TYPE: DNA
; ORGANISM: Bovine 19866880791558
US-10-750-623-54418

Query Match      76.0%; Score 15.2; DB 8; Length 2828;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 245 AAGGAACACTGCCACCAA 226

RESULT 95
US-10-330-773-916/c
; Sequence 916, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 916
; LENGTH: 23367
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(23367)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-916

Query Match      76.0%; Score 15.2; DB 7; Length 23367;
Best Local Similarity 85.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 12303 AAGGAACACGGACAGACAA 12284

RESULT 96
US-10-330-773-829/c
; Sequence 829, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 829
; LENGTH: 123331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)...(123331)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-829

Query Match      76.0%; Score 15.2; DB 7; Length 123331;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 32548 AAGGAATATGGACACCAA 32529

RESULT 97
US-11-121-086-75
; Sequence 75, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 161874
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-75

Query Match      76.0%; Score 15.2; DB 12; Length 161874;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 51954 AAGGAACACGTCACAGCAA 51973

RESULT 98
US-11-121-086-85
; Sequence 85, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 171423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-85

Query Match      76.0%; Score 15.2; DB 12; Length 171423;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 36823 AAGGAACACTGCACAGCAA 36842
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Search completed: March 9, 2006, 01:19:05
Job time : 448.728 secs

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RESULT 99
US-11-091-018-1/c
; Sequence 1, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Greta Sottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1691140)
; OTHER INFORMATION: n=A,T,C or G
US-11-091-018-1

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Query Match 76.0%; Score 15.2; DB 12; Length 1691140;
Best Local Similarity 85.0%; Pred. No. 9.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACCGACCCCAA 20
Db 1440757 AAGGAACACCGACCCCAA 1440738

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RESULT 100
US-10-995-561-51045/c
; Sequence 51045, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51045
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-51045

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Query Match 75.0%; Score 15; DB 8; Length 201;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACACCGACCCCAA 20
Db 108 GAACACCGACCCCAA 92

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:15:52 ; Search time 580.194 Seconds
(without alignments)
285.056 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaacacggacacccaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications NA Main.*

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	9	US-10-829-474-2
2	20	100.0	21	9	US-10-829-474-25
3	20	100.0	21	9	US-10-829-474-26
4	20	100.0	26	9	US-10-829-474-27
C 5	20	100.0	107	9	US-10-760-048-53
C 6	20	100.0	110	9	US-10-760-048-52
C 7	20	100.0	126	9	US-10-760-048-18
C 8	20	100.0	236	9	US-10-760-048-55
C 9	20	100.0	237	9	US-10-760-048-21
C 10	20	100.0	237	9	US-10-760-048-44
C 11	20	100.0	237	9	US-10-760-048-45
C 12	20	100.0	237	9	US-10-760-048-56
C 13	20	100.0	237	9	US-10-760-048-57
C 14	20	100.0	237	9	US-10-760-048-59
C 15	20	100.0	237	9	US-10-760-048-60
C 16	20	100.0	237	9	US-10-760-048-63
C 17	20	100.0	237	9	US-10-760-048-64
C 18	20	100.0	237	9	US-10-760-048-66
C 19	20	100.0	238	9	US-10-760-048-15
C 20	20	100.0	238	9	US-10-760-048-30
C 21	20	100.0	238	9	US-10-760-048-31
C 22	20	100.0	238	9	US-10-760-048-33
C 23	20	100.0	238	9	US-10-760-048-33

C 24	20	100.0	238	9	US-10-760-048-38	Sequence 38, Appl
C 25	20	100.0	238	9	US-10-760-048-42	Sequence 42, Appl
C 26	20	100.0	238	9	US-10-760-048-43	Sequence 43, Appl
C 27	20	100.0	238	9	US-10-760-048-46	Sequence 46, Appl
C 28	20	100.0	238	9	US-10-760-048-47	Sequence 47, Appl
C 29	20	100.0	238	9	US-10-760-048-48	Sequence 48, Appl
C 30	20	100.0	238	9	US-10-760-048-58	Sequence 58, Appl
C 31	20	100.0	238	9	US-10-760-048-61	Sequence 61, Appl
C 32	20	100.0	238	9	US-10-760-048-65	Sequence 65, Appl
C 33	20	100.0	709	9	US-10-614-283-1	Sequence 1, Appl
C 34	20	100.0	743	8	US-10-839-729-21	Sequence 21, Appl
C 35	20	100.0	745	8	US-10-489-136-10	Sequence 10, Appl
C 36	20	100.0	2076	3	US-03-884-586A-3	Sequence 3, Appl
C 37	20	100.0	10448	6	US-10-408-456-4	Sequence 4, Appl
C 38	20	100.0	11058	6	US-10-408-456-5	Sequence 5, Appl
C 39	20	100.0	11622	6	US-10-408-456-34	Sequence 34, Appl
C 40	20	100.0	11622	8	US-10-873-573-7	Sequence 7, Appl
C 41	19.6	100.0	62	6	US-10-366-823-5	Sequence 5, Appl
C 42	19.2	100.0	53	6	US-10-408-519-3	Sequence 3, Appl
C 43	19	95.0	19	9	US-10-829-474-21	Sequence 21, Appl
C 44	19	95.0	19	9	US-10-829-474-22	Sequence 22, Appl
C 45	19	95.0	238	9	US-10-760-048-34	Sequence 34, Appl
C 46	19	95.0	238	9	US-10-760-048-35	Sequence 35, Appl
C 47	19	95.0	238	9	US-10-760-048-36	Sequence 36, Appl
C 48	19	95.0	238	9	US-10-760-048-62	Sequence 62, Appl
C 49	19	95.0	521	7	US-10-332-123-53	Sequence 53, Appl
C 50	18.4	92.0	235	9	US-10-760-048-41	Sequence 41, Appl
C 51	18.4	92.0	236	9	US-10-760-048-37	Sequence 37, Appl
C 52	18.4	92.0	237	9	US-10-760-048-16	Sequence 16, Appl
C 53	18.4	92.0	237	9	US-10-760-048-52	Sequence 52, Appl
C 54	18.4	92.0	238	9	US-10-760-048-14	Sequence 14, Appl
C 55	18.4	92.0	238	9	US-10-760-048-19	Sequence 19, Appl
C 56	18.4	92.0	238	9	US-10-760-048-23	Sequence 23, Appl
C 57	18.4	92.0	238	9	US-10-760-048-25	Sequence 25, Appl
C 58	18.4	92.0	238	9	US-10-760-048-26	Sequence 26, Appl
C 59	18.4	92.0	238	9	US-10-760-048-27	Sequence 27, Appl
C 60	18.4	92.0	238	9	US-10-760-048-28	Sequence 28, Appl
C 61	18.4	92.0	238	9	US-10-760-048-29	Sequence 29, Appl
C 62	18.4	92.0	520	7	US-10-332-123-54	Sequence 54, Appl
C 63	18.4	92.0	7399	6	US-10-136-819-7	Sequence 7, Appl
C 64	18	90.0	18	9	US-10-829-474-17	Sequence 17, Appl
C 65	18	90.0	18	9	US-10-829-474-18	Sequence 18, Appl
C 66	18	90.0	18	9	US-10-829-474-20	Sequence 20, Appl
C 67	18	90.0	225734	7	US-10-322-696-13	Sequence 13, Appl
C 68	17.8	89.0	40	9	US-10-760-048-10	Sequence 10, Appl
C 69	17	85.0	17	9	US-10-829-474-23	Sequence 23, Appl
C 70	17	85.0	17	9	US-10-829-474-24	Sequence 24, Appl
C 71	17	85.0	20	8	US-10-938-005-4	Sequence 4, Appl
C 72	17	85.0	21	6	US-10-179-082A-3	Sequence 3, Appl
C 73	17	85.0	21	6	US-10-938-005-3	Sequence 3, Appl
C 74	17	85.0	33	6	US-10-175-247-20	Sequence 20, Appl
C 75	17	85.0	40	9	US-10-760-048-9	Sequence 9, Appl
C 76	17	85.0	92	8	US-10-938-005-9	Sequence 9, Appl
C 77	17	85.0	117	9	US-10-760-048-39	Sequence 39, Appl
C 78	17	85.0	117	9	US-10-760-048-40	Sequence 40, Appl
C 79	17	85.0	627	5	US-10-104-611-31	Sequence 31, Appl
C 80	17	85.0	627	5	US-10-112-547-31	Sequence 31, Appl
C 81	17	85.0	627	5	US-10-112-241-31	Sequence 31, Appl
C 82	17	85.0	627	6	US-10-109-368-31	Sequence 31, Appl
C 83	17	85.0	627	8	US-10-867-798-31	Sequence 31, Appl
C 84	16.8	84.0	230	8	US-10-425-115-173501	Sequence 173501, Appl
C 85	16.8	84.0	238	9	US-10-760-048-12	Sequence 12, Appl
C 86	16.8	84.0	238	9	US-10-760-048-22	Sequence 22, Appl
C 87	16.8	84.0	238	9	US-10-760-048-24	Sequence 24, Appl
C 88	16.8	84.0	370	9	US-10-950-009-1102	Sequence 1102, Appl
C 89	16.8	84.0	585	4	US-09-925-065A-156382	Sequence 156382, Appl
C 90	16.8	84.0	585	4	US-09-925-065A-156383	Sequence 156383, Appl
C 91	16.8	84.0	660	4	US-10-760-048-67	Sequence 67, Appl
C 92	16.8	84.0	906	8	US-10-363-345A-23361	Sequence 23361, A
C 93	16.8	84.0	906	8	US-10-363-345A-23362	Sequence 23362, A
C 94	16.8	84.0	906	9	US-10-363-483A-23361	Sequence 23361, A
C 95	16.8	84.0	906	9	US-10-363-483A-23362	Sequence 23362, A
C 96	16.8	84.0	147300	9	US-10-723-681-3	Sequence 3, Appl

97	16.4	82.0	578	4	US-09-925-065A-319374	Sequence 319374, App	c 170	15.4	77.0	2690	3	US-09-978-192A-514	Sequence 514, App
c 98	16.4	82.0	47493	7	US-10-052-482-55	Sequence 55, Appl	c 171	15.4	77.0	2690	3	US-09-999-832A-514	Sequence 514, App
99	16	80.0	16	9	US-10-829-474-19	Sequence 19, Appl	c 172	15.4	77.0	2690	3	US-09-978-189-514	Sequence 514, App
100	16	80.0	484	8	US-10-425-115-83354	Sequence 83354, A	c 173	15.4	77.0	2690	3	US-09-978-608A-514	Sequence 514, App
c 101	15.8	79.0	169	4	US-09-925-065A-187976	Sequence 187976, A	c 174	15.4	77.0	2690	3	US-09-978-585A-514	Sequence 514, App
c 102	15.8	79.0	201	8	US-10-719-993-25361	Sequence 25361, A	c 175	15.4	77.0	2690	3	US-09-978-191A-514	Sequence 514, App
c 103	15.8	79.0	201	8	US-10-719-993-40170	Sequence 40170, A	c 176	15.4	77.0	2690	3	US-09-978-403A-514	Sequence 514, App
c 104	15.8	79.0	212	7	US-10-437-963-46575	Sequence 46575, A	c 177	15.4	77.0	2690	3	US-09-978-564A-514	Sequence 514, App
c 105	15.8	79.0	357	8	US-10-425-115-50529	Sequence 50529, A	c 178	15.4	77.0	2690	3	US-09-999-833A-514	Sequence 514, App
c 106	15.8	79.0	377	7	US-10-424-599-63366	Sequence 63366, A	c 179	15.4	77.0	2690	3	US-09-981-915A-514	Sequence 514, App
c 107	15.8	79.0	385	7	US-10-437-963-71490	Sequence 71490, A	c 180	15.4	77.0	2690	3	US-09-978-824-514	Sequence 514, App
c 108	15.8	79.0	385	8	US-10-425-115-108968	Sequence 108968, A	c 181	15.4	77.0	2690	3	US-09-918-585A-514	Sequence 514, App
c 109	15.8	79.0	449	4	US-09-925-065A-527437	Sequence 527437, A	c 182	15.4	77.0	2690	3	US-09-999-834A-514	Sequence 514, App
c 110	15.8	79.0	449	4	US-09-925-065A-527438	Sequence 527438, A	c 183	15.4	77.0	2690	3	US-09-978-423A-514	Sequence 514, App
c 111	15.8	79.0	470	9	US-10-972-079-92721	Sequence 92721, A	c 184	15.4	77.0	2690	3	US-09-978-193A-514	Sequence 514, App
c 112	15.8	79.0	500	4	US-09-925-065A-287845	Sequence 287845, A	c 185	15.4	77.0	2690	3	US-09-999-830A-514	Sequence 514, App
c 113	15.8	79.0	532	4	US-09-925-065A-216395	Sequence 216395, A	c 186	15.4	77.0	2690	3	US-09-978-757A-514	Sequence 514, App
c 114	15.8	79.0	532	6	US-10-029-386-10669	Sequence 10669, A	c 187	15.4	77.0	2690	3	US-09-978-187B-514	Sequence 514, App
c 115	15.8	79.0	560	4	US-09-925-065A-187867	Sequence 187867, A	c 188	15.4	77.0	2690	3	US-09-978-643A-514	Sequence 514, App
c 116	15.8	79.0	595	5	US-10-027-632-285012	Sequence 285012, A	c 189	15.4	77.0	2690	3	US-09-978-375A-514	Sequence 514, App
c 117	15.8	79.0	595	6	US-10-027-632-285012	Sequence 285012, A	c 190	15.4	77.0	2690	3	US-09-978-298A-514	Sequence 514, App
c 118	15.8	79.0	612	5	US-10-027-632-230060	Sequence 230060, A	c 191	15.4	77.0	2690	3	US-09-978-188A-514	Sequence 514, App
c 119	15.8	79.0	612	6	US-10-027-632-230060	Sequence 230060, A	c 192	15.4	77.0	2690	3	US-09-978-681A-514	Sequence 514, App
c 120	15.8	79.0	634	4	US-09-925-065A-708503	Sequence 708503, A	c 193	15.4	77.0	2690	3	US-09-999-829A-514	Sequence 514, App
c 121	15.8	79.0	634	4	US-09-925-065A-136278	Sequence 136278, A	c 194	15.4	77.0	2690	3	US-09-978-824-514	Sequence 514, App
c 122	15.8	79.0	647	4	US-09-925-065A-879054	Sequence 879054, A	c 195	15.4	77.0	2690	3	US-09-978-299A-514	Sequence 514, App
c 123	15.8	79.0	660	3	US-09-778-320-224	Sequence 224, App	c 196	15.4	77.0	2690	3	US-09-978-544A-514	Sequence 514, App
c 124	15.8	79.0	660	3	US-09-910-689-224	Sequence 224, App	c 197	15.4	77.0	2690	3	US-09-978-665A-514	Sequence 514, App
c 125	15.8	79.0	660	5	US-10-010-742-224	Sequence 224, App	c 198	15.4	77.0	2690	3	US-09-978-802A-514	Sequence 514, App
c 126	15.8	79.0	660	7	US-10-714-389-224	Sequence 224, App	c 199	15.4	77.0	2690	3	US-09-999-831A-514	Sequence 514, App
c 127	15.8	79.0	660	7	US-10-717-296-224	Sequence 224, App	c 200	15.4	77.0	2690	3	US-09-978-824-514	Sequence 514, App
c 128	15.8	79.0	807	7	US-10-424-599-94135	Sequence 94135, A	c 201	15.4	77.0	2690	5	US-10-052-586-35	Sequence 35, Appl
c 129	15.8	79.0	963	4	US-09-925-065A-722637	Sequence 722637, A	c 202	15.4	77.0	2690	5	US-10-174-590-35	Sequence 35, Appl
c 130	15.8	79.0	1013	7	US-10-437-963-38704	Sequence 38704, A	c 203	15.4	77.0	2690	5	US-10-176-758-35	Sequence 35, Appl
c 131	15.8	79.0	1463	4	US-09-925-065A-65977	Sequence 65977, A	c 204	15.4	77.0	2690	5	US-10-175-737-35	Sequence 35, Appl
c 132	15.8	79.0	1616	7	US-10-437-963-98627	Sequence 98627, A	c 205	15.4	77.0	2690	5	US-10-176-481-35	Sequence 35, Appl
c 133	15.8	79.0	1817	3	US-09-452-599-1	Sequence 1, Appl	c 206	15.4	77.0	2690	5	US-10-176-483-35	Sequence 35, Appl
c 134	15.8	79.0	1817	6	US-10-121-120-1	Sequence 1, Appl	c 207	15.4	77.0	2690	5	US-10-176-749-35	Sequence 35, Appl
c 135	15.8	79.0	1817	8	US-10-121-120-1	Sequence 1, Appl	c 208	15.4	77.0	2690	5	US-10-176-914-35	Sequence 35, Appl
c 136	15.8	79.0	1936	8	US-10-739-930-4243	Sequence 4243, Ap	c 209	15.4	77.0	2690	5	US-10-176-915-35	Sequence 35, Appl
c 137	15.8	79.0	2328	7	US-10-437-963-48056	Sequence 48056, A	c 210	15.4	77.0	2690	5	US-10-173-706-35	Sequence 35, Appl
c 138	15.8	79.0	2364	10	US-11-097-143-42710	Sequence 42710, A	c 211	15.4	77.0	2690	5	US-10-175-738-35	Sequence 35, Appl
c 139	15.8	79.0	4670	10	US-11-097-143-42709	Sequence 42709, A	c 212	15.4	77.0	2690	5	US-10-175-752-35	Sequence 35, Appl
c 140	15.8	79.0	4951	3	US-09-070-927A-261	Sequence 261, App	c 213	15.4	77.0	2690	5	US-10-176-482-35	Sequence 35, Appl
c 141	15.8	79.0	12590	8	US-10-719-993-6975	Sequence 6975, Ap	c 214	15.4	77.0	2690	5	US-10-176-757-35	Sequence 35, Appl
c 142	15.8	79.0	70780	8	US-10-719-993-6819	Sequence 6819, Ap	c 215	15.4	77.0	2690	5	US-10-176-913-35	Sequence 35, Appl
c 143	15.8	79.0	175590	3	US-09-911-077A-13	Sequence 13, Appl	c 216	15.4	77.0	2690	5	US-10-180-552-35	Sequence 35, Appl
c 144	15.8	79.0	175590	8	US-10-724-806-13	Sequence 13, Appl	c 217	15.4	77.0	2690	5	US-10-180-557-35	Sequence 35, Appl
c 145	15.8	79.0	204621	5	US-10-087-192-958	Sequence 958, App	c 218	15.4	77.0	2690	5	US-10-173-700-35	Sequence 35, Appl
c 146	15.8	79.0	290367	8	US-10-719-993-6887	Sequence 6887, Ap	c 219	15.4	77.0	2690	5	US-10-174-572-35	Sequence 35, Appl
c 147	15.8	79.0	374849	8	US-10-087-192-1627	Sequence 1627, Ap	c 220	15.4	77.0	2690	5	US-10-174-579-35	Sequence 35, Appl
c 148	15.4	77.0	236	9	US-10-760-048-49	Sequence 49, Appl	c 221	15.4	77.0	2690	5	US-10-174-582-35	Sequence 35, Appl
c 149	15.4	77.0	236	9	US-10-760-048-50	Sequence 50, Appl	c 222	15.4	77.0	2690	5	US-10-174-588-35	Sequence 35, Appl
c 150	15.4	77.0	236	9	US-10-760-048-51	Sequence 51, Appl	c 223	15.4	77.0	2690	5	US-10-175-739-35	Sequence 35, Appl
c 151	15.4	77.0	355	7	US-10-424-599-70907	Sequence 70907, A	c 224	15.4	77.0	2690	5	US-10-175-740-35	Sequence 35, Appl
c 152	15.4	77.0	372	7	US-10-424-599-124060	Sequence 124060, A	c 225	15.4	77.0	2690	5	US-10-175-743-35	Sequence 35, Appl
c 153	15.4	77.0	478	8	US-10-425-115-5826	Sequence 5826, Ap	c 226	15.4	77.0	2690	5	US-10-176-488-35	Sequence 35, Appl
c 154	15.4	77.0	525	7	US-09-332-123-55	Sequence 55, Appl	c 227	15.4	77.0	2690	5	US-10-176-492-35	Sequence 35, Appl
c 155	15.4	77.0	537	4	US-09-925-065A-366331	Sequence 366331, A	c 228	15.4	77.0	2690	5	US-10-176-497-35	Sequence 35, Appl
c 156	15.4	77.0	537	4	US-09-925-065A-366333	Sequence 366333, A	c 229	15.4	77.0	2690	5	US-10-176-750-35	Sequence 35, Appl
c 157	15.4	77.0	620	4	US-09-925-065A-544937	Sequence 544937, A	c 230	15.4	77.0	2690	5	US-10-176-985-35	Sequence 35, Appl
c 158	15.4	77.0	632	8	US-10-363-345A-27321	Sequence 27321, A	c 231	15.4	77.0	2690	5	US-10-176-987-35	Sequence 35, Appl
c 159	15.4	77.0	632	8	US-10-363-345A-27322	Sequence 27322, A	c 232	15.4	77.0	2690	5	US-10-176-992-35	Sequence 35, Appl
c 160	15.4	77.0	632	9	US-10-363-483A-27321	Sequence 27321, A	c 233	15.4	77.0	2690	5	US-10-176-993-35	Sequence 35, Appl
c 161	15.4	77.0	632	9	US-10-363-483A-27322	Sequence 27322, A	c 234	15.4	77.0	2690	5	US-10-184-658-35	Sequence 35, Appl
c 162	15.4	77.0	657	5	US-10-027-632-25021	Sequence 25021, A	c 235	15.4	77.0	2690	5	US-10-176-991-35	Sequence 35, Appl
c 163	15.4	77.0	657	6	US-10-027-632-25021	Sequence 25021, A	c 236	15.4	77.0	2690	5	US-10-173-695-35	Sequence 35, Appl
c 164	15.4	77.0	1663	7	US-10-437-963-643	Sequence 643, App	c 237	15.4	77.0	2690	5	US-10-173-697-35	Sequence 35, Appl
c 165	15.4	77.0	1781	9	US-10-487-078-141	Sequence 141, App	c 238	15.4	77.0	2690	5	US-10-173-705-35	Sequence 35, Appl
c 166	15.4	77.0	2667	8	US-10-643-795A-50	Sequence 50, Appl	c 239	15.4	77.0	2690	5	US-10-174-576-35	Sequence 35, Appl
c 167	15.4	77.0	2667	9	US-10-948-518-50	Sequence 50, Appl	c 240	15.4	77.0	2690	5	US-10-174-585-35	Sequence 35, Appl
c 168	15.4	77.0	2690	3	US-09-978-295A-514	Sequence 514, App	c 241	15.4	77.0	2690	5	US-10-174-586-35	Sequence 35, Appl
c 169	15.4	77.0	2690	3	US-09-978-295A-514	Sequence 514, App	c 242	15.4	77.0	2690	5	US-10-175-747-35	Sequence 35, Appl

C 389	15.4	77.0	2690	5	US-10-198-764-35	Sequence 35, Appl
C 390	15.4	77.0	2690	5	US-10-198-765-35	Sequence 35, Appl
C 391	15.4	77.0	2690	5	US-10-198-768-35	Sequence 35, Appl
C 392	15.4	77.0	2690	5	US-10-198-769-35	Sequence 35, Appl
C 393	15.4	77.0	2690	5	US-10-199-305-35	Sequence 35, Appl
C 394	15.4	77.0	2690	5	US-10-199-306-35	Sequence 35, Appl
C 395	15.4	77.0	2690	5	US-10-199-310-35	Sequence 35, Appl
C 396	15.4	77.0	2690	5	US-10-199-311-35	Sequence 35, Appl
C 397	15.4	77.0	2690	5	US-10-199-314-35	Sequence 35, Appl
C 398	15.4	77.0	2690	5	US-10-199-317-35	Sequence 35, Appl
C 399	15.4	77.0	2690	5	US-10-199-665-35	Sequence 35, Appl
C 400	15.4	77.0	2690	5	US-10-199-666-35	Sequence 35, Appl
C 401	15.4	77.0	2690	5	US-10-199-669-35	Sequence 35, Appl
C 402	15.4	77.0	2690	5	US-10-201-534-35	Sequence 35, Appl
C 403	15.4	77.0	2690	5	US-10-201-770-35	Sequence 35, Appl
C 404	15.4	77.0	2690	5	US-10-201-855-35	Sequence 35, Appl
C 405	15.4	77.0	2690	5	US-10-201-856-35	Sequence 35, Appl
C 406	15.4	77.0	2690	5	US-10-202-469-35	Sequence 35, Appl
C 407	15.4	77.0	2690	5	US-10-202-470-35	Sequence 35, Appl
C 408	15.4	77.0	2690	5	US-10-202-476-35	Sequence 35, Appl
C 409	15.4	77.0	2690	5	US-10-202-934-35	Sequence 35, Appl
C 410	15.4	77.0	2690	5	US-10-202-935-35	Sequence 35, Appl
C 411	15.4	77.0	2690	5	US-10-202-936-35	Sequence 35, Appl
C 412	15.4	77.0	2690	5	US-10-202-939-35	Sequence 35, Appl
C 413	15.4	77.0	2690	5	US-10-205-504-35	Sequence 35, Appl
C 414	15.4	77.0	2690	5	US-10-205-509-35	Sequence 35, Appl
C 415	15.4	77.0	2690	5	US-10-205-895-35	Sequence 35, Appl
C 416	15.4	77.0	2690	5	US-10-205-899-35	Sequence 35, Appl
C 417	15.4	77.0	2690	5	US-10-205-900-35	Sequence 35, Appl
C 418	15.4	77.0	2690	5	US-10-205-903-35	Sequence 35, Appl
C 419	15.4	77.0	2690	5	US-10-195-890-35	Sequence 35, Appl
C 420	15.4	77.0	2690	5	US-10-183-002-35	Sequence 35, Appl
C 421	15.4	77.0	2690	5	US-10-184-621-35	Sequence 35, Appl
C 422	15.4	77.0	2690	5	US-10-184-638-35	Sequence 35, Appl
C 423	15.4	77.0	2690	5	US-10-187-752-35	Sequence 35, Appl
C 424	15.4	77.0	2690	5	US-10-187-861-35	Sequence 35, Appl
C 425	15.4	77.0	2690	5	US-10-194-461-35	Sequence 35, Appl
C 426	15.4	77.0	2690	5	US-10-195-892-35	Sequence 35, Appl
C 427	15.4	77.0	2690	5	US-10-196-751-35	Sequence 35, Appl
C 428	15.4	77.0	2690	5	US-10-197-694-35	Sequence 35, Appl
C 429	15.4	77.0	2690	5	US-10-197-697-35	Sequence 35, Appl
C 430	15.4	77.0	2690	5	US-10-197-707-35	Sequence 35, Appl
C 431	15.4	77.0	2690	5	US-10-199-303-35	Sequence 35, Appl
C 432	15.4	77.0	2690	5	US-10-199-318-35	Sequence 35, Appl
C 433	15.4	77.0	2690	5	US-10-199-458-35	Sequence 35, Appl
C 434	15.4	77.0	2690	5	US-10-199-462-35	Sequence 35, Appl
C 435	15.4	77.0	2690	5	US-10-201-324-35	Sequence 35, Appl
C 436	15.4	77.0	2690	5	US-10-201-328-35	Sequence 35, Appl
C 437	15.4	77.0	2690	5	US-10-201-527-35	Sequence 35, Appl
C 438	15.4	77.0	2690	5	US-10-201-528-35	Sequence 35, Appl
C 439	15.4	77.0	2690	5	US-10-201-529-35	Sequence 35, Appl
C 440	15.4	77.0	2690	5	US-10-201-530-35	Sequence 35, Appl
C 441	15.4	77.0	2690	5	US-10-202-408-35	Sequence 35, Appl
C 442	15.4	77.0	2690	5	US-10-202-409-35	Sequence 35, Appl
C 443	15.4	77.0	2690	5	US-10-202-411-35	Sequence 35, Appl
C 444	15.4	77.0	2690	5	US-10-202-472-35	Sequence 35, Appl
C 445	15.4	77.0	2690	5	US-10-205-502-35	Sequence 35, Appl
C 446	15.4	77.0	2690	5	US-10-205-507-35	Sequence 35, Appl
C 447	15.4	77.0	2690	5	US-10-205-511-35	Sequence 35, Appl
C 448	15.4	77.0	2690	5	US-10-205-902-35	Sequence 35, Appl
C 449	15.4	77.0	2690	5	US-10-205-907-35	Sequence 35, Appl
C 450	15.4	77.0	2690	5	US-10-167-749-514	Sequence 514, Appl
C 451	15.4	77.0	2690	5	US-10-176-484-35	Sequence 35, Appl
C 452	15.4	77.0	2690	5	US-10-194-456-35	Sequence 35, Appl
C 453	15.4	77.0	2690	5	US-10-196-758-35	Sequence 35, Appl
C 454	15.4	77.0	2690	5	US-10-198-770-35	Sequence 35, Appl
C 455	15.4	77.0	2690	5	US-10-199-308-35	Sequence 35, Appl
C 456	15.4	77.0	2690	5	US-10-200-617-35	Sequence 35, Appl
C 457	15.4	77.0	2690	5	US-10-205-893-35	Sequence 35, Appl
C 458	15.4	77.0	2690	5	US-10-205-897-35	Sequence 35, Appl
C 459	15.4	77.0	2690	5	US-10-195-896-35	Sequence 35, Appl
C 460	15.4	77.0	2690	5	US-10-180-550-35	Sequence 35, Appl
C 461	15.4	77.0	2690	5	US-10-183-014-35	Sequence 35, Appl

C 462	15.4	77.0	2690	5	US-10-187-738-35	Sequence 35, Appl
C 463	15.4	77.0	2690	5	US-10-187-740-35	Sequence 35, Appl
C 464	15.4	77.0	2690	5	US-10-187-883-35	Sequence 35, Appl
C 465	15.4	77.0	2690	5	US-10-194-363-35	Sequence 35, Appl
C 466	15.4	77.0	2690	5	US-10-194-460-35	Sequence 35, Appl
C 467	15.4	77.0	2690	5	US-10-194-463-35	Sequence 35, Appl
C 468	15.4	77.0	2690	5	US-10-194-484-35	Sequence 35, Appl
C 469	15.4	77.0	2690	5	US-10-195-884-35	Sequence 35, Appl
C 470	15.4	77.0	2690	5	US-10-196-744-35	Sequence 35, Appl
C 471	15.4	77.0	2690	5	US-10-196-755-35	Sequence 35, Appl
C 472	15.4	77.0	2690	5	US-10-197-704-35	Sequence 35, Appl
C 473	15.4	77.0	2690	5	US-10-197-710-35	Sequence 35, Appl
C 474	15.4	77.0	2690	5	US-10-198-758-35	Sequence 35, Appl
C 475	15.4	77.0	2690	5	US-10-198-766-35	Sequence 35, Appl
C 476	15.4	77.0	2690	5	US-10-199-304-35	Sequence 35, Appl
C 477	15.4	77.0	2690	5	US-10-199-309-35	Sequence 35, Appl
C 478	15.4	77.0	2690	5	US-10-199-313-35	Sequence 35, Appl
C 479	15.4	77.0	2690	5	US-10-199-456-35	Sequence 35, Appl
C 480	15.4	77.0	2690	5	US-10-201-329-35	Sequence 35, Appl
C 481	15.4	77.0	2690	5	US-10-202-412-35	Sequence 35, Appl
C 482	15.4	77.0	2690	5	US-10-206-919-35	Sequence 35, Appl
C 483	15.4	77.0	2690	5	US-10-206-922-35	Sequence 35, Appl
C 484	15.4	77.0	2690	5	US-10-206-924-35	Sequence 35, Appl
C 485	15.4	77.0	2690	5	US-10-206-928-35	Sequence 35, Appl
C 486	15.4	77.0	2690	5	US-10-207-914-35	Sequence 35, Appl
C 487	15.4	77.0	2690	5	US-10-207-921-35	Sequence 35, Appl
C 488	15.4	77.0	2690	5	US-10-207-922-35	Sequence 35, Appl
C 489	15.4	77.0	2690	5	US-10-208-027-35	Sequence 35, Appl
C 490	15.4	77.0	2690	5	US-10-196-757-35	Sequence 35, Appl
C 491	15.4	77.0	2690	5	US-10-196-754-35	Sequence 35, Appl
C 492	15.4	77.0	2690	5	US-10-013-921A-514	Sequence 514, Appl
C 493	15.4	77.0	2690	5	US-10-174-571-35	Sequence 35, Appl
C 494	15.4	77.0	2690	5	US-10-176-746-35	Sequence 35, Appl
C 495	15.4	77.0	2690	5	US-10-176-923-35	Sequence 35, Appl
C 496	15.4	77.0	2690	5	US-10-183-011-35	Sequence 35, Appl
C 497	15.4	77.0	2690	5	US-10-184-633-35	Sequence 35, Appl
C 498	15.4	77.0	2690	5	US-10-184-639-35	Sequence 35, Appl
C 499	15.4	77.0	2690	5	US-10-187-742-35	Sequence 35, Appl
C 500	15.4	77.0	2690	10	US-11-129-762-514	Sequence 514, Appl

ALIGNMENTS

RESULT 1
US-10-829-474-2
; Sequence 2, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: GENETICS & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-2

Query Match		100.0%;	Score 20;	DB 9;	Length 20;
Best Local Similarity		100.0%;	Pred. No. 6.8;		
Matches		20;	Conservative	0;	Mismatches
				0;	Indels
				0;	Gaps
				0;	
Qy	1	AAGGAAACACGGACACCAA	20		
Db	1	AAGGAAACACGGACACCAA	20		

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RESULT 2
US-10-829-474-25
; Sequence 25, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-25

Query Match      100.0%; Score 20; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 1 AAGGAAACACGGACACCCAA 20

RESULT 3
US-10-829-474-26
; Sequence 26, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-26

Query Match      100.0%; Score 20; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 2 AAGGAAACACGGACACCCAA 21

RESULT 4
US-10-829-474-27
; Sequence 27, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
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; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-27

Query Match      100.0%; Score 20; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 7 AAGGAAACACGGACACCCAA 26

RESULT 5
US-10-760-048-53/c
; Sequence 53, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 53
; LENGTH: 107
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-53

Query Match      100.0%; Score 20; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 102 AAGGAAACACGGACACCCAA 83

RESULT 6
US-10-760-048-52/c
; Sequence 52, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 52
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
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Ov 1 AAGGAAACACGGAC

; FUNCTION NO: 0520
: GENERAL INFORMATION:
: GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 45
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-45

Query Match 100.0%; Score 20; DB 9; Length 237;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 12

US-10-760-048-56/c
; Sequence 56, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 56
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-56

Query Match 100.0%; Score 20; DB 9; Length 237;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 13

US-10-760-048-57/c
; Sequence 57, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 57
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-57

Query Match 100.0%; Score 20; DB 9; Length 237;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 14

US-10-760-048-59/c
; Sequence 59, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 59
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-59

Query Match 100.0%; Score 20; DB 9; Length 237;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 15

US-10-760-048-60/c
; Sequence 60, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 60
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-60

FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 15
LENGTH: 238
TYPE: DNA
ORGANISM: Unknown Organism

FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Viral

OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-15

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 21

US-10-760-048-30/c
Sequence 30, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 30
LENGTH: 238
TYPE: DNA
ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral
OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-30

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 22

US-10-760-048-31/c
Sequence 31, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 31
LENGTH: 238
TYPE: DNA
ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral
OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-38

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

Db 105 AAGGAAACACGGACACCCAA 86

Db 105 AAGGAAACACGGACACCCAA 86

Db 105 AAGGAAACACGGACACCCAA 86

Db 105 AAGGAAACACGGACACCCAA 86

Db 105 AAGGAAACACGGACACCCAA 86

Db 105 AAGGAAACACGGACACCCAA 86

Db 105 AAGGAAACACGGACACCCAA 86

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral
OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-31

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 23

US-10-760-048-33/c
Sequence 33, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 33
LENGTH: 238
TYPE: DNA
ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral
OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-33

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 24

US-10-760-048-38/c
Sequence 38, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 38
LENGTH: 238
TYPE: DNA
ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral
OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-38

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 25

US-10-760-048-39/c
Sequence 39, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 39
LENGTH: 238
TYPE: DNA
ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral
OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-39

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
| | | | | | | | | | | | | | | | | |
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 25

US-10-760-048-42/c
; Sequence 42, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 42
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-42

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
| | | | | | | | | | | | | | | | | |
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 26

US-10-760-048-43/c
; Sequence 43, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 43
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-43

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
| | | | | | | | | | | | | | | | | |
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 27

US-10-760-048-46/c
; Sequence 46, Application US/10760048
; Publication No. US20050158710A1

; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 46
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-46

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
| | | | | | | | | | | | | | | | | |
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 28

US-10-760-048-47/c
; Sequence 47, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 47
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-47

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
| | | | | | | | | | | | | | | | | |
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 29

US-10-760-048-48/c
; Sequence 48, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 3.2

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQUENCE: 5'-AAGGAAACACGGACACCCAA-3'
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-48

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 105 AAGGAAACACGGACACCCAA 86

RESULT 30

US-10-760-048-58/c
; Sequence 58, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 58
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-58

QY 1 AAGGAAACACGGACACCCAA 20
DB 106 AAGGAAACACGGACACCCAA 87

RESULT 31

US-10-760-048-61/c
; Sequence 61, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 61
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-61

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 106 AAGGAAACACGGACACCCAA 87

RESULT 33

US-10-614-283-1/c
; Sequence 1, Application US/10614283
; Publication No. US20050112095A1
; GENERAL INFORMATION:
; APPLICANT: HSU, TSUNG-YUAN
; APPLICANT: LEE, JIN-CHING
; TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN
; FILE REFERENCE: 08842.0002-00000
; CURRENT APPLICATION NUMBER: US/10/614,283
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/394,269
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-10-614-283-1

QY 1 AAGGAAACACGGACACCCAA 20
DB 105 AAGGAAACACGGACACCCAA 86

Query Match 100.0%; Score 20; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 105 AAGGAAACACGGACACCCAA 86

RESULT 32
US-10-760-048-65/c
; Sequence 65, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 65
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-65

QY 1 AAGGAAACACGGACACCCAA 20
DB 105 AAGGAAACACGGACACCCAA 86

Query Match 100.0%; Score 20; DB 9; Length 709;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 534 AAGGAAACACGGACACCCAA 515

```
RESULT 34
US-10-839-729-21/c
; Sequence 21, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 743
; TYPE: DNA
; ORGANISM: Mahoney Strain Poliovirus Type I
US-10-839-729-21

Query Match      100.0%; Score 20; DB 8; Length 743;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 563 AAGGAAACACGGACACCCAA 544

RESULT 35
US-10-489-136-10/c
; Sequence 10, Application US/10489136
; Publication No. US20050014150A1
; GENERAL INFORMATION:
; APPLICANT: Atabekov, Joseph
; APPLICANT: Dorokhov, Yuri
; APPLICANT: Skulachev, Maxim
; APPLICANT: Ivanov, Peter
; APPLICANT: Gleba, Yuri
; TITLE OF INVENTION: IDENTIFICATION OF EUKARYOTIC INTERNAL RIBOSOME ENTRY SITE (IRES)
; TITLE OF INVENTION: ELEMENTS
; FILE REFERENCE: 9286.30
; CURRENT APPLICATION NUMBER: US/10/489,136
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: PCT/EP02/09844
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: DE 101 43 238.0
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 745
; TYPE: DNA
; ORGANISM: Poliovirus
US-10-489-136-10

Query Match      100.0%; Score 20; DB 8; Length 745;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 568 AAGGAAACACGGACACCCAA 549

RESULT 36
US-09-884-586A-3/c
; Sequence 3, Application US/09884586A
; Publication No. US20030046716A1
; GENERAL INFORMATION:
; APPLICANT: Echelard, Yann
```

```
; APPLICANT: Meade, Harry M.
; APPLICANT: Eichner, Wolfram
; APPLICANT: Sommermeyer, Klaus
; TITLE OF INVENTION: TRANSGENICALLY PRODUCED PLATELET DERIVED
; TITLE OF INVENTION: GROWTH FACTOR
; FILE REFERENCE: 10275-120001
; CURRENT APPLICATION NUMBER: US/09/884,586A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/212,406
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-586A-3

Query Match      100.0%; Score 20; DB 3; Length 2076;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 1317 AAGGAAACACGGACACCCAA 1298

RESULT 37
US-10-408-456-4/c
; Sequence 4, Application US/10408456
; Publication No. US20040013648A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: KINGSMAN, et al., Alan John
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-4

Query Match      100.0%; Score 20; DB 6; Length 10448;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 1541 AAGGAAACACGGACACCCAA 1522

RESULT 38
US-10-408-456-5/c
; Sequence 5, Application US/10408456
; Publication No. US20040013648A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: KINGSMAN, et al., Alan John
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
```

; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 11058
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-5

Query Match 100.0%; Score 20; DB 6; Length 11058;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
|||
DB 3813 AAGGAAACACGACACCCAA 3794

RESULT 39
US-10-408-456-34/c
; Sequence 34, Application US/10408456
; Publication No. US20040013648A1
; GENERAL INFORMATION:
; APPLICANT: KINGSMAN, et al., Alan John
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 11622
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-34

Query Match 100.0%; Score 20; DB 6; Length 11622;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
|||
DB 7244 AAGGAAACACGACACCCAA 7225

RESULT 40
US-10-873-573-7/c
; Sequence 7, Application US/10873573
; Publication No. US20050002907A1
; GENERAL INFORMATION:
; APPLICANT: MITRAPHANOUS, KYRI
; APPLICANT: ROHL, JONATHAN
; APPLICANT: MISKIN, JAMES
; APPLICANT: KINGSMAN, SUSAN MARIE
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 674523-2016.1
; CURRENT APPLICATION NUMBER: US/10/873,573
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 10/408,456
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 11622

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-873-573-7

Query Match 100.0%; Score 20; DB 8; Length 11622;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
|||
DB 7244 AAGGAAACACGACACCCAA 7225

RESULT 41
US-10-366-823-5/c
; Sequence 5, Application US/10366823
; Publication No. US20030211526A1
; GENERAL INFORMATION:
; APPLICANT: Juang, Jyh-Lyh
; APPLICANT: Hsiung, Chao Agnes
; APPLICANT: Lin, Chung-Yen
; TITLE OF INVENTION: CROSS-SPECIES NUCLEIC ACID PROBES
; FILE REFERENCE: 12563-006001
; CURRENT APPLICATION NUMBER: US/10/366,823
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,541
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-10-366-823-5

Query Match 100.0%; Score 20; DB 6; Length 62;
Best Local Similarity 95.0%; Pred. No. 11;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
|||
DB 57 AAGGAAACACGACACCCAA 38

RESULT 42
US-10-408-519-3/c
; Sequence 3, Application US/10408519
; Publication No. US20030228683A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Kan-Hung
; APPLICANT: Shih, Yu-Hau
; APPLICANT: Tsai, Chuan-Wei
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Hsiao, Hsiung
; APPLICANT: Bahr, Chi-Horng
; APPLICANT: Wang, Shin-Hwan
; TITLE OF INVENTION: BIOMOLECULE-BOUND SUBSTRATES
; FILE REFERENCE: 12674-002002
; CURRENT APPLICATION NUMBER: US/10/408,519
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 09/522,417
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence

;
; FEATURE:
; OTHER INFORMATION: Probe from 5' ends of enterovirus genes
US-10-408-519-3

Query Match 100.0%; Score 20; DB 6; Length 53;
Best Local Similarity 95.0%; Pred. No. 17;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||:|||||
Db 49 AAGGAACACGACACCCAA 30

RESULT 43

US-10-829-474-21
; Sequence 21, Application US/10829474
; Publication No. US20050239055A1

; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
US-10-829-474-21

Query Match 95.0%; Score 19; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCAA 20
|||||
Db 1 AGGAACACGACACCCAA 19

RESULT 44

US-10-829-474-22
; Sequence 22, Application US/10829474
; Publication No. US20050239055A1

; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
US-10-829-474-22

Query Match 95.0%; Score 19; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCCA 19
|||||
Db 1 AAGGAACACGACACCCCA 19

RESULT 45

US-10-760-048-34/c
; Sequence 34, Application US/10760048
; Publication No. US20050158710A1

; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 34
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism

; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-34

Query Match 95.0%; Score 19; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCAA 20
|||||
Db 104 AGGAACACGACACCCAA 86

RESULT 46

US-10-760-048-35/c
; Sequence 35, Application US/10760048
; Publication No. US20050158710A1

; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 35
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism

; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-35

Query Match 95.0%; Score 19; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCAA 20
|||||
Db 104 AGGAACACGACACCCAA 86

RESULT 47

US-10-760-048-36/c
; Sequence 36, Application US/10760048
; Publication No. US20050158710A1

; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.

; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-36

Query Match 95.0%; Score 19; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAAACACGGACACCCAA 20
|||||
Db 104 AGGAAACACGGACACCCAA 86

RESULT 48
US-10-760-048-62/c
; Sequence 62, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 62
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-62

Query Match 95.0%; Score 19; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAAACACGGACACCCAA 20
|||||
Db 104 AGGAAACACGGACACCCAA 86

RESULT 49
US-10-332-123-53/c
; Sequence 53, Application US/10332123
; Publication No. US20040072239A1
; GENERAL INFORMATION:
; APPLICANT: RENAUD, Patricia
; APPLICANT: GUILLOT, Emmanuelle
; APPLICANT: MABILAT, Claude
; APPLICANT: VACHON, Carole
; APPLICANT: LACROIX, Bruno
; APPLICANT: VERNET, Guy
; APPLICANT: ARMAND, Marie-Astrid
; APPLICANT: LARFAIRE, Philippe
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
; TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
; FILE REFERENCE: 114502

; CURRENT APPLICATION NUMBER: US/10/332,123
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: PCT/FR01/02191
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: FR00-08839
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Poliovirus (X00595)
US-10-332-123-53

Query Match 95.0%; Score 19; DB 7; Length 521;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAAACACGGACACCCAA 20
|||||
Db 500 AGGAAACACGGACACCCAA 482

RESULT 50
US-10-760-048-41/c
; Sequence 41, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 41
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-41

Query Match 92.0%; Score 18.4; DB 9; Length 235;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 105 ATGGAACACGGACACCCAA 86

RESULT 51
US-10-760-048-37/c
; Sequence 37, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Unknown Organism

;
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-37

Query Match 92.0%; Score 18.4; DB 9; Length 236;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 ATGGAACACGGACACCCAA 86
|||

RESULT 52

US-10-760-048-16/c
; Sequence 16, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-16

Query Match 92.0%; Score 18.4; DB 9; Length 237;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AGGGAACACGGACACCCAA 86
|||

RESULT 53

US-10-760-048-32/c
; Sequence 32, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-32

Query Match 92.0%; Score 18.4; DB 9; Length 237;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AAGAAACACGGACACCCAA 86
|||

RESULT 54

US-10-760-048-14/c
; Sequence 14, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-14

Query Match 92.0%; Score 18.4; DB 9; Length 238;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AAGAAACACGGACACCCAA 86
|||

RESULT 55

US-10-760-048-19/c
; Sequence 19, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760.048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-19

Query Match 92.0%; Score 18.4; DB 9; Length 238;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AATGAAACACGGACACCCAA 86
|||

RESULT 56

US-10-760-048-23/c
; Sequence 23, Application US/10760048
; Publication No. US20050158710A1

;; GENERAL INFORMATION:
;; APPLICANT: TSANG, SHIRLEY
;; APPLICANT: PRICE, JAMES A.
;; APPLICANT: HELLYER, TOBIN J.
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
;; FILE REFERENCE: 020187.0187PTUS
;; CURRENT APPLICATION NUMBER: US/10/760,048
;; CURRENT FILING DATE: 2004-01-16
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 23
;; LENGTH: 238
;; TYPE: DNA
;; ORGANISM: Unknown Organism
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: Viral
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-23

Query Match 92.0%; Score 18.4; DB 9; Length 238;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AATGAACACGGACACCCAA 86

RESULT 57

US-10-760-048-25/c
;; Sequence 25, Application US/10760048
;; Publication No. US20050158710A1
;; GENERAL INFORMATION:
;; APPLICANT: TSANG, SHIRLEY
;; APPLICANT: PRICE, JAMES A.
;; APPLICANT: HELLYER, TOBIN J.
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
;; FILE REFERENCE: 020187.0187PTUS
;; CURRENT APPLICATION NUMBER: US/10/760,048
;; CURRENT FILING DATE: 2004-01-16
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 25
;; LENGTH: 238
;; TYPE: DNA
;; ORGANISM: Unknown Organism
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: Viral
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-25

Query Match 92.0%; Score 18.4; DB 9; Length 238;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AATGAACACGGACACCCAA 86

RESULT 58

US-10-760-048-26/c
;; Sequence 26, Application US/10760048
;; Publication No. US20050158710A1
;; GENERAL INFORMATION:
;; APPLICANT: TSANG, SHIRLEY
;; APPLICANT: PRICE, JAMES A.
;; APPLICANT: HELLYER, TOBIN J.
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
;; FILE REFERENCE: 020187.0187PTUS
;; CURRENT APPLICATION NUMBER: US/10/760,048
;; CURRENT FILING DATE: 2004-01-16
;; NUMBER OF SEQ ID NOS: 67

;; -SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 26
;; LENGTH: 238
;; TYPE: DNA
;; ORGANISM: Unknown Organism
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: Viral
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-26

Query Match 92.0%; Score 18.4; DB 9; Length 238;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AATGAACACGGACACCCAA 86

RESULT 59

US-10-760-048-27/c
;; Sequence 27, Application US/10760048
;; Publication No. US20050158710A1
;; GENERAL INFORMATION:
;; APPLICANT: TSANG, SHIRLEY
;; APPLICANT: PRICE, JAMES A.
;; APPLICANT: HELLYER, TOBIN J.
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
;; FILE REFERENCE: 020187.0187PTUS
;; CURRENT APPLICATION NUMBER: US/10/760,048
;; CURRENT FILING DATE: 2004-01-16
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 27
;; LENGTH: 238
;; TYPE: DNA
;; ORGANISM: Unknown Organism
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: Viral
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-27

Query Match 92.0%; Score 18.4; DB 9; Length 238;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AATGAACACGGACACCCAA 86

RESULT 60

US-10-760-048-28/c
;; Sequence 28, Application US/10760048
;; Publication No. US20050158710A1
;; GENERAL INFORMATION:
;; APPLICANT: TSANG, SHIRLEY
;; APPLICANT: PRICE, JAMES A.
;; APPLICANT: HELLYER, TOBIN J.
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
;; FILE REFERENCE: 020187.0187PTUS
;; CURRENT APPLICATION NUMBER: US/10/760,048
;; CURRENT FILING DATE: 2004-01-16
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 28
;; LENGTH: 238
;; TYPE: DNA
;; ORGANISM: Unknown Organism
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: Viral
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-28

Query Match 92.0%; Score 18.4; DB 9; Length 238;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AATGAAACACGGACACCCAA 86
|||

RESULT 61

US-10-760-048-29/c
; Sequence 29, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187, 0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 29
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-29

Query Match 92.0%; Score 18.4; DB 9; Length 238;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 105 AATGAAACACGGACACCCAA 86
|||

RESULT 62

US-10-332-123-54/c
; Sequence 54, Application US/10332123
; Publication No. US20040072239A1
; GENERAL INFORMATION:
; APPLICANT: RENAUD, Patricia
; APPLICANT: GUILLOT, Emmanuelle
; APPLICANT: MABILAT, Claude
; APPLICANT: VACHON, Carole
; APPLICANT: LACROIX, Bruno
; APPLICANT: VERNET, Guy
; APPLICANT: ARMAND, Marie-Astrid
; APPLICANT: LAPFAIRE, Philippe
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
; TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
; FILE REFERENCE: 114502
; CURRENT APPLICATION NUMBER: US/10/332,123
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: PCT/FR01/02191
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: FR00-08839
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Coxsackievirus (D00538)
US-10-332-123-54

Query Match 92.0%; Score 18.4; DB 7; Length 520;

Best Local Similarity 95.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 500 AGGGAACACGGACACCCAA 481
|||

RESULT 63

US-10-136-819-7/c
; Sequence 7, Application US/10136819
; Publication No. US20030166593A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific gen
; FILE REFERENCE: 6627-PAIL98
; CURRENT APPLICATION NUMBER: US/10/136,819
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/287,423
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 7399
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-136-819-7

Query Match 92.0%; Score 18.4; DB 6; Length 7399;
Best Local Similarity 95.0%; Pred. No. 46;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||
Db 568 AATGAAACACGGACACCCAA 549
|||

RESULT 64

US-10-829-474-17
; Sequence 17, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-17

Query Match 90.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCC 18
|||
Db 1 AAGGAAACACGGACACCCC 18
|||

RESULT 65

US-10-829-474-18
; Sequence 18, Application US/10829474
; Publication No. US20050239055A1

```
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-18

Query Match          90.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACACGCGACACCCAA 20
   |||||
Db 1 GGAACACGCGACACCCAA 18

RESULT 66
US-10-829-474-20
; Sequence 20, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-20
```

```
Query Match          90.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAACACGCGACACCCA 19
   |||||
Db 1 AGGAACACGCGACACCCA 18
```

```
RESULT 67
US-10-322-696-13
; Sequence 13, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morrie, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 225734
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(225734)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-696-13
```

```
Query Match          90.0%; Score 18; DB 7; Length 225734;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 GGAACACGCGACACCCAA 20
   |||||
Db 57400 GGAACACGCGACACCCAA 57417
```

```
RESULT 68
US-10-760-048-10
; Sequence 10, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 10
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-760-048-10
```

```
Query Match          89.0%; Score 17.8; DB 9; Length 40;
Best Local Similarity 89.5%; Pred. No. 81;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AAGGAACACGCGACACCCA 19
   |||||
Db 22 AADRAAACACGCGACACCCA 40
```

```
RESULT 69
US-10-829-474-23
; Sequence 23, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-23
```

```
Query Match          85.0%; Score 17; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 3 GGAACACGGACACCCA 19
Db 1 GGAACACGGACACCCA 17

RESULT 70

US-10-829-474-24
; Sequence 24, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-24

Qy 2 AGGAACACGGACACCC 18
Db 1 AGGAACACGGACACCC 17

RESULT 71

US-10-938-005-4/c
; Sequence 4, Application US/10938005
; Publication No. US20050048475A1
; GENERAL INFORMATION:
; APPLICANT: Paul, John H.
; APPLICANT: Casper, Erica T.
; APPLICANT: Patterson, Stacey S.
; TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus
; FILE REFERENCE: USF-114XC621
; CURRENT APPLICATION NUMBER: US/10/938,005
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 10/857,109
; PRIOR FILING DATE: 2004-05-28
; PRIOR FILING DATE: 2002-06-25
; PRIOR FILING DATE: 2002-06-25
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Ent P3
US-10-938-005-4

Qy 1 AAGGAACACGGACACCC 17
Db 17 AAGGAACACGGACACCC 1

RESULT 72
US-10-179-082A-3/c
; Sequence 3, Application US/10179082A
; Publication No. US20030186222A1
; GENERAL INFORMATION:
; APPLICANT: Paul, John H.
; TITLE OF INVENTION: RAPID DETECTION OF ENTEROVIRUSES IN ENVIRONMENTAL SAMPLES BY NASBA
; FILE REFERENCE: USF-114XC6
; CURRENT APPLICATION NUMBER: US/10/179,082A
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Poliovirus sp.
US-10-179-082A-3

Query Match 85.0%; Score 17; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
Db 21 GAAACACGGACACCCAA 5

RESULT 73

US-10-938-005-3/c
; Sequence 3, Application US/10938005
; Publication No. US20050048475A1
; GENERAL INFORMATION:
; APPLICANT: Paul, John H.
; APPLICANT: Casper, Erica T.
; APPLICANT: Patterson, Stacey S.
; TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus
; FILE REFERENCE: USF-114XC621
; CURRENT APPLICATION NUMBER: US/10/938,005
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 10/857,109
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/179,082
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/301,218
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe for poliovirus
US-10-938-005-3

Query Match 85.0%; Score 17; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
Db 21 GAAACACGGACACCCAA 5

RESULT 74

US-10-175-247-20
; Sequence 20, Application US/10175247
; Publication No. US20030165466A1
; GENERAL INFORMATION:
; APPLICANT: Gromeier PhD, Matthias
; APPLICANT: Wimmer Prof, Eckard
; TITLE OF INVENTION: Recombinant Poliovirus For The Treatment of Cancer

```
; FILE REFERENCE: Recomb Poliovirus for Cancer Treatment
; CURRENT APPLICATION NUMBER: US/10/175,247
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/129,686
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Human rhinovirus 2
US-10-175-247-20

Query Match      85.0%; Score 17; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACC 17
      |||||
Db      17 AAGGAAACACGGACACC 33

RESULT 75
US-10-760-048-9/c
; Sequence 9, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-760-048-9

Query Match      85.0%; Score 17; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAAACACGGACACCCAA 20
      |||||
Db      40 GAAACACGGACACCCAA 24

RESULT 76
US-10-938-005-9/c
; Sequence 9, Application US/10938005
; Publication No. US20050048475A1
; GENERAL INFORMATION:
; APPLICANT: Casper, John H.
; APPLICANT: Casper, Erica T.
; APPLICANT: Patterson, Stacey S.
; TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus
; FILE REFERENCE: USF-114XC621
; CURRENT APPLICATION NUMBER: US/10/938,005
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 10/857,109
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/179,082
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/301,218
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 9
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Enteroviral Internal Control
US-10-938-005-9

Query Match      85.0%; Score 17; DB 8; Length 92;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACC 17
      |||||
Db      17 AAGGAAACACGGACACC 1

RESULT 77
US-10-760-048-39/c
; Sequence 39, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 39
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-39

Query Match      85.0%; Score 17; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAAACACGGACACCCAA 20
      |||||
Db      102 GAAACACGGACACCCAA 86

RESULT 78
US-10-760-048-40/c
; Sequence 40, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 40
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-40

Query Match      85.0%; Score 17; DB 9; Length 117;
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
|||||
Db 102 GAAACACGGACACCCAA 86

RESULT 79

US-10-104-611-31/c
; Sequence 31, Application US/10104611
; Publication No. US20020160976A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.

TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,611
FILING DATE: 22-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31

Query Match 85.0%; Score 17; DB 5; Length 627;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
|||||
Db 568 GAAACACGGACACCCAA 552

RESULT 80

US-10-112-547-31/c
; Sequence 31, Application US/10112547
; Publication No. US20020160977A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.

Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,547
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-112-547-31

Query Match 85.0%; Score 17; DB 5; Length 627;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
|||||
Db 568 GAAACACGGACACCCAA 552

RESULT 81

US-10-112-241-31/c
; Sequence 31, Application US/10112241
; Publication No. US20020165194A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.

TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711

```

; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rna
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-109-368-31

Query Match      85.0%; Score 17; DB 6; Length 627;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

QY      4 GAAACACGGCACCCCAA 20
|||||
Db      568 GAAACACGGCACCCCAA 552

RESULT 83
US-10-867-798-31/c
; Sequence 31, Application US/10867798
; Publication No. US20040254140A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/867,798
; FILING DATE: 14-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```
;
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-867-798-31

Query Match      85.0%; Score 17; DB 8; Length 627;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
Db 568 GAAACACGGACACCCAA 552
|||||
|

RESULT 84
US-10-425-115-173501
; Sequence 173501, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 173501
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_89813C.1
US-10-425-115-173501

Query Match      84.0%; Score 16.8; DB 8; Length 230;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 53 AGGGAACACGGAAACCCAA 72
|||||
|

RESULT 85
US-10-760-048-17/c
; Sequence 17, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187, 0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-17

Query Match      84.0%; Score 16.8; DB 9; Length 238;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGTACCCAA 86
|||||
|

RESULT 86
US-10-760-048-22/c
; Sequence 22, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187, 0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-22

Query Match      84.0%; Score 16.8; DB 9; Length 238;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAAGAAACACGGTACCCAA 86
|||||
|

RESULT 87
US-10-760-048-24/c
; Sequence 24, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187, 0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-24

Query Match      84.0%; Score 16.8; DB 9; Length 238;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAAGAAACACGGTACCCAA 86
|||||
|

RESULT 88
US-10-950-009-1102/c
; Sequence 1102, Application US/10950009
; Publication No. US20050069934A1
; GENERAL INFORMATION:
```

```
; APPLICANT: BERKA, Randy
; APPLICANT: BASHKIROVA, Elena
; APPLICANT: REY, Michael
; TITLE OF INVENTION: Methods For Monitoring Gene Expression
; FILE REFERENCE: 10541.200-US
; CURRENT APPLICATION NUMBER: US/10/950,009
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/506,140
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 1190
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1102
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Trichoderma reesei
US-10-950-009-1102

Query Match      84.0%; Score 16.8; DB 9; Length 370;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 262 AAGGAAACACGACACCCAA 243

RESULT 89
US-09-925-065A-156382
; Sequence 156382, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156382
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-156382

Query Match      84.0%; Score 16.8; DB 4; Length 585;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 85 AAGGAAACACGACACCCAA 104

RESULT 90
US-09-925-065A-156383
; Sequence 156383, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156382
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-156383

Query Match      84.0%; Score 16.8; DB 4; Length 585;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 85 AAGGAAACACGACACCCAA 104

RESULT 91
US-10-760-048-67/c
; Sequence 67, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 67
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-760-048-67

Query Match      84.0%; Score 16.8; DB 9; Length 660;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
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Db 487 AAGGAAACACGACACCCAA 468

RESULT 92
US-10-363-345A-23361/c
; Sequence 23361, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23361
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; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156383
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-156383

Query Match      84.0%; Score 16.8; DB 4; Length 585;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 85 AAGGAAACACGACACCCAA 104

RESULT 91
US-10-760-048-67/c
; Sequence 67, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 67
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-760-048-67

Query Match      84.0%; Score 16.8; DB 9; Length 660;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 487 AAGGAAACACGACACCCAA 468

RESULT 92
US-10-363-345A-23361/c
; Sequence 23361, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23361
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Db 50059 ATGGAACACGGGACCCAA 50040

RESULT 97

US-09-925-065A-319374
; Sequence 319374, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319374
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-319374

Query Match 82.0%; Score 16.4; DB 4; Length 578;
Best Local Similarity 94.4%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAACACGGGACCCAA 20

Db 89 GGAACACGGGACCCAA 106

RESULT 98

US-10-052-482-55/c
; Sequence 55, Application US/10052482
; Publication No. US20040072264A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 47493
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1241)..(1975)
; OTHER INFORMATION: "n" at positions 1241 to 1975 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13629)..(13648)
; OTHER INFORMATION: "n" at positions 13629 to 13648 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15882)..(16151)

; OTHER INFORMATION: "n" at positions 15882 to 16151 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22065)..(22084)
; OTHER INFORMATION: "n" at positions 22065 to 22084 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26226)..(26285)
; OTHER INFORMATION: "n" at positions 26226 to 26285 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30454)..(30473)
; OTHER INFORMATION: "n" at positions 30454 to 30473 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31687)..(32259)
; OTHER INFORMATION: "n" at positions 31687 to 32259 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (40899)..(41095)
; OTHER INFORMATION: "n" at positions 40899 to 41095 can be any base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42909)..(43118)
; OTHER INFORMATION: "n" at positions 42909 to 43118 can be any base
US-10-052-482-55

Query Match 82.0%; Score 16.4; DB 7; Length 47493;
Best Local Similarity 94.4%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGAACACGGGACCCCA 19

Db 11461 AGGAACACGGGACCCCA 11444

RESULT 99

US-10-829-474-19
; Sequence 19, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
; OTHER INFORMATION: RNA
US-10-829-474-19

Query Match 80.0%; Score 16; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGAACACGGGACCC 18

Db 1 GGAACACGGGACCC 16

RESULT 100

US-10-425-115-83354
; Sequence 83354, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

```

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 83354
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MET4577_176031C.1
US-10-425-115-83354

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Query Match      80.0%; Score 16; DB 8; Length 484;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      4 GAAACACGGACACCCA 19
        |||||
Db      29 GAAACACGGACACCCA 44

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Search completed: March 9, 2006, 08:33:39
Job time : 588.194 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:06:59 ; Search time 200.388 Seconds
(without alignments)
665.178 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaaacacggacacccaa 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

100% Processing: Maximum Match 0%
Maximum Match 100%

Listing first 500 summaries

Database : N Geneseq 21: *

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1: geneseqm1980s:*

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2: geneseqn1990s:*

3: geneseqn200s:*

4: geneseqn2001as:

5: geneseqn2001bs:

6: geneseqn2002as:

7: geneseqn2002bs:

8: geneseqn2003as:

9: geneseqn2003bs:

10: geneseqn2003cs

11: geneseqn2003db

12: geneseqn2004as

13: geneseqn2004bs

14: geneseqn2005s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	20	100.0	105	14	AEB56869	Aeb56869 Human ech
C 2	20	100.0	106	14	AEB56868	Aeb56868 Human ech
C 3	20	100.0	107	14	AEB56814	Aeb56814 Viral 5'
C 4	20	100.0	110	14	AEB56813	Aeb56813 Viral 5'
C 5	20	100.0	126	14	AEB56779	Aeb56779 Viral 5'
C 6	20	100.0	176	3	Az58488	Aaz58488 Recombina
C 7	20	100.0	180	14	AEB56834	Aeb56834 Human cox
C 8	20	100.0	195	10	AEBZ69931	AebZ69931 Polioviru
C 9	20	100.0	198	14	AEB56860	Aeb56860 Human ech
C 10	20	100.0	198	14	AEB56858	Aeb56858 Human ech
C 11	20	100.0	198	14	AEB56863	Aeb56863 Human ech
C 12	20	100.0	198	14	AEB56854	Aeb56854 Human ech
C 13	20	100.0	236	14	AEB56816	Aeb56816 Viral 5'
C 14	20	100.0	237	14	AEB56837	Aeb56837 Human cox
C 15	20	100.0	237	14	AEB56862	Aeb56862 Human ech
C 16	20	100.0	237	14	AEB56879	Aeb56879 Human pol
C 17	20	100.0	237	14	AEB56861	Aeb56861 Human pol
C 18	20	100.0	237	14	AEB56827	Aeb56827 Viral 5'
C 19	20	100.0	237	14	AEB56875	Aeb56875 Human pol

C 93	20	100.0	11326	2	AAV12373	Aav12373 Chimexic	C 166	17	85.0	608	5	AAC93057	Aac93057 Human rhi
C 94	20	100.0	11746	12	ADO07659	Ado07659 Viral vec	C 167	17	85.0	610	1	AAH81398	Aan81398 Sequence
C 95	20	100.0	38246	12	ADO07662	Ado07662 Viral vec	C 168	17	85.0	627	8	ABX11923	Abx11923 Human rhi
C 96	19.6	100.0	62	12	ADK66744	Adk66744 Picornavi	C 169	17	85.0	627	8	ABX11971	Abx11971 Human rhi
C 97	19.6	100.0	62	14	AEC07516	Aec07516 Picornavi	C 170	17	85.0	627	10	ADB84230	Adb84230 Rhinoviru
C 98	19.2	100.0	28	8	ACD26711	AcD26711 Enterovir	C 171	17	85.0	627	10	ADA15642	Ada15642 Human rhi
C 99	19.2	100.0	28	13	ADU47464	Adu47464 p3 probe	C 172	17	85.0	627	14	ADV78854	Adv78854 Novel ant
C 100	19	95.0	70	14	ADM75017	Adm75017 Human rhi	C 173	17	85.0	627	14	ADW71616	Adw71616 Human rhi
C 101	19	95.0	238	14	AEBS6850	Aeb56850 Human cox	C 174	17	85.0	681	12	ADP82874	Adp82874 Human rhi
C 102	19	95.0	238	14	AEBS6878	Aeb56878 Human pol	C 175	17	85.0	7100	2	AAQ03360	Aaq03360 Complete
C 103	19	95.0	238	14	AEBS6797	Aeb56797 Viral 5'	C 176	17	85.0	7100	2	AAQ03418	Aaq03418 Complete
C 104	19	95.0	238	14	AEBS6851	Aeb56851 Human cox	C 177	17	85.0	7102	1	AAH60044	Aan60044 Sequence
C 105	19	95.0	238	14	AEBS6852	Aeb56852 Human cox	C 178	17	85.0	7102	1	AAH81393	Aan81393 Rhinoviru
C 106	19	95.0	238	14	AEBS6795	Aeb56795 Viral 5'	C 179	17	85.0	7227	1	AAH60194	Aan60194 Sequence
C 107	19	95.0	238	14	AEBS6796	Aeb56796 Viral 5'	C 180	16.8	84.0	41	ADZ76557	Adz76557 Enterovir	
C 108	19	95.0	238	14	AEBS6823	Aeb56823 Viral 5'	C 181	16.8	84.0	238	14	AEBS6840	Aeb56840 Human cox
C 109	19	95.0	521	6	ABL53111	AbL53111 Micro-org	C 182	16.8	84.0	238	14	AEBS6838	Aeb56838 Human cox
C 110	19	95.0	618	1	AAH81397	Aan81397 Sequence	C 183	16.8	84.0	238	14	AEBS6785	Aeb56785 Viral 5'
C 111	19	95.0	7152	1	AAH81390	Aan81390 Sequence	C 184	16.8	84.0	238	14	AEBS6783	Aeb56783 Viral 5'
C 112	19	95.0	7152	1	AAH80153	Aan80153 Sequence	C 185	16.8	84.0	238	14	AEBS6833	Aeb56833 Human cox
C 113	18.4	92.0	198	14	AEBS6853	Aeb56853 Human ech	C 186	16.8	84.0	238	14	AEBS6778	Aeb56778 Viral 5'
C 114	18.4	92.0	235	14	AEBS6802	Aeb56802 Viral 5'	C 187	16.8	84.0	370	14	AAZ99748	Adz99748 T. reesei
C 115	18.4	92.0	236	14	AEBS6798	Aeb56798 Viral 5'	C 188	16.8	84.0	660	4	AAC85174	Aac85174 Coxsackie
C 116	18.4	92.0	237	14	AEBS6848	Aeb56848 Human cox	C 189	16.8	84.0	660	14	AEBS6828	Aeb56828 Coxsackie
C 117	18.4	92.0	237	14	AEBS6777	Aeb56777 Viral 5'	C 190	16.8	84.0	750	2	AAQ21315	Aaq21315 DNA encod
C 118	18.4	92.0	237	14	AEBS6793	Aeb56793 Viral 5'	C 191	16.8	84.0	906	6	ABQ36770	Abq36770 Oligonucl
C 119	18.4	92.0	237	14	AEBS6857	Aeb56857 Human ech	C 192	16.8	84.0	906	6	ABQ36771	Abq36771 Oligonucl
C 120	18.4	92.0	238	14	AEBS6839	Aeb56839 Human cox	C 193	16.8	84.0	147300	12	ADP45593	Adp45593 Human Rho
C 121	18.4	92.0	238	14	AEBS6789	Aeb56789 Viral 5'	C 194	16.8	84.0	147700	14	ADX98570	Adx98570 Human gua
C 122	18.4	92.0	238	14	AEBS6775	Aeb56775 Viral 5'	C 195	16.4	82.0	47493	9	ADA02549	Ada02549 Mouse Wnt
C 123	18.4	92.0	238	14	AEBS6842	Aeb56842 Human cox	C 196	16.4	82.0	47493	10	ADB72287	Adb72287 Mouse Wnt
C 124	18.4	92.0	238	14	AEBS6832	Aeb56832 Human cox	C 197	16.4	82.0	47493	10	ADB95797	Adb95797 Mouse Wnt
C 125	18.4	92.0	238	14	AEBS6835	Aeb56835 Human cox	C 198	16.4	82.0	63079	14	ADZ12509	Adz12509 Murine ca
C 126	18.4	92.0	238	14	AEBS6780	Aeb56780 Viral 5'	C 199	16	80.0	20	10	ABZ79843	Abz79843 Exemplary
C 127	18.4	92.0	238	14	AEBS6784	Aeb56784 Viral 5'	C 200	15.8	79.0	532	12	ACH77474	Ach77474 Human gen
C 128	18.4	92.0	238	14	AEBS6843	Aeb56843 Human cox	C 201	15.8	79.0	568	4	AAH13480	Aah13480 Human CDN
C 129	18.4	92.0	238	14	AEBS6845	Aeb56845 Human cox	C 202	15.8	79.0	660	4	AAH55696	Aah55696 Human bre
C 130	18.4	92.0	238	14	AEBS6788	Aeb56788 Viral 5'	C 203	15.8	79.0	660	7	ADU01443	Adu01443 Breast ca
C 131	18.4	92.0	238	14	AEBS6786	Aeb56786 Viral 5'	C 204	15.8	79.0	660	7	ADZ41707	Adz41707 Human bre
C 132	18.4	92.0	238	14	AEBS6787	Aeb56787 Viral 5'	C 205	15.8	79.0	660	12	ADN40469	Adn40469 Human bre
C 133	18.4	92.0	238	14	AEBS6830	Aeb56830 Human cox	C 206	15.8	79.0	1530	14	ADV16700	Adv16700 E. faecal
C 134	18.4	92.0	238	14	AEBS6790	Aeb56790 Viral 5'	C 207	15.8	79.0	1560	10	ADH83192	Adh83192 Enterococ
C 135	18.4	92.0	238	14	AEBS6841	Aeb56841 Human cox	C 208	15.8	79.0	1817	2	AAT28545	Aat28545 E. faecal
C 136	18.4	92.0	238	14	AEBS6844	Aeb56844 Human cox	C 209	15.8	79.0	1817	2	ABA76825	Aba76825 Enterococ
C 137	18.4	92.0	497	8	ABX12446	Abx12446 Coxsackie	C 210	15.8	79.0	1936	13	ADT18917	Adt18917 Plant CDN
C 138	18.4	92.0	502	8	ABX12451	Abx12451 Coxsackie	C 211	15.8	79.0	2008	4	AAH16730	Aah16730 Human CDN
C 139	18.4	92.0	520	6	ABL53112	AbL53112 Micro-org	C 212	15.8	79.0	2364	4	ABL30313	AbL30313 Drosophil
C 140	18.4	92.0	556	8	ABX12449	Abx12449 Coxsackie	C 213	15.8	79.0	2378	4	AAH23696	Aah23696 Human tum
C 141	18.4	92.0	654	4	AAC85173	Aac85173 Coxsackie	C 214	15.8	79.0	4670	4	ABL30312	AbL30312 Drosophil
C 142	18.4	92.0	745	4	AAC85152	Aac85152 Coxsackie	C 215	15.8	79.0	4951	2	AAH13198	Aah13198 Enterococ
C 143	18.4	92.0	810	12	ADP82873	Adp82873 Human cox	C 216	15.8	79.0	4951	6	ABS98993	Abs98993 Enterococ
C 144	18.4	92.0	1560	13	ADU47469	Adu47469 Enterovir	C 217	15.8	79.0	13294	4	AAK85255	Aak85255 Human imm
C 145	18.4	92.0	7399	2	AAQ11816	Aaq11816 RNA encod	C 218	15.8	79.0	28906	4	AAH23705	Aah23705 Human tum
C 146	18.4	92.0	7399	10	ABV76134	Abv76134 Coxsackie	C 219	15.8	79.0	98638	12	ADQ97919	Adq97919 Mouse can
C 147	18	90.0	225734	12	ADQ93777	Adq93777 Human can	C 220	15.8	79.0	110000	11	ACN44932	Acn44932
C 148	18	90.0	225734	14	ADZ13617	Adz13617 Murine ca	C 221	15.8	79.0	110000	12	ADQ97960	Adq97960
C 149	17.8	89.0	40	14	AEBS6771	Aeb56771 Enterovir	C 222	15.8	79.0	110000	13	ABQ32921	Abq32921
C 150	17	85.0	21	14	ADY39814	Ady39814 Enterovir	C 223	15.8	79.0	137454	12	ADQ97388	Adq97388 Mouse can
C 151	17	85.0	21	14	AAQ06252	Aaq06252 Probe for	C 224	15.8	79.0	175590	10	ADP50650	Adp50650 BAC sequ
C 152	17	85.0	21	3	AAV65062	Aav65062 Enterovir	C 225	15.8	79.0	175590	14	ADV77908	Adv77908 Human BAC
C 153	17	85.0	21	3	AAH14164	Aah14164 Enterovir	C 226	15.8	79.0	204621	11	ACN44486	Acn44486 Human gen
C 154	17	85.0	21	10	ADZ37351	Adz37351 Polioviru	C 227	15.8	79.0	209613	14	ADY25743	Ady25743 Uridine p
C 155	17	85.0	21	14	ADY39813	Ady39813 Polioviru	C 228	15.4	77.0	25	6	ABK12649	Abk12649 P. patens
C 156	17	85.0	21	14	ADZ68662	Adz68662 Enterovir	C 229	15.4	77.0	198	14	AEBS6865	Aeb56865 Human ech
C 157	17	85.0	25	2	AAT37522	Aat37522 Enterovir	C 230	15.4	77.0	236	14	AEBS6811	Aeb56811 Viral 5'
C 158	17	85.0	33	3	AZ59478	Aaz59478 Polioviru	C 231	15.4	77.0	236	14	AEBS6810	Aeb56810 Viral 5'
C 159	17	85.0	39	4	AA09940	Aa09940 Probe EVP	C 232	15.4	77.0	236	14	AEBS6812	Aeb56812 Viral 5'
C 160	17	85.0	40	14	AEBS6770	Aeb56770 Enterovir	C 233	15.4	77.0	238	14	AEBS6867	Aeb56867 Human ech
C 161	17	85.0	92	14	ADY39819	Ady39819 Enterovir	C 234	15.4	77.0	238	14	AEBS6866	Aeb56866 Human ech
C 162	17	85.0	117	14	AEBS6800	Aeb56800 Viral 5'	C 235	15.4	77.0	525	6	ABL53113	AbL53113 Micro-org
C 163	17	85.0	117	14	AEBS6801	Aeb56801 Viral 5'	C 236	15.4	77.0	632	6	ABQ40730	Abq40730 Oligonucl
C 164	17	85.0	173	14	AEBS6856	Aeb56856 Human ech	C 237	15.4	77.0	632	6	ABQ40731	Abq40731 Oligonucl
C 165	17	85.0	173	14	AEBS6855	Aeb56855 Human ech	C 238	15.4	77.0	646	4	AAC85153	Aac85153 Echo viru

C 239	15.4	77.0	1596	14	ADM16475	Adw16475 Eucalyptu	C 312	15.4	77.0	2690	8	ACC81149	Acc81149 Human sec
C 240	15.4	77.0	1781	10	ACC79086	Acc79086 Human sec	C 313	15.4	77.0	2690	8	ACA95473	ACA95473 Novel hum
C 241	15.4	77.0	2000	8	ADA72841	Ada72841 Rice gene	C 314	15.4	77.0	2690	8	ACA66430	ACA66430 Human cDN
C 242	15.4	77.0	2000	11	ACL317757	ACL317757 Rice stre	C 315	15.4	77.0	2690	8	ACD04391	ACD04391 Novel hum
C 243	15.4	77.0	2624	6	ABK12639	Abk12639 DNA encod	C 316	15.4	77.0	2690	8	ACC87832	ACC87832 Human sec
C 244	15.4	77.0	2690	2	AAC234317	Aac234317 Human PRO	C 317	15.4	77.0	2690	8	ACF12494	ACF12494 Human sec
C 245	15.4	77.0	2690	3	AAZ78588	Aaz78588 Human PRO	C 318	15.4	77.0	2690	8	ACA96209	ACA96209 Human PRO
C 246	15.4	77.0	2690	4	AA545942	Aa545942 Human DNA	C 319	15.4	77.0	2690	8	ACA64983	ACA64983 Human PRO
C 247	15.4	77.0	2690	8	ACA63885	Aac63885 Novel hum	C 320	15.4	77.0	2690	8	ACA73709	ACA73709 Human sec
C 248	15.4	77.0	2690	8	ACA89392	ACA89392 cDNA enco	C 321	15.4	77.0	2690	8	ACA74121	ACA74121 Novel hum
C 249	15.4	77.0	2690	8	ACA73402	ACA73402 Human sec	C 322	15.4	77.0	2690	8	ACA96516	ACA96516 Human PRO
C 250	15.4	77.0	2690	8	ACA05717	ACA05717 Human sec	C 323	15.4	77.0	2690	8	ACD10622	ACD10622 cDNA enco
C 251	15.4	77.0	2690	8	ACA66551	ACA66551 cDNA enco	C 324	15.4	77.0	2690	8	ACC91318	ACC91318 Human sec
C 252	15.4	77.0	2690	8	ACF20126	ACf20126 Human sec	C 325	15.4	77.0	2690	8	ACD02653	ACD02653 cDNA enco
C 253	15.4	77.0	2690	8	ACF19512	ACf19512 Human sec	C 326	15.4	77.0	2690	8	ACC87218	ACC87218 Human sec
C 254	15.4	77.0	2690	8	ACD21800	ACd21800 Human sec	C 327	15.4	77.0	2690	8	ACC85802	ACC85802 Human sec
C 255	15.4	77.0	2690	8	ACF12965	ACf12965 Human sec	C 328	15.4	77.0	2690	8	ACA65290	ACA65290 Human PRO
C 256	15.4	77.0	2690	8	ACD25068	ACd25068 Human sec	C 329	15.4	77.0	2690	8	ACA94107	ACA94107 Human sec
C 257	15.4	77.0	2690	8	ACF00117	ACf00117 Human sec	C 330	15.4	77.0	2690	8	ACA97851	ACA97851 Human PRO
C 258	15.4	77.0	2690	8	ACA72174	ACA72174 Novel hum	C 331	15.4	77.0	2690	8	ACA91353	ACA91353 Novel hum
C 259	15.4	77.0	2690	8	ACD04698	ACd04698 Novel hum	C 332	15.4	77.0	2690	8	ACA90567	ACA90567 Novel hum
C 260	15.4	77.0	2690	8	ACD18159	ACd18159 Human sec	C 333	15.4	77.0	2690	8	ACD16114	ACD16114 Human sec
C 261	15.4	77.0	2690	8	ACD08166	ACD08166 Human sec	C 334	15.4	77.0	2690	8	ACD17275	ACD17275 Human sec
C 262	15.4	77.0	2690	8	ACA88600	ACA88600 Novel hum	C 335	15.4	77.0	2690	8	ACC91932	ACC91932 Human sec
C 263	15.4	77.0	2690	8	ACA70042	ACA70042 Human sec	C 336	15.4	77.0	2690	8	ACA74789	ACA74789 cDNA enco
C 264	15.4	77.0	2690	8	ACD12264	ACd12264 Novel hum	C 337	15.4	77.0	2690	8	ACA91660	ACA91660 Human PRO
C 265	15.4	77.0	2690	8	ACC74179	ACC74179 Human sec	C 338	15.4	77.0	2690	8	ACA71304	ACA71304 Human sec
C 266	15.4	77.0	2690	8	ACD15807	ACd15807 Human sec	C 339	15.4	77.0	2690	8	ACC90704	ACC90704 Human sec
C 267	15.4	77.0	2690	8	ACD25375	ACD25375 Novel hum	C 340	15.4	77.0	2690	8	ACA65714	ACA65714 cDNA enco
C 268	15.4	77.0	2690	8	ACD17852	ACd17852 Human sec	C 341	15.4	77.0	2690	8	ACA94859	ACA94859 cDNA enco
C 269	15.4	77.0	2690	8	ACC88139	ACC88139 Human sec	C 342	15.4	77.0	2690	8	ACD16421	ACD16421 Human sec
C 270	15.4	77.0	2690	8	ACD21493	ACd21493 Human sec	C 343	15.4	77.0	2690	8	ACD15500	ACD15500 Human sec
C 271	15.4	77.0	2690	8	ACD18560	ACd18560 Human sec	C 344	15.4	77.0	2690	8	ABX16603	ABX16603 Human cDN
C 272	15.4	77.0	2690	8	ACA72049	ACA72049 Human sec	C 345	15.4	77.0	2690	9	ACA97544	ACA97544 Human PRO
C 273	15.4	77.0	2690	8	ABX98170	ABx98170 Human cDN	C 346	15.4	77.0	2690	9	ACA98993	ACA98993 Novel hum
C 274	15.4	77.0	2690	8	ABD13921	ABd13921 Human PRO	C 347	15.4	77.0	2690	9	ACC91625	ACC91625 Human sec
C 275	15.4	77.0	2690	8	ACD09701	ACD09701 Human sec	C 348	15.4	77.0	2690	9	ACD11036	ACD11036 Novel hum
C 276	15.4	77.0	2690	8	ACC88446	ACC88446 Human sec	C 349	15.4	77.0	2690	9	ACD14886	ACD14886 Human sec
C 277	15.4	77.0	2690	8	ACD21186	ACD21186 Human sec	C 350	15.4	77.0	2690	9	ACD11650	ACD11650 Human sec
C 278	15.4	77.0	2690	8	ABX75558	ABx75558 Human cDN	C 351	15.4	77.0	2690	9	ACC95779	ACC95779 Human sec
C 279	15.4	77.0	2690	8	ABX92689	ABx92689 cDNA enco	C 352	15.4	77.0	2690	9	ACF16342	ACF16342 Human sec
C 280	15.4	77.0	2690	8	ABX97761	ABx97761 Human PRO	C 353	15.4	77.0	2690	9	ACF02460	ACF02460 Human sec
C 281	15.4	77.0	2690	8	ACA97237	ACA97237 Novel hum	C 354	15.4	77.0	2690	9	ACF02767	ACF02767 Human sec
C 282	15.4	77.0	2690	8	ACA57700	ACA57700 Human PRO	C 355	15.4	77.0	2690	9	ACF21354	ACF21354 Human sec
C 283	15.4	77.0	2690	8	ACD14228	ACd14228 Human PRO	C 356	15.4	77.0	2690	9	ACF10038	ACF10038 Human sec
C 284	15.4	77.0	2690	8	ACC91011	ACC91011 Human sec	C 357	15.4	77.0	2690	9	ACF77931	ACF77931 Human sec
C 285	15.4	77.0	2690	8	ACC88753	ACC88753 Human sec	C 358	15.4	77.0	2690	9	ACD46636	ACD46636 Human sec
C 286	15.4	77.0	2690	8	ACD06950	ACD06950 Human PRO	C 359	15.4	77.0	2690	9	ACD49399	ACD49399 Human sec
C 287	15.4	77.0	2690	8	ACA67401	ACA67401 Human PRO	C 360	15.4	77.0	2690	9	ACF28166	ACF28166 Human sec
C 288	15.4	77.0	2690	8	ACC81456	ACC81456 Human sec	C 361	15.4	77.0	2690	9	ACD88856	ACD88856 Human sec
C 289	15.4	77.0	2690	8	ACC89060	ACC89060 Human sec	C 362	15.4	77.0	2690	9	ACD84251	ACD84251 Human PRO
C 290	15.4	77.0	2690	8	ACC86416	ACC86416 Human sec	C 363	15.4	77.0	2690	9	ACD99025	ACD99025 cDNA enco
C 291	15.4	77.0	2690	8	ACC89674	ACC89674 Human sec	C 364	15.4	77.0	2690	9	ADA77787	ADA77787 Human sec
C 292	15.4	77.0	2690	8	ACC92853	ACC92853 Human sec	C 365	15.4	77.0	2690	9	ACF48767	ACF48767 Human sec
C 293	15.4	77.0	2690	8	ACA72481	ACA72481 Human PRO	C 366	15.4	77.0	2690	9	ACD09087	ACD09087 Human sec
C 294	15.4	77.0	2690	8	ACA88999	ACA88999 Human sec	C 367	15.4	77.0	2690	9	ACF11880	ACF11880 Human sec
C 295	15.4	77.0	2690	8	ACA69735	ACA69735 Human sec	C 368	15.4	77.0	2690	9	ACF41114	ACF41114 Human sec
C 296	15.4	77.0	2690	8	ACA96878	ACA96878 Novel hum	C 369	15.4	77.0	2690	9	ACF15728	ACF15728 Human sec
C 297	15.4	77.0	2690	8	ACA90874	ACA90874 Novel hum	C 370	15.4	77.0	2690	9	ACF16035	ACF16035 Human sec
C 298	15.4	77.0	2690	8	ACA70856	ACA70856 Human sec	C 371	15.4	77.0	2690	9	ACD31862	ACD31862 Human sec
C 299	15.4	77.0	2690	8	ACA95166	ACA95166 Novel hum	C 372	15.4	77.0	2690	9	ACF18670	ACF18670 Human sec
C 300	15.4	77.0	2690	8	ACC86109	ACC86109 Human sec	C 373	15.4	77.0	2690	9	ACF09117	ACF09117 Human sec
C 301	15.4	77.0	2690	8	ACC89981	ACC89981 Human sec	C 374	15.4	77.0	2690	9	ACF78238	ACF78238 Human sec
C 302	15.4	77.0	2690	8	ACD12589	ACd12589 Human sec	C 375	15.4	77.0	2690	9	ACF51837	ACF51837 Human sec
C 303	15.4	77.0	2690	8	ACF19819	ACf19819 Human sec	C 376	15.4	77.0	2690	9	ACF26324	ACF26324 Human sec
C 304	15.4	77.0	2690	8	ABX76763	ABx76763 Human PRO	C 377	15.4	77.0	2690	9	ACF24117	ACF24117 Human sec
C 305	15.4	77.0	2690	8	ACA73095	ACA73095 Novel hum	C 378	15.4	77.0	2690	9	ACF63428	ACF63428 Human sec
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C 307	15.4	77.0	2690	8	ACA74482	ACA74482 cDNA enco	C 380	15.4	77.0	2690	9	ACH07773	ACH07773 Human sec
C 308	15.4	77.0	2690	8	ACA70349	ACA70349 Human sec	C 381	15.4	77.0	2690	9	ACF13579	ACF13579 Human sec
C 309	15.4	77.0	2690	8	ACD14535	ACd14535 Human PRO	C 382	15.4	77.0	2690	9	ACD41505	ACD41505 Human sec
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C 311	15.4	77.0	2690	8	ABX98672	ABx98672 Novel hum	C 384	15.4	77.0	2690	9	ACF23196	ACF23196 Human sec

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ALIGNMENTS

RESULT 1
AEB56869/c
ID AEB56869 standard; DNA; 105 BP.
XX AC AEB56869;
XX AC
XX AC
DT 22-SEP-2005 (first entry)
XX Human echovirus 30 5' untranslated polynucleotide sequence.
DE Human detection; enteroviral detection; ds.
XX DNA detection; enteroviral detection; ds.
XX Human echovirus 30.
XX US2005158710-A1.
XX PD 21-JUL-2005.
XX PD
XX 16-JAN-2004; 2004US-00760048.
XX PF
XX 16-JAN-2004; 2004US-00760048.
XX PR
XX (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; S76769.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (KI) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of ABB56764
 CC to ABB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX Sequence 105 BP; 22 A; 27 C; 27 G; 29 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 20; DB 14; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAGGAACACGGACACCCAA 20
 DB 100 AAGGAACACGGACACCCAA 81

RESULT 2
 ABB56868/c
 ID ABB56868 standard; DNA; 106 BP.
 AC ABB56868;
 XX 22-SEP-2005 (first entry)
 XX Human echovirus 30 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 XX Human echovirus 30.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; S76768.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (KI) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of ABB56764
 CC to ABB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX Sequence 106 BP; 21 A; 26 C; 27 G; 32 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 20; DB 14; Length 106;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAGGAACACGGACACCCAA 20
 DB 101 AAGGAACACGGACACCCAA 82

RESULT 3
 ABB56814/c
 ID ABB56814 standard; DNA; 107 BP.
 XX ABB56814;
 XX 22-SEP-2005 (first entry)
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:53.
 XX DNA detection; enteroviral detection; ds.
 XX Unidentified.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (KI) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of ABB56764
 CC to ABB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX Sequence 107 BP; 21 A; 26 C; 27 G; 32 T; 0 U; 0 Other;
 SQ

CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 107 BP; 22 A; 28 C; 28 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 107;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
 |||||
 Db 102 AAGGAACACGGACACCCAA 83

RESULT 4

AEB56813/c

ID AEB56813 standard; DNA; 110 BP.

XX AC AEB56813;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:52.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Teang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 52; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 110 BP; 21 A; 28 C; 29 G; 32 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 110;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
 |||||
 Db 105 AAGGAACACGGACACCCAA 86

RESULT 5

AEB56779/c

ID AEB56779 standard; DNA; 126 BP.

XX AC AEB56779;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:18.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Teang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 18; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 126 BP; 26 A; 36 C; 31 G; 33 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 126;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
 |||||
 Db 105 AAGGAACACGGACACCCAA 86

RESULT 6
ID AA258488 standard; RNA; 176 BP.
XX
AC AA258488;
XX
DT 15-SEP-2003 (revised)
DT 23-MAY-2000 (first entry)
XX
DE Recombinant poliovirus PVI(pr) IRES domain V-VI region.
XX
KW Internal ribosomal entry site; IRES; picornavirus; PVI(pr); tumour;
KW cancer; glioblastoma multiforme; medulloblastoma; mammary carcinoma;
KW prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;
KW bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.
XX
OS Human poliovirus 1.
OS Human rhinovirus sp; type 2.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT stem_loop . 1..109
FT /*tag= a
FT /*note= "domain V"
FT stem_loop 138..176
FT /*tag= b
FT /*note= "domain VI"
XX
FN WO200008166-A1.
XX
PD 17-FEB-2000.
XX
PF 09-APR-1999; 99WO-US007839.
XX
PR 05-AUG-1998; 98US-00129686.
XX
PA (UUNY) UNIV NEW YORK STATE RES FOUND.
XX
PI Gromeier M, Wimmer E;
XX
DR WPI; 2000-205717/18.
XX
PT Chimeric recombinant poliovirus useful for treating malignant tumors
PT comprises internal ribosomal entry site derived from picornaviruses.
XX
PS Example 6; Fig 7; 99pp; English.
XX
CC This sequence represents domains V-VI of the internal ribosomal entry
CC site (IRES) of PVI(pr), a recombinant, non-pathogenic oncolytic
CC poliovirus that carries the IRES of poliovirus type 1 Mahoney where the
CC terminal loop of regions of domain V and domain VI are substituted with
CC the corresponding fragments of human rhinovirus type 2 (HRV2). PVI(pr)
CC was characterized by a loss of neurovirulence, demonstrated by its
CC reduced ability to propagate within cells of neuronal origin and failure
CC to cause neurological disease in C57BL/6 mice. Oncolytic potential was
CC demonstrated against a panel of malignant cell lines. PVI(pr) is an
CC example of novel recombinant polioviruses (I) of the invention in which
CC the IRES of wild-type poliovirus is exchanged with the IRES of another
CC picornavirus, such as HRV2, and optionally the P1, P3 or 3' untranslated
CC region is exchanged with that of Sabin poliovirus. (I) are useful for
CC treating malignant tumors such as glioblastoma multiforme,
CC medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial
CC and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 176 BP; 42 A; 43 C; 40 G; 0 T; 51 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||

Db 118 AAGGAAACACGGACACCCAA 99
RESULT 7
ID AEB56834/c
XX AEB56834 standard; DNA; 180 BP.
XX AC AEB56834;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human coxsackievirus B1 5' untranslated polynucleotide sequence.
XX DNA detection; enteroviral detection; ds.
XX Human coxsackievirus B1.
XX US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PF 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
DR WPI; 2005-512251/52.
XX GENBANK; S76767.
XX
PT Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
PS Disclosure; Fig 1A-D; 34pp; English.
XX
CC The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||

Db 159 AAGGAAACACGGACACCCAA 140

RESULT 8
ID ABZ69931/c
XX ABZ69931 standard; DNA; 195 BP.
XX AC ABZ69931;
XX

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DT 04-APR-2003 (first entry)
XX Poliovirus type 3 sequence.
DE Analysis; detection; quantification; ss.
XX Poliovirus.
OS FR2824001-A1.
XX 31-OCT-2002.
XX 26-APR-2001; 2001FR-00005639.
XX 26-APR-2001; 2001FR-00005639.
XX (INMR ) BTO MERIEUX.
XX Perrin A, Theretz A, Delair T, Mandrand B;
XX WPI; 2003-186349/19.
XX Preparing a spot on a substrate surface, the sample is contained within a
XX liquid with magnetic particles to be deposited as a droplet, to be dried
XX together with a magnetic field to distribute the particles/molecules
XX evenly in the spot.
XX Example 3; Page 17; 26pp; French.
XX The present invention relates to a method for depositing a spot on a
XX substrate, containing a sample for study, comprising preparing the sample
XX in a liquid vehicle together with a magnetic support, to be deposited on
XX the surface of a substrate as a droplet. The sample bonds to the magnetic
XX support as particles. The sample material for analysis/ detection/
XX quantification can be cells, organisms, viruses and bacteria, antibodies,
XX antibody fragments, antigens, haptens, lectins, sugars, RNA and DNA,
XX proteins, hormones, hormone receptors, natural or synthetic molecules and
XX macro molecules, and the like. The present oligonucleotide from
XX Poliovirus type 3 was used in an example from the invention
XX SQ Sequence 195 BP; 42 A; 51 C; 50 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 122 AAGGAAACACGGACACCCAA 103

RESULT 9
AEB56860/c
ID AEB56860 standard; DNA; 198 BP.
XX AEB56860;
AC AEB56860;
XX 22-SEP-2005 (first entry)
XX Human echovirus 9 5' untranslated polynucleotide sequence.
DE DNA detection; enteroviral detection; ds.
XX Human echovirus 9.
OS US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX

DT 04-APR-2003 (first entry)
XX Poliovirus type 3 sequence.
DE Analysis; detection; quantification; ss.
XX Poliovirus.
OS FR2824001-A1.
XX 31-OCT-2002.
XX 26-APR-2001; 2001FR-00005639.
XX 26-APR-2001; 2001FR-00005639.
XX (INMR ) BTO MERIEUX.
XX Perrin A, Theretz A, Delair T, Mandrand B;
XX WPI; 2003-186349/19.
XX Preparing a spot on a substrate surface, the sample is contained within a
XX liquid with magnetic particles to be deposited as a droplet, to be dried
XX together with a magnetic field to distribute the particles/molecules
XX evenly in the spot.
XX Example 3; Page 17; 26pp; French.
XX The present invention relates to a method for depositing a spot on a
XX substrate, containing a sample for study, comprising preparing the sample
XX in a liquid vehicle together with a magnetic support, to be deposited on
XX the surface of a substrate as a droplet. The sample bonds to the magnetic
XX support as particles. The sample material for analysis/ detection/
XX quantification can be cells, organisms, viruses and bacteria, antibodies,
XX antibody fragments, antigens, haptens, lectins, sugars, RNA and DNA,
XX proteins, hormones, hormone receptors, natural or synthetic molecules and
XX macro molecules, and the like. The present oligonucleotide from
XX Poliovirus type 3 was used in an example from the invention
XX SQ Sequence 195 BP; 42 A; 51 C; 50 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 122 AAGGAAACACGGACACCCAA 103

RESULT 9
AEB56860/c
ID AEB56860 standard; DNA; 198 BP.
XX AEB56860;
AC AEB56860;
XX 22-SEP-2005 (first entry)
XX Human echovirus 9 5' untranslated polynucleotide sequence.
DE DNA detection; enteroviral detection; ds.
XX Human echovirus 9.
OS US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX

PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11709.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX SQ Sequence 198 BP; 39 A; 49 C; 52 G; 58 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 198;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 121 AAGGAAACACGGACACCCAA 102

RESULT 10
AEB56858/c
ID AEB56858 standard; DNA; 198 BP.
XX AEB56858;
AC AEB56858;
XX 22-SEP-2005 (first entry)
XX Human echovirus 6 5' untranslated polynucleotide sequence.
DE DNA detection; enteroviral detection; ds.
XX Human echovirus 6.
OS US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11709.
XX

```

PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 198 BP; 37 A; 47 C; 55 G; 59 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 198;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGACACCCAA 20

DB 121 AAGGAACACGACACCCAA 102

RESULT 11

AEB56863/c

ID AEB56863 standard; DNA; 198 BP.

XX AEB56863;

XX 22-SEP-2005 (first entry)

XX Human echovirus 11 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human echovirus 11.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; U11705.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit

CC (KI) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 198;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGACACCCAA 20

DB 121 AAGGAACACGACACCCAA 102

RESULT 12

AEB56854/c

ID AEB56854 standard; DNA; 198 BP.

XX AEB56854;

XX 22-SEP-2005 (first entry)

XX Human echovirus 4 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human echovirus 4.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; U11708.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

XX SQ Sequence 198 BP; 43 A; 48 C; 50 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 198;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 121 AAGGAAACACGGACACCCAA 102

RESULT 13

AEBS6816/c
ID AEB56816 standard; DNA; 236 BP.

XX AC AEB56816;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:55.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX FA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 55; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

XX SQ Sequence 236 BP; 59 A; 51 C; 46 G; 80 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 236;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 14

AEBS6837/c
ID AEB56837 standard; DNA; 237 BP.

XX AC AEB56837;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B2 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B2.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX FA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX DR GENBANK; AF081485.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

XX SQ Sequence 237 BP; 46 A; 54 C; 66 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 161 AAGGAAACACGGACACCCAA 142

RESULT 15

AEBS6862/c
ID AEB56862 standard; DNA; 237 BP.

XX

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AC AEB56862;
AD 22-SEP-2005 (first entry)
DE Human echovirus 9 5' untranslated polynucleotide sequence.
KW DNA detection; enteroviral detection; ds.
XX Human echovirus 9.
OS
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; X92886.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX Sequence 237 BP; 51 A; 55 C; 62 G; 69 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 14; Length 237;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAGGAAACACGGACACCCAA 20
XX |||||
XX DB 160 AAGGAAACACGGACACCCAA 141
XX
XX RESULT 16
XX AEB56879/c
XX ID AEB56879 standard; DNA; 237 BP.
XX AC AEB56879;
XX XX
XX DT 22-SEP-2005 (first entry)
XX DE Human poliovirus 3 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS
XX Human poliovirus 3.

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XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; K01392.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX Sequence 237 BP; 54 A; 57 C; 65 G; 61 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 14; Length 237;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAGGAAACACGGACACCCAA 20
XX |||||
XX DB 161 AAGGAAACACGGACACCCAA 142
XX
XX RESULT 17
XX AEB56881/c
XX ID AEB56881 standard; DNA; 237 BP.
XX AC AEB56881;
XX XX
XX DT 22-SEP-2005 (first entry)
XX DE Human poliovirus 3 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS
XX Human poliovirus 3.
XX FN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX

```

PA (TSAN//) TSANG S.
PA (PRIC//) PRICE J A.
PA (HELL//) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
DR GENBANK; X00925.
DR
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX Sequence 237 BP; 54 A; 56 C; 65 G; 62 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAACACGGACACCCAA 20
DB 161 AAGGAACACGGACACCCAA 142
RESULT 18
AEB56827/C
ID AEB56827 standard; DNA; 237 BP.
XX
XX AEB56827;
XX
XX 22-SEP-2005 (first entry)
XX
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:66.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Unidentified.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN//) TSANG S.
XX (PRIC//) PRICE J A.
XX (HELL//) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
DR
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX Sequence 237 BP; 53 A; 58 C; 55 G; 71 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAACACGGACACCCAA 20
DB 105 AAGGAACACGGACACCCAA 86
RESULT 19
AEB56875/C
ID AEB56875 standard; DNA; 237 BP.
XX
XX AEB56875;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human poliovirus 1 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Human poliovirus 1.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN//) TSANG S.
XX (PRIC//) PRICE J A.
XX (HELL//) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
DR GENBANK; V01149.
DR
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX Sequence 237 BP; 53 A; 58 C; 55 G; 71 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAACACGGACACCCAA 20
DB 105 AAGGAACACGGACACCCAA 86

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (1), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (1) and
 CC specifically and selectively recognizes the enterovirus genome. (1)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 237 BP; 57 A; 54 C; 62 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
 |||||
 DB 161 AAGGAACACGACACCCAA 142

RESULT 20
 AEB56876/C
 ID AEB56876 standard; DNA; 237 BP.
 XX
 AC AEB56876;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human poliovirus 1 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human poliovirus 1.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; V01150.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (1) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (1), and one or more container that contains (1); and (2)
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequences. (1), (M1) and
 XX (K1) are useful for detecting enterovirus target sequences. (1)
 XX specifically and selectively recognizes the enterovirus genome. (1)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 237 BP; 56 A; 54 C; 63 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGGAACACGACACCCAA 20
 |||||
 DB 161 AAGGAACACGACACCCAA 142

RESULT 21
 AEB56880/C
 ID AEB56880 standard; DNA; 237 BP.
 XX
 AC AEB56880;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human poliovirus 3 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human poliovirus 3.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; X00596.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (1) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (1), and one or more container that contains (1); and (2)
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequences. (1), (M1) and
 XX (K1) are useful for detecting enterovirus target sequences. (1)
 XX specifically and selectively recognizes the enterovirus genome. (1)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The
 XX present sequence represents a viral 5' untranslated polynucleotide
 XX sequence given in the exemplification of the present invention.
 XX Sequence 237 BP; 55 A; 56 C; 65 G; 61 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGGAACACGACACCCAA 20
 |||||
 DB 161 AAGGAACACGACACCCAA 142

RESULT 21
 AEB56880/C
 ID AEB56880 standard; DNA; 237 BP.
 XX
 AC AEB56880;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human poliovirus 3 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human poliovirus 3.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX GENBANK; X00596.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (1) consisting of: (a) the
 XX target binding sequence of an oligonucleotide chosen from any one of the
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 XX selected amplification or detection reaction. Also described: (1) a kit
 XX (K1) comprising (1), and one or more container that contains (1); and (2)
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 XX the target sequence using first amplification primer having a sequence
 XX consisting essentially of target binding sequence of any one of AEB56764
 XX to AEB56771 and optionally a sequence required for selected amplification
 XX reaction; and (b) detecting the amplified target sequences. (1), (M1) and
 XX (K1) are useful for detecting enterovirus target sequences. (1)
 XX specifically and selectively recognizes the enterovirus genome. (1)
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral
 XX genome and allows detection of broad range of enterovirus serotypes. The

Qy 1 AAGGAACACGGACACCCAA 20
 |||||
 Db 161 AAGGAACACGGACACCCAA 142

RESULT 22
 AEB56825/c

ID AEB56825 standard; DNA; 237 BP.

XX AC AEB56825;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:64.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 64; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I), (M1) and (K1) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

XX SQ Sequence 237 BP; 53 A; 58 C; 55 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

|||||
 Db 105 AAGGAACACGGACACCCAA 86

RESULT 23

AEB56805/c

ID AEB56805 standard; DNA; 237 BP.

XX AC AEB56805;

XX 22-SEP-2005 (first entry)
 DT Viral 5' untranslated polynucleotide sequence SEQ ID NO:44.
 DE DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 44; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I) sensitively and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

XX SQ Sequence 237 BP; 54 A; 53 C; 56 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

|||||
 Db 105 AAGGAACACGGACACCCAA 86

RESULT 24

AEB56818/c

ID AEB56818 standard; DNA; 237 BP.

XX AC AEB56818;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:57.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.
 XX PF 16-JAN-2004; 2004US-00760048.
 XX PR 16-JAN-2004; 2004US-00760048.
 XX PA (TSAN//) TSANG S.
 XX PA (PRIC//) PRICE J A.
 XX PA (HELL//) HELLYER T J.
 XX PI Tsang S, Price JA, Hellyer TJ;
 XX DR WPI; 2005-512251/52.
 XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
 XX PT detecting target, useful for detecting enterovirus nucleic acids.
 XX PS Disclosure; SEQ ID NO 57; 34pp; English.
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 237 BP; 50 A; 55 C; 59 G; 73 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAGGAACACGACACCCAA 20
 DB ||||||||||||||||||||
 105 AAGGAACACGACACCCAA 86
 RESULT 25
 AEB56873/c
 ID AEB56873 standard; DNA; 237 BP.
 XX AC AEB56873;
 XX DT 22-SEP-2005 (first entry)
 XX DE Human poliovirus 1 5' untranslated polynucleotide sequence.
 XX KW DNA detection; enteroviral detection; ds.
 XX OS Human poliovirus 1.
 XX FN US2005158710-A1.
 XX PD 21-JUL-2005.
 XX PF 16-JAN-2004; 2004US-00760048.
 XX PR 16-JAN-2004; 2004US-00760048.
 XX PA (TSAN//) TSANG S.
 XX PA (PRIC//) PRICE J A.
 XX PA (HELL//) HELLYER T J.
 XX PI Tsang S, Price JA, Hellyer TJ;
 XX DR WPI; 2005-512251/52.
 XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
 XX PT detecting target, useful for detecting enterovirus nucleic acids.
 XX PS Disclosure; SEQ ID NO 57; 34pp; English.
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 237 BP; 50 A; 55 C; 59 G; 73 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAGGAACACGACACCCAA 20
 DB ||||||||||||||||||||
 105 AAGGAACACGACACCCAA 86
 RESULT 26
 AEB56806/c
 ID AEB56806 standard; DNA; 237 BP.
 XX AC AEB56806;
 XX DT 22-SEP-2005 (first entry)
 XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:45.
 XX KW DNA detection; enteroviral detection; ds.
 XX OS Unidentified.
 XX FN US2005158710-A1.
 XX PD 21-JUL-2005.
 XX PF 16-JAN-2004; 2004US-00760048.
 XX PR 16-JAN-2004; 2004US-00760048.
 XX PA (TSAN//) TSANG S.
 XX PA (PRIC//) PRICE J A.
 XX PA (HELL//) HELLYER T J.
 XX PI Tsang S, Price JA, Hellyer TJ;
 XX DR WPI; 2005-512251/52.
 XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
 XX PT detecting target, useful for detecting enterovirus nucleic acids.
 XX PS Disclosure; SEQ ID NO 45; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 237 BP; 54 A; 53 C; 56 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 105 AAGGAACACGACACCCAA 86
|||||

RESULT 27
AEB56861/c
ID AEB56861 standard; DNA; 237 BP.
XX
AC AEB56861;
XX
XX 22-SEP-2005 (first entry)
XX Human echovirus 9 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Human echovirus 9.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Teang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Teang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; X84981.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX

CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 237 BP; 48 A; 54 C; 65 G; 70 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 160 AAGGAACACGACACCCAA 141
|||||

RESULT 28
AEB56817/c
ID AEB56817 standard; DNA; 237 BP.
XX
AC AEB56817;
XX
XX 22-SEP-2005 (first entry)
XX
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:56.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Unidentified.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Teang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; SEQ ID NO 56; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 237 BP; 52 A; 56 C; 58 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 29
AEB56820/c
ID AEB56820 standard; DNA; 237 BP.
AC AEB56820;
XX
DT 22-SEP-2005 (first entry)
XX
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:59.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Unidentified.
XX
PN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PF 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
DR
DR GENBANK; D00820.
XX
PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
PS Disclosure; SEQ ID NO 59; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and
CC (K1) are useful for detecting enterovirus target sequences. (I) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX Sequence 237 BP; 50 A; 53 C; 60 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 30
AEB56871/c
ID AEB56871 standard; DNA; 237 BP.
XX
AC AEB56871;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human enterovirus 70 5' untranslated polynucleotide sequence.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Human enterovirus 70.
XX
PN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PF 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
DR
DR GENBANK; D00820.
XX
PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
PS Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and
CC (K1) are useful for detecting enterovirus target sequences. (I) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX Sequence 237 BP; 54 A; 52 C; 60 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 161 AAGGAAACACGGACACCCAA 142

RESULT 31
AEB56821/c
ID AEB56821 standard; DNA; 237 BP.
XX
AC AEB56821;
XX
DT 22-SEP-2005 (first entry)
XX
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:60.

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XX DNA detection; enteroviral detection; ds.
XX Unidentified.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 60; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 237 BP; 49 A; 51 C; 61 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db ||||| ||||| ||||| ||||| |||||

RESULT 32
AEB56872/c
ID AEB56872 standard; DNA; 237 BP.
XX AC AEB56872;
XX DT 22-SEP-2005 (first entry)
XX DE Human poliovirus 1 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human poliovirus 1.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.

XX DNA detection; enteroviral detection; ds.
XX Unidentified.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 60; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 237 BP; 54 A; 56 C; 64 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db ||||| ||||| ||||| ||||| |||||

RESULT 33
AEB56782/c
ID AEB56782 standard; DNA; 237 BP.
XX AC AEB56782;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:21.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;

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DR WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 21; 34pp; English.

PS

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 46 A; 52 C; 61 G; 78 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20

DB 105 AAGGAACACGGACACCCAA 86

RESULT 34

AEB56824/C

ID AEB56824 standard; DNA; 237 BP.

XX

AC AEB56824;

XX

DT 22-SEP-2005 (first entry)

XX

DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:63.

XX

KW DNA detection; enteroviral detection; ds.

XX

OS Unidentified.

XX

PN US2005158710-A1.

XX

PD 21-JUL-2005.

XX

PP 16-JAN-2004; 2004US-00760048.

XX

PR 16-JAN-2004; 2004US-00760048.

XX

PA (TSAN/) TSANG S.

XX

PA (PRIC/) PRICE J A.

XX

PA (HELL/) HELLYER T J.

XX

PI Tsang S, Price JA, Hellyer TJ;

XX

DR WPI; 2005-512251/52.

XX

PT Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX

PS Disclosure; SEQ ID NO 63; 34pp; English.

XX

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 46 A; 52 C; 61 G; 78 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20

DB 105 AAGGAACACGGACACCCAA 86

RESULT 35

AEB56791/C

ID AEB56791 standard; DNA; 238 BP.

XX

AC AEB56791;

XX

DT 22-SEP-2005 (first entry)

XX

DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:30.

XX

KW DNA detection; enteroviral detection; ds.

XX

OS Unidentified.

XX

PN US2005158710-A1.

XX

PD 21-JUL-2005.

XX

PP 16-JAN-2004; 2004US-00760048.

XX

PR 16-JAN-2004; 2004US-00760048.

XX

PA (TSAN/) TSANG S.

XX

PA (PRIC/) PRICE J A.

XX

PA (HELL/) HELLYER T J.

XX

PI Tsang S, Price JA, Hellyer TJ;

XX

DR WPI; 2005-512251/52.

XX

PT Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX

PS Disclosure; SEQ ID NO 30; 34pp; English.

XX

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 53 A; 59 C; 55 G; 70 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20

DB 105 AAGGAACACGGACACCCAA 86

RESULT 35

AEB56791/C

ID AEB56791 standard; DNA; 238 BP.

XX

AC AEB56791;

XX

DT 22-SEP-2005 (first entry)

XX

DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:30.

XX

KW DNA detection; enteroviral detection; ds.

XX

OS Unidentified.

XX

PN US2005158710-A1.

XX

PD 21-JUL-2005.

XX

PP 16-JAN-2004; 2004US-00760048.

XX

PR 16-JAN-2004; 2004US-00760048.

XX

PA (TSAN/) TSANG S.

XX

PA (PRIC/) PRICE J A.

XX

PA (HELL/) HELLYER T J.

XX

PI Tsang S, Price JA, Hellyer TJ;

XX

DR WPI; 2005-512251/52.

XX

PT Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX

PS Disclosure; SEQ ID NO 30; 34pp; English.

XX

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 53 A; 59 C; 55 G; 70 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20

DB 105 AAGGAACACGGACACCCAA 86

CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

XX
SQ Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
|||||
Db 105 AAGGAACACGGACACCCAA 86

RESULT 36
AEB56826/c
ID AEB56826 standard; DNA; 238 BP.

XX AC AEB56826;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:65.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PA US2005158710-A1.

XX PN 21-JUL-2005.

XX PP 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 65; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 56 A; 52 C; 55 G; 75 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
|||||
Db 105 AAGGAACACGGACACCCAA 86

RESULT 37

AEB56849/c

ID AEB56849 standard; DNA; 238 BP.

XX AC AEB56849;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B5 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B5.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PP 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Teang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX DR GENBANK; X67706.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 53 A; 57 C; 61 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
|||||
Db 161 AAGGAACACGGACACCCAA 142

RESULT 38

AEB56846/c

ID AEB56846 standard; DNA; 238 BP.

XX

AC AEB56846;
 XX 22-SEP-2005 (first entry)
 DT Human coxsackievirus B4 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 DE
 XX
 KW
 XX
 OS Human coxsackievirus B4.
 XX
 XX
 PN US2005158710-A1.
 XX 21-JUL-2005.
 PD
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 PR
 XX (TSAN//) TSANG S.
 PA (PRIC//) PRICE J A.
 PA (HELL//) HELLYER T J.
 XX
 PI Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; D00149.
 DR
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 PT
 XX Disclosure; Fig 1A-D; 34pp; English.
 PS
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAGGAACACGGACACCCAA 20
 |||||
 Db 161 AAGGAACACGGACACCCAA 142
 RESULT 39
 AEB56847/C
 ID AEB56847 standard; DNA; 238 BP.
 AC
 XX AEB56847;
 XX 22-SEP-2005 (first entry)
 DT Human coxsackievirus B4 5' untranslated polynucleotide sequence.
 DE
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human coxsackievirus B4.

XX US2005158710-A1.
 PN 21-JUL-2005.
 PD
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 PR
 XX (TSAN//) TSANG S.
 PA (PRIC//) PRICE J A.
 PA (HELL//) HELLYER T J.
 XX
 PI Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; X05690.
 DR
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 PT
 XX Disclosure; Fig 1A-D; 34pp; English.
 PS
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAGGAACACGGACACCCAA 20
 |||||
 Db 161 AAGGAACACGGACACCCAA 142
 RESULT 40
 AEB56819/C
 ID AEB56819 standard; DNA; 238 BP.
 AC
 XX AEB56819;
 XX 22-SEP-2005 (first entry)
 DT Viral 5' untranslated polynucleotide sequence SEQ ID NO:58.
 DE DNA detection; enteroviral detection; ds.
 XX
 OS Unidentified.
 XX
 PN US2005158710-A1.
 XX 21-JUL-2005.
 PD
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 PR
 XX

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PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 58; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 50 A; 53 C; 60 G; 75 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAACACGGACACCCAA 20
Db 106 AAGGAACACGGACACCCNA 87
RESULT 41
AEB56807/c
ID AEB56807 standard; DNA; 238 BP.
AC AEB56807;
XX 22-SEP-2005 (first entry)
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:46.
XX DNA detection; enteroviral detection; ds.
XX Unidentified.
XX OS
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 61; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 53 A; 53 C; 58 G; 74 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAACACGGACACCCAA 20
Db 105 AAGGAACACGGACACCCNA 86
RESULT 42
AEB56822/c
ID AEB56822 standard; DNA; 238 BP.
XX AEB56822;
XX 22-SEP-2005 (first entry)
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:61.
XX DNA detection; enteroviral detection; ds.
XX Unidentified.
XX OS
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 61; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
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CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

XX
SQ Sequence 238 BP; 55 A; 51 C; 56 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
|||||
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 43

AEB56799/c
ID AEB56799 standard; DNA; 238 BP.

XX
AC AEB56799;

DT 22-SEP-2005 (first entry)

DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:38.

KW DNA detection; enteroviral detection; ds.

XX Unidentified.

PN US2005158710-A1.

XX 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; SEQ ID NO 38; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (i), and one or more container that contains (i); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

XX

SQ Sequence 238 BP; 57 A; 50 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
|||||
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 44

AEB56874/c
ID AEB56874 standard; DNA; 238 BP.

XX
AC AEB56874;

DT 22-SEP-2005 (first entry)

DE Human poliovirus 1 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

PN US2005158710-A1.

XX 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

DR GENBANK; V01148.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (i), and one or more container that contains (i); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
|||||
Db 162 AAGGAAACACGGACACCCAA 143

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RESULT 45
AEB56803/c
ID AEB56803 standard; DNA; 238 BP.
XX
XX AC AEB56803;
XX
XX DT 22-SEP-2005 (first entry)
XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:42.
XX
XX KW DNA detection; enteroviral detection; ds.
XX
XX OS Unidentified.
XX
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.
XX
XX PF 16-JAN-2004; 2004US-00760048.
XX
XX PR 16-JAN-2004; 2004US-00760048.
XX
XX PA (TSAN/) TSANG S.
XX
XX PA (PRIC/) PRICE J A.
XX
XX PA (HELL/) HELLYER T J.
XX
XX PI Tsang S, Price JA, Hellyer TJ;
XX
XX DR WPI; 2005-512251/52.
XX
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX PS Disclosure; SEQ ID NO 42; 34pp; English.
XX
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (KI) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX SQ Sequence 238 BP; 49 A; 52 C; 60 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
| | | | | | | | | | | | | |
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 46
AEB56829/c
ID AEB56829 standard; DNA; 238 BP.
XX
XX AC AEB56829;
XX
XX DT 22-SEP-2005 (first entry)
XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:13.
XX
XX KW DNA detection; enteroviral detection; ds.
XX
XX OS Unidentified.
XX
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.
XX
XX PF 16-JAN-2004; 2004US-00760048.
XX
XX PR 16-JAN-2004; 2004US-00760048.
XX
XX PA (TSAN/) TSANG S.
XX
XX PA (PRIC/) PRICE J A.
XX
XX PA (HELL/) HELLYER T J.
XX
XX PI Tsang S, Price JA, Hellyer TJ;
XX
XX DR WPI; 2005-512251/52.
XX
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX PS Disclosure; SEQ ID NO 42; 34pp; English.
XX
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (KI) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX SQ Sequence 238 BP; 51 A; 55 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
| | | | | | | | | | | | | |
Db 161 AAGGAAACACGGACACCCAA 142

RESULT 47
AEB56774/c
ID AEB56774 standard; DNA; 238 BP.
XX
XX AC AEB56774;
XX
XX DT 22-SEP-2005 (first entry)
XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:13.
XX
XX KW DNA detection; enteroviral detection; ds.
XX
XX OS Unidentified.
XX
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.

Consensus viral 5' untranslated polynucleotide sequence.
DNA detection; enteroviral detection; ds.
Synthetic.
US2005158710-A1.
21-JUL-2005.
16-JAN-2004; 2004US-00760048.
16-JAN-2004; 2004US-00760048.
(TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
Tsang S, Price JA, Hellyer TJ;
WPI; 2005-512251/52.
Novel oligonucleotide comprising sequences for binding and amplifying or
detecting target, useful for detecting enterovirus nucleic acids.
Disclosure; Fig 1A-D; 34pp; English.
The invention relates to an oligonucleotide (I) consisting of: (a) the
target binding sequence of an oligonucleotide chosen from any one of the
10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
selected amplification or detection reaction. Also described: (1) a kit
(KI) comprising (I), and one or more container that contains (I); and (2)
detecting (MI) an enterovirus target sequence, involving: (a) amplifying
the target sequence using first amplification primer having a sequence
consisting essentially of target binding sequence of any one of AEB56764
to AEB56771 and optionally a sequence required for selected amplification
reaction; and (b) detecting the amplified target sequences. (I), (M1) and
(KI) are useful for detecting enterovirus target sequences. (I)
specifically and selectively recognizes the enterovirus genome. (I)
sensitively and rapidly detects fewer than 500 copies of enteroviral
genome and allows detection of broad range of enterovirus serotypes. The
present sequence represents a consensus viral 5' untranslated
polynucleotide sequence given in the exemplification of the present
invention.
Sequence 238 BP; 51 A; 55 C; 65 G; 67 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
| | | | | | | | | | | | | |
Db 161 AAGGAAACACGGACACCCAA 142
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XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX DR Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; SEQ ID NO 13; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX CC (K1) are useful for detecting enterovirus target sequences. (I)
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 59 A; 51 C; 54 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCCAA 20
DB ||||| ||||| ||||| ||||| |||||
105 AAGGAACACGGACACCCAA 86

RESULT 48
AEB56792/c
ID AEB56792 standard; DNA; 238 BP.
XX AC AEB56792;
XX XX 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:31.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX XX US2005158710-A1.
XX FN 21-JUL-2005.
XX PD 16-JAN-2004; 2004US-00760048.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX DR GENBANK; X80059.
XX XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the

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CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
| | | | | | | | | | | | | | | | | |
Db 161 AAGGAACACGACACCCAA 142

RESULT 50
AEB56877/c
ID AEB56877 standard; DNA; 238 BP.
XX
AC AEB56877;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human poliovirus 2 5' untranslated polynucleotide sequence.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Human poliovirus 2.
XX
FN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PF 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.

(TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
XX
Tsang S, Price JA, Hellyer TJ;
XX
WPI; 2005-512251/52.
XX
GENBANK; M12197.
XX
Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
Disclosure; Fig 1A-D; 34pp; English.
XX
The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 238 BP; 56 A; 56 C; 63 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
| | | | | | | | | | | | | | | | | |
Db 161 AAGGAACACGACACCCAA 142

RESULT 51
AEB56794/c
ID AEB56794 standard; DNA; 238 BP.
XX
AC AEB56794;
XX
DT 22-SEP-2005 (first entry)
XX
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:33.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Unidentified.
XX
FN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PF 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.

(TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
XX
Tsang S, Price JA, Hellyer TJ;
XX
WPI; 2005-512251/52.
XX
Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
Disclosure; SEQ ID NO 33; 34pp; English.
XX
The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX (KI) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
SQ Sequence 238 BP; 59 A; 53 C; 53 G; 73 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;

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Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 52
AEB56859/c
ID AEB56859 standard; DNA; 238 BP.
XX AC AEB56859;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:15.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 15; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 238 BP; 47 A; 53 C; 66 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 161 AAGGAAACACGGACACCCAA 142

RESULT 53
AEB56859/c
ID AEB56859 standard; DNA; 238 BP.
XX AC AEB56859;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 238 BP; 47 A; 53 C; 66 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 161 AAGGAAACACGGACACCCAA 142

RESULT 54
AEB56809/c
ID AEB56809 standard; DNA; 238 BP.
XX AC AEB56809;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 15; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 238 BP; 58 A; 55 C; 55 G; 70 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 54
AEB56809/c
ID AEB56809 standard; DNA; 238 BP.
XX AC AEB56809;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.
XX KW DNA detection; enteroviral detection; ds.
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XX OS Unidentified.
XX PA
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX TS (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX DR WPI; 2005-512251/52.
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; SEQ ID NO 48; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
Db 105 AAGGAAACACGACACCCAA 86

RESULT 55
AEB56831/c
ID AEB56831 standard; DNA; 238 BP.
XX AC AEB56831;
XX DT 22-SEP-2005 (first entry)
XX DE Human coxsackievirus A16 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human coxsackievirus A16.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.

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XX TS (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX DR WPI; 2005-512251/52.
XX DR GENBANK; U05876.
XX TS Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
Db 161 AAGGAAACACGACACCCAA 142

RESULT 56
AEB56808/c
ID AEB56808 standard; DNA; 238 BP.
XX AC AEB56808;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:47.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX TS (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX DR WPI; 2005-512251/52.

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PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; SEQ ID NO 47; 34pp; English.
 XX
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGGAAACACGGACACCCAA 20
 DB 105 AAGGAAACACGGACACCCAA 86

RESULT 57
 AEB5682/c
 ID AEB5682 standard; DNA; 238 BP.
 XX
 AC AEB5682;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human poliovirus 3 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 3.
 OS US2005158710-A1.
 PN
 XX
 PD 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 DR GENBANK; X04468.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGGAAACACGGACACCCAA 20
 DB 161 AAGGAAACACGGACACCCAA 142

RESULT 58
 AEB56804/c
 ID AEB56804 standard; DNA; 238 BP.

XX AEB56804;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:43.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 43; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 48 A; 52 C; 60 G; 78 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACCCCAA 20
 Db 105 AAGGAACACGACCCCAA 86

RESULT 59
 AA258487/C
 ID AA258487 standard; RNA; 514 BP.

XX AA258487;
 XX 15-SEP-2003 (revised)
 DT 23-MAY-2000 (first entry)
 XX Poliovirus IRES domain II-VI region.

XX Internal ribosomal entry site; IRES; picornavirus; tumour; cancer;
 KW glioblastoma multiforme; medulloblastoma; mammary carcinoma;
 KW prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;
 KW bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.
 XX Human poliovirus 1.

XX Key Location/Qualifiers
 FT stem_loop 25..63
 FT /*tag= a
 FT /note= "domain II"
 FT stem_loop 70..83
 FT /*tag= b
 FT stem_loop 84..120
 FT /*tag= c
 FT /note= "domain III"
 FT stem_loop 132..338
 FT /*tag= d
 FT /note= "domain IV"
 FT stem_loop 183..209
 FT /*tag= e
 FT stem_loop 273..292
 FT /*tag= f
 FT stem_loop 346..454
 FT /*tag= g
 FT /note= "domain V"
 FT stem_loop 481..513
 FT /*tag= h
 FT /note= "domain VI"

XX WO200008166-A1.
 XX 17-FEB-2000.
 XX 09-APR-1999; 99WO-US007839.
 XX 05-AUG-1998; 98US-00129686.
 XX (UYNV) UNIV NEW YORK STATE RES FOUND.

XX Gromeier M, Wimmer E;
 XX WPI; 2000-205717/18.

XX Chimeric recombinant poliovirus useful for treating malignant tumors
 FT comprises internal ribosomal entry site derived from picornaviruses.
 XX Disclosure; Fig 2; 99pp; English.

XX This sequence represents domains II-VI of the internal ribosomal entry
 CC site (IRES) of wild-type poliovirus type 1 Mahoney. The invention
 CC provides non-pathogenic, oncolytic, recombinant polioviruses (I) in which
 CC the IRES of the wild-type poliovirus is exchanged with the IRES of
 CC another picornavirus, such as human rhinovirus type 2, and optionally the
 CC P1, P3 or 3' untranslated region is exchanged with that of Sabin
 CC poliovirus. (I) may contain a composite IRES encompassing IRES domains
 CC from both wild-type poliovirus and from another virus. (I) are useful for
 CC treating malignant tumors such as glioblastoma multiforme,
 CC medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial
 CC and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to
 XX standardise OS field)

SQ Sequence 514 BP; 122 A; 134 C; 132 G; 0 T; 126 U; 0 Other;
 Query Match 100.0%; Score 20; DB 3; Length 514;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACCCCAA 20
 Db 463 AAGGAACACGACCCCAA 444

RESULT 60
 AAQ58715/C
 ID AAQ58715 standard; DNA; 628 BP.

XX AAQ58715;
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 29-SEP-1994 (first entry)
 XX Poliovirus type 1 5'-UTR with C to G substn. at position 610.
 XX Platelet-Derived Growth Factor; heterodimer; PDGF-AB;
 KW recombinant protein production; PDGF-A chain; PDGF-B chain;
 KW bicistronic vector system; ss.

XX Human poliovirus 1 Mahoney.

XX Key Location/Qualifiers
 FT 5'UTR 1..628
 FT /*tag= a
 FT mutation 610
 FT /*tag= b
 FT /note= "wild-type C has been substituted by G"

XX WO9405786-A1.
 XX 17-MAR-1994.
 XX 26-AUG-1993; 93WO-EP002295.
 XX 27-AUG-1992; 92DE-04228457.
 XX (BEIE) BEIERSDORF AG.
 XX (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.

XX Eichner W, Achterberg V, Doerschner A, Meyer-Ingold W, Mielke H;
 XX Dirks W, Wirth M, Hauser H;
 XX WPI; 1994-101191/12.

XX Heterodimer platelet-derived-growth factor (PDGF) prodn. - using a
 FT polycistronic vector system in mammalian host cells for equimolar prodn
 FT of A- and B-chains.
 XX Claim 5; Page 41; 64pp; German.
 XX A PDGF-AB heterodimer is recombinantly produced using a bicistronic

CC expression unit in which a sequence responsible for internal translation
CC start (designated "IRES") is located between cistrons coding for the PDGF
CC -B and PDGF-A chains. The preferred IRES sequence for inclusion in the
CC bicistronic construct is the 5'-UTR from Poliovirus type 1 Mahoney strain
CC of sequence AAQ58715. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 628;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
DB 565 AAGGAACACGACACCCAA 546

RESULT 61
AAQ58726/c
ID AAQ58726 standard; DNA; 628 BP.
XX
AC AAQ58726;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 29-SEP-1994 (first entry)
XX
DE Poliovirus type 1 5'-UTR with C to G substn. at position 610.
XX
KW Multicistronic expression unit; recombinant protein production;
KW internal translation start; initiation; 5'-untranslated region; ss.
XX
OS Human poliovirus 1 Mahoney.

Key Location/Qualifiers

5'UTR 1..628
mutation /*tag= a
610 /*tag= b
/note= "wild-type C has been substituted by G"
XX
FN WO9405785-A1.

PD 17-MAR-1994.

PF 26-AUG-1993; 93WO-EP002294.

PR 27-AUG-1992; 92DE-04228458.

XX (BEIE) BEIERSDORF AG.
PA (GBPB) GBF GES BIOTECH FORSCHUNG GMBH.

XX Dirks W, Wirth M, Hauser H, Eichner W, Achterberg V;
PI Doerschner A, Meyer-Ingold W, Mielke H;
XX WPI; 1994-101190/12.

XX New multicistronic expression units - for producing equimolar amts. of
PT polypeptide(s) in mammalian cells as hosts.

PS Claim 6; Page 50; 109pp; German.

XX Heterodimeric proteins can be recombinantly produced using a
CC multicistronic (esp. bicistronic) expression unit in which a sequence
CC responsible for internal translation start (designated "IRES") is located
CC between cistrons coding for the different subunits. The preferred IRES
CC sequence is the 5'-UTR from Poliovirus type 1 Mahoney strain of sequence
CC AAQ58726. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
CC AUG-2003 to correct OS field.)

XX Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 628;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAACACGACACCCAA 20
DB 565 AAGGAACACGACACCCAA 546

RESULT 62
ADP74707/c
ID ADP74707 standard; DNA; 639 BP.

XX
AC ADP74707;
XX
DT 26-AUG-2004 (first entry)
XX

XX Novel bicistronic retroviral vector related poliovirus IRES sequence.
XX immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
KW severe combined immune deficiency syndrome; protein expression;
KW antisense; ds; gene.

XX Unidentified.

XX EP1428886-A1.

XX 16-JUN-2004.

XX 09-DEC-2002; 2002EP-00027555.

XX 09-DEC-2002; 2002EP-00027555.

XX (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.

XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;

XX WPI; 2004-452367/43.

XX Bicistronic retroviral vector, useful in gene therapy, particularly of
PT graft versus host disease, contains components of both murine embryonic
PT stem cell and myeloproliferative sarcoma viruses.

XX Disclosure; Page 70; 91pp; German.

XX The present invention relates to a new bicistronic retroviral vector.
CC These are used for (over)expression of proteins, suppressing expression
CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
CC suppress a dominant-negative phenotype, also infectious viral particles
CC that contain the vectors, in gene therapy, particularly for control of
CC guest versus host disease, especially where haematopoietic cells are
CC transduced with the vector or where T cells are transduced, for adoptive
CC immunotherapy, but also for treating severe combined immune deficiency
CC syndrome and for expression cloning of genes. The present sequence is a
CC vector sequence fragment shown in the exemplification of the invention.

XX Sequence 639 BP; 146 A; 171 C; 164 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 639;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
DB 569 AAGGAACACGACACCCAA 550

RESULT 63

ID ADU77356 standard; DNA; 682 BP.

XX
AC ADU77356;

```
DT 10-FEB-2005 (first entry)
XX DT
XX DE
XX DE Prima7 virus 5' UTR region DNA.
XX KW
XX KW Enteroviral genus related disease; Prima7-related disease; gene therapy;
XX KW ds.
XX OS
XX OS Prima7 virus.
XX XX
XX XX EPI479761-A1.
XX XX
XX XX 24-NOV-2004.
XX XX
XX XX 21-MAY-2003; 2003EP-00076529.
XX XX
XX XX 21-MAY-2003; 2003EP-00076529.
XX XX
XX XX (PRIM-) PRIMAGEN HOLDING BV.
XX XX
XX XX Maas HCGI, Van Den Broek PJM, Mang R;
XX XX
XX XX WPI; 2004-823915/82.
XX DR
XX XX New isolated or recombinant virus, useful for detecting a molecule
XX PT capable of specifically binding the virus in a sample, and as a vaccine
XX PT or medicament for treating or preventing Prima7-related disease.
XX PT
XX PS Example; SEQ ID NO 39; 5lpp; English.
XX XX
XX CC The present invention provides a new isolated or recombinant virus called
XX CC Prima7 (which belong to enteroviral species) comprising a nucleic acid
XX CC sequence or its functional part, derivative or analogue of the said
XX CC virus. The invention is useful for detecting and/or identifying a Prima7
XX CC enterovirus in a sample and for diagnosing an enteroviral genus related
XX CC disease. The vaccine or medicament prepared from the Prima7 virus is
XX CC useful for preventing and/or treating a Prima7-related disease. The
XX CC invention is also useful in gene therapy. The present sequence is Prima7
XX CC virus 5' UTR region DNA.
XX XX
XX SQ Sequence 682 BP; 176 A; 157 C; 159 G; 190 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 13; Length 682;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAACACGACACCCAA 20
Db 504 AAGGAACACGACACCCAA 485
RESULT 64
AEA00424/c
ID AEA00424 standard; DNA; 709 BP.
XX XX
XX AC AEA00424;
XX XX
XX DT 28-JUL-2005 (first entry)
XX XX
XX DE Enterovirus 71 5' untranslated region internal ribosome entry site DNA.
XX XX
XX KW vector; neurological disease; ds; gene therapy;
XX KW internal ribosome entry site; cystic fibrosis; cns-gen.;
XX KW respiratory-gen.; factor VIII deficiency; hemostatic; genetic disorder;
XX KW factor IX deficiency; Duchenne dystrophy; muscular-gen.;
XX KW Becker's disease; cancer; cytostatic; neoplasm;
XX KW acquired immune deficiency syndrome; anti-hiv; infectious disease;
XX KW antimicrobial.
XX XX
XX OS Human enterovirus 71; strain TW/2086/98.
XX XX
XX XX US2005112095-A1.
XX XX
XX XX 26-MAY-2005.
XX XX
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XX 08-JUL-2003; 2003US-00614283.
XX PF
XX XX
XX PR 09-JUL-2002; 2002US-0394269P.
XX XX
XX XX (HSUT/) HSU T.
XX PA (WUTJ/) WU T.
XX PA (LEEJ/) LEE J.
XX XX
XX FI Hsu T, Wu T, Lee J;
XX XX
XX DR WPI; 2005-371616/38.
XX XX
XX PT New nucleic acid vector for the expression of at least two cistrons
XX PT comprising a nucleotide sequence comprising an internal ribosome entry
XX PT site (IRES) e.g. enterovirus 71 (EV71), useful for treating a patient
XX PT having e.g. AIDS.
XX XX
XX PS Example 2; SEQ ID NO 1; 23pp; English.
XX XX
XX CC The present invention relates to a nucleic acid vector for the expression
XX CC of at least two cistrons. The vector comprises a promoter operably linked
XX CC to a nucleotide sequence comprising at least two cistrons and at least
XX CC one nucleotide sequence comprising an internal ribosome entry site (IRES)
XX CC selected from Human enterovirus 71 (EV71), Hepatitis C virus (HCV), or
XX CC Encephalomyocarditis virus (EMCV). The invention also provides a method
XX CC for screening of anti-viral compounds using the IRES. The invention is
XX CC useful for the genetic treatment of patients with cystic fibrosis,
XX CC hemophilia A or B, Duchenne or Becker type myopathy, cancer, AIDS and
XX CC other bacterial or infectious diseases due to a pathogenic organism and
XX CC in gene therapy. The present sequence is the enterovirus 71 5'
XX CC untranslated region (UTR) IRES DNA.
XX XX
XX SQ Sequence 709 BP; 165 A; 185 C; 172 G; 187 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 709;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAACACGACACCCAA 20
Db 534 AAGGAACACGACACCCAA 515
RESULT 65
ADW37919/c
ID ADW37919 standard; cDNA; 743 BP.
XX XX
XX AC ADW37919;
XX XX
XX DT 24-MAR-2005 (first entry)
XX XX
XX DE Poliovirus type 1 strain mahoney internal ribosomal entry site cDNA.
XX XX
XX KW SARS-coronavirus virus-like particle; SARS-CoV-VLP;
XX KW cellular immune response; humoral immune response; vaccine;
XX KW immunogenicity; cytotoxic T-lymphocyte; internal ribosomal entry site;
XX KW IRES; ss.
XX XX
XX OS Human poliovirus 1.
XX XX
XX XX US2005002953-A1.
XX XX
XX PD 06-JAN-2005.
XX XX
XX PF 04-MAY-2004; 2004US-00839729.
XX XX
XX PR 06-MAY-2003; 2003US-0468703P.
XX XX
XX PA (HERO/) HEROLD J.
XX XX
XX PI Herold J;
XX XX
```

DR WPI; 2005-065191/07.
 XX
 PT New system comprising one or more recombinant vectors that expresses the
 PT SARS-CoV E-protein, SARS-CoV M-protein, and SARS-CoV S-protein, useful
 PT for making SARS-coronavirus virus-like particles.
 XX
 PS Example 2; SEQ ID NO 21; 111pp; English.
 XX
 CC The present invention provides a system for making SARS-coronavirus virus
 CC -like particles (SARS-CoV-VLPs) comprising one or more recombinant
 CC vectors that express the SARS-CoV E (small membrane)-protein, SARS-CoV
 CC M (membrane)-protein and SARS-CoV S (spike)-protein. The invention is
 CC useful for inducing cellular and/or humoral immune response. The
 CC invention is also useful to reduce the symptoms of SARS-CoV infections
 CC and in vaccine preparations. The present sequence is Poliovirus type 1
 CC strain mahoney internal ribosomal entry site (IRES) cDNA. This cDNA
 CC sequence is used in the preparation of plasmid for the expression of SARS
 CC -CoV M, E and S proteins.
 XX
 SQ Sequence 743 BP; 175 A; 185 C; 181 G; 202 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 14; Length 743;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGGAACACGGACACCCAA 20
 DB 563 AAGGAACACGGACACCCAA 544
 RESULT 66
 ACC48197/c
 ID ACC48197 standard; cDNA; 745 BP.
 XX
 AC ACC48197;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Poliovirus internal ribosome entry site-containing mRNA 5' UTR.
 XX
 KW Internal ribosome entry site; IRES; translation; ss.
 XX
 OS Poliovirus.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..742
 FT /*tag= a
 XX
 PN WO200302927-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 03-SEP-2002; 2002WO-EP009843.
 XX
 PR 04-SEP-2001; 2001DE-01043237.
 XX
 PA (ICON-) ICON GENETICS INC.
 XX
 PI Atabekov J, Dorokhov Y, Skulachev M, Ivanov P, Gleba Y;
 DR WPI; 2003-313089/30.
 XX
 PT Creating nucleic acid sequence for carrying out translation by internal
 PT ribosome entry site element and expressing nucleotide sequence of
 PT interest in eukaryotic cell, by creating a nucleic acid having adenine-
 PT rich block.
 XX
 PS Disclosure; Fig 3; 48pp; English.
 XX
 CC The present sequence is that of a known internal ribosome entry site
 CC (IRES) element contained in the 5' untranslated region of poliovirus
 CC mRNA. The invention provides a method of creating an artificial IRES
 CC element having an adenine-rich (40-100 mol%) nucleic acid block of at

CC least 25 nucleotides and capable of causing cap-independent translation
 CC of a downstream nucleotide sequence of interest in eukaryotic cells, such
 CC as plant, animal or yeast cells (claimed). A method of identifying
 CC nucleic acid elements having IRES activity involving genome database
 CC searches is also provided. The methods allow the creation or
 CC identification of IRES elements that are universal with cross-kingdom and
 CC tailor-made activity
 XX
 SQ Sequence 745 BP; 163 A; 202 C; 193 G; 187 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 8; Length 745;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGGAACACGGACACCCAA 20
 DB 568 AAGGAACACGGACACCCAA 549
 RESULT 67
 ABK14791/c
 ID ABK14791 standard; DNA; 2076 BP.
 XX
 AC ABK14791;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Platelet-derived growth factor expression cassette insert used in pBC701.
 XX
 KW Platelet-derived growth factor; PDGF; transgenic; milk; gene;
 KW wound healing; diabetic foot ulcer; decubitus ulcer; ophthalmic disease;
 KW venous stasis ulcer; periodontal regeneration; bone formation;
 KW prosthetic vascular graft; pBC701; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200198520-A1.
 XX
 PD 27-DEC-2001.
 XX
 PF 19-JUN-2001; 2001WO-US041044.
 XX
 PR 19-JUN-2000; 2000US-0212406P.
 XX
 PA (GENZ) GENZYME TRANSGENICS CORP.
 XX
 PI Echelard Y, Meade H, Eichner W, Sommermeyer K;
 DR WPI; 2002-083329/11.
 XX
 PT Production of platelet derived growth factor (PDGF) comprises expression
 PT in the milk of a non-human transgenic animal.
 XX
 PS Example 1; Fig 1; 59pp; English.
 XX
 CC The invention relates to the production of platelet-derived growth factor
 CC (PDGF) comprising a transgenic mammal whose somatic and germ cells
 CC comprise a nucleic acid sequence (I) encoding PDGF, operably linked to a
 CC promoter directing expression into mammalian gland epithelial cells, and
 CC obtaining the milk from the transgenic mammal where at least 30% of the
 CC PDGF in the milk is as a dimer. Also described is a method of producing a
 CC transgenic mammal capable of expressing an active PDGF molecule in milk.
 CC Pharmaceutical compositions can be obtained from this milk and can be
 CC used to stimulate or enhance the wound healing process, in particular
 CC diabetic foot ulcers, decubitus ulcers and venous stasis ulcers.
 CC Transgenic PGF (II) can also be used in the treatment of periodontal
 CC regeneration, stimulation of bone formation, ophthalmic diseases or
 CC healing of prosthetic vascular grafts. (II) can also be used for non-
 CC medical applications, e.g., as a supplement for cell culture media or as
 CC a component of diagnostic kits. The present sequence represents the
 CC platelet-derived growth factor expression cassette insert used in pBC701
 CC vector of the invention

SQ Sequence 2076 BP; 441 A; 612 C; 607 G; 416 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 2076;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAGGAACACGACCCCAA 20
 |||||
 Db 1317 AAGGAACACGACCCCAA 1298
 RESULT 68
 AAH20890/c
 ID AAH20890 standard; DNA; 4148 BP.
 AC AAH20890;
 XX
 DT 11-SEP-2003 (revised)
 DT 24-AUG-2001 (first entry)
 XX
 DE Vector containing HIV gp41 DNA SEQ ID 1.
 KW Transmembrane anchor; gene therapy; endoplasmic reticulum; gp41;
 KW antiviral; HIV replication inhibitor; T lymphocyte; viral infection;
 KW hematopoietic stem cell; ds.
 XX
 OS Human immunodeficiency virus 1.
 XX
 XX Key Location/Qualifiers
 FH CDS 1438..1773
 FT /*tag= a
 FT
 XX WO200137881-A2.
 PN
 XX
 XX 31-MAY-2001.
 PD
 XX
 XX 24-NOV-2000; 2000WO-EP011733.
 PF
 XX
 XX 25-NOV-1999; 99DE-01057838.
 PR
 XX
 XX (PETT-) PETTE INST HEINRICH.
 FA
 XX
 XX Von Laer M;
 PI
 XX
 XX WPI; 2001-367622/38.
 DR
 XX P-PSDB; AAB86198.
 DR
 XX
 PT New nucleic acid encoding membrane-anchored gp41 fusion protein, useful
 PT for gene therapy of human immunodeficiency virus (HIV) infection,
 PT prevents entry of virus into cells.
 PT
 XX
 XX Claim 11; Page 28-30; 39pp; German.
 PS
 XX This invention describes a novel nucleic acid (I) comprising elements
 CC that encode a signal peptide (SP) that provides transfer of expressed
 CC polypeptide into the endoplasmic reticulum, a fragment (FI) of HIV gp41
 CC protein, containing a segment from a heptad repeat region, a
 CC transmembrane anchor (MSD) of a type I membrane protein and a flexible
 CC linker (hinge) linking FI and MSD, therefore the formula of (I) is SP-FI-
 CC hinge-MSD. The products of the invention have antiviral activity and act
 CC as HIV replication inhibitors. Vectors containing (I), also T lymphocytes
 CC or hematopoietic stem cells transfected in vitro with (I), are used in
 CC gene therapy of HIV infection. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 4148 BP; 880 A; 1177 C; 1103 G; 988 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 5; Length 4148;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAGGAACACGACCCCAA 20
 |||||

Db 2359 AAGGAACACGACCCCAA 2340
 RESULT 69
 ADO07652/c
 ID ADO07652 standard; DNA; 5252 BP.
 XX
 AC ADO07652;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Tricistronic expression cassette containing murine coding sequences.
 DE cytosstatic; virucide; anti-HIV; hepatotropic; neuroprotective;
 KW immunostimulant; expression cassette; viral vector; interleukin-12;
 KW co-stimulatory protein; cancer; infection; ds; gene.
 XX
 XX Mus sp.
 OS Synthetic.
 OS Unidentified.
 XX
 FN WO2004035799-A2.
 PD
 XX 29-APR-2004.
 XX
 PF 10-OCT-2003; 2003WO-EP011252.
 XX
 XX 11-OCT-2002; 2002DE-01048141.
 PR
 XX (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
 PA
 XX Waehler R, Schnieders F;
 XX
 XX WPI; 2004-357221/33.
 DR
 XX
 PT Viral vector that expresses single-chain interleukin-12 and costimulator,
 PT useful for treatment of tumors, viral infections, e.g. human
 PT immunodeficiency virus, and prion diseases.
 XX
 PS Disclosure; Fig 18; 129pp; German.
 XX
 CC The present invention relates to a viral vector that includes a nucleic
 CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
 CC protein. Viral vectors and virus particles derived from them are useful
 CC for treatment of tumors, infectious diseases (e.g. HIV, hepatitis A, B
 CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
 CC present sequence is a tricistronic expression cassette used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 5252 BP; 1347 A; 1386 C; 1300 G; 1219 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 12; Length 5252;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAGGAACACGACCCCAA 20
 |||||
 Db 2853 AAGGAACACGACCCCAA 2834
 RESULT 70
 ADP74699/c
 ID ADP74699 standard; DNA; 7185 BP.
 XX
 AC ADP74699;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Novel bicistronic retroviral vector related vector #1.
 XX
 KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
 KW severe combined immune deficiency syndrome; protein expression;
 KW antisense; ds; gene.

```

XX OS Synthetic.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT LTR 424..994
XX FT /tag= a
XX FT /standard_name= "5'-LTR"
XX FT 995..1487
XX FT 5'UTR /tag= b
XX FT CDS 1488..2615
XX FT /tag= c
XX FT /product= "HSV-TK"
XX FT misc_RNA 2626..3250
XX FT /tag= d
XX FT /standard_name= "IRES"
XX FT CDS 3298..4098
XX FT /tag= e
XX FT /product= "neo"
XX FT LTR 4345..4931
XX FT /tag= f
XX FT /standard_name= "3'-LTR"
XX PN EP1428886-A1.
XX XX
XX PD 16-JUN-2004.
XX PF 09-DEC-2002; 2002EP-00027555.
XX PR 09-DEC-2002; 2002EP-00027555.
XX PA (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
XX PI Heberlein C, Gindullis F, Hannemann J, Strathmann G;
XX DR WPI; 2004-452367/43.
XX DR
XX PS Disclosure; Page 58-59; 91pp; German.
XX CC The present invention relates to a new bicistronic retroviral vector.
XX CC These are used for (over)expression of proteins, suppressing expression
XX CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
XX CC suppress a dominant-negative phenotype, also infectious viral particles
XX CC that contain the vectors, in gene therapy, particularly for control of
XX CC guest versus host disease, especially where haematopoietic cells are
XX CC transduced with the vector or where T cells are transduced, for adoptive
XX CC immunotherapy, but also for treating severe combined immune deficiency
XX CC syndrome and for expression cloning of genes. The present sequence is a
XX CC vector sequence shown in the exemplification of the invention.
XX SQ Sequence 7185 BP; 1579 A; 2013 C; 1943 G; 1650 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 7185;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 3188 AAGGAAACACGGACACCCAA 3169

RESULT 71
ADP74701/c
ID ADP74701 standard; DNA; 7185 BP.
XX AC ADP74701;
XX DT 26-AUG-2004 (first entry)
XX ID ADP74714 standard; DNA; 7235 BP.

```

```

DE Novel bicistronic retroviral vector related vector #3.
XX immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
XX severe combined immune deficiency syndrome; protein expression;
XX antisense; ds; gene.
XX OS Synthetic.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT LTR 424..994
XX FT /tag= a
XX FT /standard_name= "5'-LTR"
XX FT 995..1487
XX FT 5'UTR /tag= b
XX FT CDS 1488..2615
XX FT /tag= c
XX FT /product= "HSV-TK splice variant"
XX FT misc_RNA 2626..3250
XX FT /tag= d
XX FT /standard_name= "IRES"
XX FT CDS 3298..4098
XX FT /tag= e
XX FT /product= "neo"
XX FT LTR 4345..4931
XX FT /tag= f
XX FT /standard_name= "3'-LTR"
XX PN EP1428886-A1.
XX XX
XX PD 16-JUN-2004.
XX PF 09-DEC-2002; 2002EP-00027555.
XX PR 09-DEC-2002; 2002EP-00027555.
XX PA (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
XX PI Heberlein C, Gindullis F, Hannemann J, Strathmann G;
XX DR WPI; 2004-452367/43.
XX DR
XX PS Disclosure; Page 63-65; 91pp; German.
XX CC The present invention relates to a new bicistronic retroviral vector.
XX CC These are used for (over)expression of proteins, suppressing expression
XX CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
XX CC suppress a dominant-negative phenotype, also infectious viral particles
XX CC that contain the vectors, in gene therapy, particularly for control of
XX CC guest versus host disease, especially where haematopoietic cells are
XX CC transduced with the vector or where T cells are transduced, for adoptive
XX CC immunotherapy, but also for treating severe combined immune deficiency
XX CC syndrome and for expression cloning of genes. The present sequence is a
XX CC vector sequence shown in the exemplification of the invention.
XX SQ Sequence 7185 BP; 1581 A; 2013 C; 1942 G; 1649 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 7185;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 3188 AAGGAAACACGGACACCCAA 3169

RESULT 72
ADP74714/c
ID ADP74714 standard; DNA; 7235 BP.

```

XX ADP74714;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Novel bicistronic retroviral vector related vector #6.
 XX
 KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
 KW severe combined immune deficiency syndrome; protein expression;
 KW antisense; ds; gene.
 XX
 XX Synthetic.
 OS Unidentified.
 XX
 XX
 FH Key Location/Qualifiers
 FT LTR 424..994
 FT /*tag= a
 FT /*standard_name= "5'-LTR"
 FT 5'UTR 995..1537
 FT /*tag= b
 FT CDS 1538..2665
 FT /*tag= c
 FT /*product= "HSV-TK splice variant"
 FT misc_RNA 2676..3300
 FT /*tag= d
 FT /*standard_name= "IRES"
 FT CDS 3348..4148
 FT /*tag= e
 FT /*product= "neo"
 FT LTR 4395..4981
 FT /*tag= f
 FT /*standard_name= "3'-LTR"
 XX
 XX EP1428886-A1.
 XX
 XX 16-JUN-2004.
 XX
 XX 09-DEC-2002; 2002EP-00027555.
 XX
 XX 09-DEC-2002; 2002EP-00027555.
 XX
 XX (CELL-) CELLTech GMBH BIOTECHNOLOGIE.
 XX
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;
 XX WPI; 2004-452367/43.
 XX
 XX Bicistronic retroviral vector, useful in gene therapy, particularly of
 XX graft versus host disease, contains components of both murine embryonic
 XX stem cell and myeloproliferative sarcoma viruses.
 XX
 XX Disclosure; Page 75-77; 91pp; German.
 XX
 XX The present invention relates to a new bicistronic retroviral vector.
 XX These are used for (over)expression of proteins, suppressing expression
 XX of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
 XX suppress a dominant-negative phenotype, also infectious viral particles
 XX that contain the vectors, in gene therapy, particularly for control of
 XX guest versus host disease, especially where haematopoietic cells are
 XX transduced with the vector or where T cells are transduced, for adoptive
 XX immunotherapy, but also for treating severe combined immune deficiency
 XX syndrome and for expression cloning of genes. The present sequence is a
 XX vector sequence shown in the exemplification of the invention.
 XX
 XX Sequence 7235 BP; 1594 A; 2025 C; 1950 G; 1666 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 20; DB 12; Length 7235;
 XX Best Local Similarity 100.0%; Pred. No. 13;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGGAACACGACCCAA 20
 Db 3238 AAGGAACACGACCCAA 3219

RESULT 73
 ADP74715/c
 ID ADP74715 standard; DNA; 7235 BP.
 XX
 AC ADP74715;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Novel bicistronic retroviral vector related vector #7.
 XX
 KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
 KW severe combined immune deficiency syndrome; protein expression;
 KW antisense; ds; gene.
 XX
 XX Synthetic.
 OS Unidentified.
 XX
 XX
 FH Key Location/Qualifiers
 FT LTR 424..994
 FT /*tag= a
 FT /*standard_name= "5'-LTR"
 FT 5'UTR 995..1537
 FT /*tag= b
 FT CDS 1538..2665
 FT /*tag= c
 FT /*product= "HSV-TK splice variant"
 FT misc_RNA 2676..3300
 FT /*tag= d
 FT /*standard_name= "IRES"
 FT CDS 3348..4148
 FT /*tag= e
 FT /*product= "neo"
 FT LTR 4395..4981
 FT /*tag= f
 FT /*standard_name= "3'-LTR"
 XX
 XX EP1428886-A1.
 XX
 XX 16-JUN-2004.
 XX
 XX 09-DEC-2002; 2002EP-00027555.
 XX
 XX 09-DEC-2002; 2002EP-00027555.
 XX
 XX (CELL-) CELLTech GMBH BIOTECHNOLOGIE.
 XX
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;
 XX WPI; 2004-452367/43.
 XX
 XX Bicistronic retroviral vector, useful in gene therapy, particularly of
 XX graft versus host disease, contains components of both murine embryonic
 XX stem cell and myeloproliferative sarcoma viruses.
 XX
 XX Disclosure; Page 78-79; 91pp; German.
 XX
 XX The present invention relates to a new bicistronic retroviral vector.
 XX These are used for (over)expression of proteins, suppressing expression
 XX of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
 XX suppress a dominant-negative phenotype, also infectious viral particles
 XX that contain the vectors, in gene therapy, particularly for control of
 XX guest versus host disease, especially where haematopoietic cells are
 XX transduced with the vector or where T cells are transduced, for adoptive
 XX immunotherapy, but also for treating severe combined immune deficiency
 XX syndrome and for expression cloning of genes. The present sequence is a
 XX vector sequence shown in the exemplification of the invention.
 XX
 XX Sequence 7235 BP; 1595 A; 2025 C; 1949 G; 1666 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 20; DB 12; Length 7235;
 XX Best Local Similarity 100.0%; Pred. No. 13;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 3238 AAGGAAACACGGACACCCAA 3219

RESULT 74
ADP74700/c
ID ADP74700 standard; DNA; 7235 BP.
XX AC
XX ADP74700;
XX 26-AUG-2004 (first entry)
XX DE Novel bicistronic retroviral vector related vector #2.
XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
XX KW severe combined immune deficiency syndrome; protein expression;
XX KW antisense; ds; gene.
XX OS Synthetic.
XX OS Unidentified.
XX FH Key
XX LTR Location/Qualifiers
424..994
/*tag= a
/standard_name= "5'-LTR"
995..1537
/*tag= b
1538..2665
/*tag= c
/product= "HSV-TK"
2676..3300
/*tag= d
/standard_name= "IRES"
3348..4148
/*tag= e
/product= "neo"
4395..4981
/*tag= f
/standard_name= "3'-LTR"
EP1428886-A1.
16-JUN-2004.
09-DEC-2002; 2002EP-00027555.
09-DEC-2002; 2002EP-00027555.
(CELL-) CELLS/TECH GMBH BIOTECHNOLOGIE.
Heberlein C, Gindullis F, Hannemann J, Strathmann G;
WPI; 2004-452367/43.
Bicistronic retroviral vector, useful in gene therapy, particularly of
graft versus host disease, contains components of both murine embryonic
stem cell and myeloproliferative sarcoma viruses.
Disclosure; Page 60-62; 91pp; German.
The present invention relates to a new bicistronic retroviral vector.
These are used for (over)expression of proteins, suppressing expression
of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
suppress a dominant-negative phenotype, also infectious viral particles
that contain the vectors, in gene therapy, particularly for control of
graft versus host disease, especially where haematopoietic cells are
transduced with the vector or where T cells are transduced, for adoptive
immunotherapy, but also for treating severe combined immune deficiency
syndrome and for expression cloning of genes. The present invention is a
vector sequence shown in the exemplification of the invention.

XX SQ Sequence 7235 BP; 1592 A; 2025 C; 1951 G; 1667 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 12; Length 7235;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 3238 AAGGAAACACGGACACCCAA 3219

RESULT 75
ADP74713/c
ID ADP74713 standard; DNA; 7235 BP.
XX AC
XX ADP74713;
XX 26-AUG-2004 (first entry)
XX DE Novel bicistronic retroviral vector related vector #5.
XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
XX KW severe combined immune deficiency syndrome; protein expression;
XX KW antisense; ds; gene.
XX OS Synthetic.
XX OS Unidentified.
XX FH Key
XX LTR Location/Qualifiers
424..994
/*tag= a
/standard_name= "5'-LTR"
995..1537
/*tag= b
1538..2665
/*tag= c
/product= "HSV-TK"
2676..3300
/*tag= d
/standard_name= "IRES"
3348..4148
/*tag= e
/product= "neo"
4395..4981
/*tag= f
/standard_name= "3'-LTR"
EP1428886-A1.
16-JUN-2004.
09-DEC-2002; 2002EP-00027555.
09-DEC-2002; 2002EP-00027555.
(CELL-) CELLS/TECH GMBH BIOTECHNOLOGIE.
Heberlein C, Gindullis F, Hannemann J, Strathmann G;
WPI; 2004-452367/43.
Bicistronic retroviral vector, useful in gene therapy, particularly of
graft versus host disease, contains components of both murine embryonic
stem cell and myeloproliferative sarcoma viruses.
Disclosure; Page 72-74; 91pp; German.
The present invention relates to a new bicistronic retroviral vector.
These are used for (over)expression of proteins, suppressing expression
of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
suppress a dominant-negative phenotype, also infectious viral particles
that contain the vectors, in gene therapy, particularly for control of

CC guest verus host disease, especially where haematopoietic cells are
CC transduced with the vector or where T cells are transduced, for adoptive
CC immunotherapy, but also for treating severe combined immune deficiency
CC syndrome and for expression cloning of genes. The present sequence is a
CC vector sequence shown in the exemplification of the invention.
XX
SQ Sequence 7235 BP; 1593 A; 2025 C; 1950 G; 1667 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 7235;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20
|||||

Db 3238 AAGGAACACGGACACCCAA 3219

RESULT 76

ABX12440/C

ID ABX12440 standard; DNA; 7392 BP.

XX AC ABX12440;

XX DT 10-MAY-2003 (first entry)

XX DE Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome.

XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.

XX OS Coxsackievirus.

XX FH Key Location/Qualifiers

FT misc_feature 1..87
/tag= a
/note= "Specifically claimed in claim 16"
FT misc_feature 88..512
/tag= b
/note= "Specifically claimed in claim 19"
FT misc_feature 513..742
/tag= c
/note= "Specifically claimed in claim 22"
FT misc_feature 742
/tag= d
/note= "Specifically claimed in claim 25"
FT CDS 743..7303
/tag= f
/product= "Polyprotein"
FT misc_feature 743..952
/tag= e
/note= "Specifically claimed in claim 26"
FT misc_feature 953..1726
/tag= g
/note= "Specifically claimed in claim 29"
FT misc_feature 1727..2441
/tag= h
/note= "Specifically claimed in claim 32"
FT misc_feature 2442..3296
/tag= i
/note= "Specifically claimed in claim 35"
FT misc_feature 3297..3737
/tag= j
/note= "Specifically claimed in claim 38"
FT misc_feature 3738..4033
/tag= k
/note= "Specifically claimed in claim 41"
FT misc_feature 4034..5029
/tag= l
/note= "Specifically claimed in claim 44"

XX PN WO2002103060-A2.

XX PD 27-DEC-2002.

XX PF 19-JUN-2002; 2002WO-IB003278.

XX PR 20-JUN-2001; 2001SE-00002198.

XX PA (INNO-) INNOVENTUS PROJECT AB.

XX FI Tuvemo HT, Friisk GE, Yin H;

XX DR WPI; 2003-278229/27.

XX DR P-PSDB; ABG75961.

XX FT Polymerase chain reaction and primers for detecting nucleic acids from
the diabetogenic coxsackie B virus-4 strain VD2921.

XX PS Example 5; Page 64-66; 79pp; English.

XX CC The invention describes a polymerase chain reaction (PCR) and primers for
detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
P3C and P3D nucleic acids). The methods and primers are used for the
detection of CBV-4 strain VD2921 which is associated with diabetes
(diabetogenic enterovirus). Early detection of the diabetes e.g.
detection of diabetogenic enteroviral RNA in peripheral mononuclear
cells, can improve prognosis by allowing treatment e.g. with antiviral
drugs, to prevent further loss of beta cells and severe long term
consequences of diabetes including blindness, renal failure and leg
amputations. This sequence represents the genome of diabetogenic
coxsackie B virus 4 (CBV-4) strain VD2921

XX SQ Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 7392;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20

Db 568 AAGGAACACGGACACCCNA 549

RESULT 77

AAZ98719/C

ID AAZ98719 standard; cDNA; 7400 BP.

XX AC AAZ98719;

XX DT 20-JUN-2000 (first entry)

XX DE Swine vesicular disease virus (SVDV) N3 mutant strain gene sequence.

XX KW Swine vesicular disease virus; SVDV; swine vesicular disease;

XX KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;

XX KW differentiation; vaccine; prevent; ss.

XX OS Swine vesicular disease virus.

XX FH Key Location/Qualifiers

XX FT misc_feature 2693..2710

FT /tag= a

FT /note= "Nucleotides in this position replace the wild-
type nucleotide sequence of strain Taiwan Yu-Li (see
AAZ98717)"

XX PN EP982403-A1.

XX PD 01-MAR-2000.

XX PF 14-AUG-1998; 98EP-00306486.

XX PR 14-AUG-1998; 98EP-00306486.

CC	(SVDV) gene sequence from the SVDV strain Taiwan Yu-Li. SVDV is the
CC	causative agent of swine vesicular disease, which is very similar to foot
CC	and mouth disease. The invention relates to the wild-type Taiwan Yu-Li
CC	strain cDNA sequence, and the gene sequences of the mutant SVDV strains
CC	N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a
CC	vaccine for the prophylaxis of swine vesicular disease. The invention
CC	also includes a method for differentiating the mutant SVDV nucleotide
CC	sequences from the wild type strain of SVDV, coxsackievirus and foot-and-
CC	mouth disease virus through the use of polymerase chain reaction
XX	
SQ	Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;
	Query Match 100.0%; Score 20; DB 3; Length 7400;
	Best Local Similarity 100.0%; Pred. No. 13;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 AAGGAACACGGACACCCAA 20
DB	568 AAGGAACACGGACACCCAA 549
RESULT 79	
AAZ98718/C	
ID	AAZ98718 standard; cDNA; 7400 BP.
XX	
AC	AAZ98718;
XX	
DT	20-JUN-2000 (first entry)
XX	
DE	Swine vesicular disease virus (SVDV) H21 mutant strain gene sequence.
XX	
KW	Swine vesicular disease virus; SVDV; swine vesicular disease;
KW	Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
KW	differentiation; vaccine; prevent; ss.
XX	
OS	Swine vesicular disease virus.
XX	
FH	Key Location/Qualifiers
FT	misc_feature 2705..2710
FT	/*tag= a
FT	/note= "Nucleotides in this position replace the wild-
FT	type nucleotide sequence of strain Taiwan Yu-Li AAZ98717"
XX	
PN	EP982403-A1.
XX	
PD	01-MAR-2000.
XX	
PF	14-AUG-1998; 98EP-00306486.
XX	
PR	14-AUG-1998; 98EP-00306486.
XX	
PA	(BIOT-) DEV CENT BIOTECHNOLOGY.
XX	
PI	Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;
XX	
DR	WPI; 2000-258616/23.
XX	
PT	Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
PT	to prevent swine vesicular disease.
XX	
PS	Claim 3; Page; 66pp; English.
XX	
CC	This sequence represents the full length Swine vesicular disease virus
CC	(SVDV) gene sequence from the SVDV strain H21. SVDV is the causative
CC	agent of swine vesicular disease, which is very similar to foot and mouth
CC	disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA
CC	sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
CC	SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
CC	prophylaxis of swine vesicular disease. The invention also includes a
CC	method for differentiating the mutant SVDV nucleotide sequences from the
CC	wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
CC	virus through the use of polymerase chain reaction. Note: This sequence
CC	is not present in the specification, but has been derived from the wild-

```

CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
CC 34-38 of the specification
XX
SQ Sequence 7400 BP; 2082 A; 1785 C; 1863 G; 1670 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 568 AAGGAACACGACACCCAA 549

RESULT 80
AAZ9863/C
ID AAA29863 standard; cDNA; 7400 BP.
XX
AC AAA29863;
XX
DT 30-AUG-2000 (first entry)
XX
DE Swine vesicular disease virus (SVDV) nucleotide sequence.
XX
KW Swine vesicular disease virus; SVDV; vesicular disease; vaccine; ss.
XX
OS Swine vesicular disease virus.
XX
CN1244583-A.
XX
FN 16-FEB-2000.
XX
PD 12-AUG-1998; 98CN-00117165.
XX
PR 12-AUG-1998; 98CN-00117165.
XX
PA (BIOL-) BIOLOGICAL TECHNOLOGY DEV CENT.
XX
FI Huang Q, Luo Z, Yang Y;
XX
DR WPI; 2000-388169/34.
XX
PT Native swine vesicular disease virus gene and its variant - useful as
XX vaccines.
XX
PS Claim 1; Page 1-5; 54pp; Chinese.
XX
CC The present invention describes a native swine vesicular disease virus
CC (SVDV) gene and its variant. Also described are: (1) an expression
CC plasmid containing the gene; (2) preparation of the gene and its variant;
CC and (3) a vaccine comprising the gene or its variant. The new gene is
CC useful for the treatment of vesicular disease. The present sequence
CC represents a specifically claimed SVDV nucleotide sequence from the
CC present invention
XX
SQ Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 568 AAGGAACACGACACCCAA 549

RESULT 81
AAZ98720/C
ID AAZ98720 standard; cDNA; 7421 BP.
XX
AC AAZ98720;
XX
DT 20-JUN-2000 (first entry)

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```

XX Swine vesicular disease virus (SVDV) SP7 mutant strain gene sequence.
DE
XX Swine vesicular disease virus; SVDV; swine vesicular disease;
KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
KW differentiation; vaccine; prevent; ss.
XX
OS Swine vesicular disease virus.
XX
FH Key Location/Qualifiers
FT misc_feature 2705..2731
FT /*tag= a
FT /note= "Nucleotides in this position replace the
FT nucleotides at position 2705-2710 of the SVDV wild-type
FT Taiwan Yu-Li strain (see AAZ98717)."
XX
XX EP982403-A1.
XX
FN 01-MAR-2000.
XX
PD 14-AUG-1998; 98EP-00306486.
XX
PR 14-AUG-1998; 98EP-00306486.
XX
PA (BIOT-) DEV CENT BIOTECHNOLOGY.
XX
PI Hong CL, Lo C, Yang Y, Jeng K, Chang EL;
XX
DR WPI; 2000-259616/23.
XX
PT Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
XX to prevent swine vesicular disease.
XX
PS Claim 5; Page: 66pp; English.
XX
CC This sequence represents the full length swine vesicular disease virus
CC (SVDV) gene sequence from the SVDV strain SP7. SVDV is the causative
CC agent of swine vesicular disease, which is very similar to foot and mouth
CC disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA
CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
CC prophylaxis of swine vesicular disease. The invention also includes a
CC method for differentiating the mutant SVDV nucleotide sequences from the
CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
CC virus through the use of polymerase chain reaction. Note: This sequence
CC is not present in the specification, but has been derived from the wild-
CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
CC 34-38 of the specification
XX
SQ Sequence 7421 BP; 2090 A; 1792 C; 1867 G; 1672 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 7421;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 568 AAGGAACACGACACCCAA 549

RESULT 82
AAQ30148/C
ID AAQ30148 standard; cDNA; 7431 BP.
XX
AC AAQ30148;
XX
DT 24-OCT-2003 (revised)
DT 16-APR-1993 (first entry)
XX
DE Attenuated (472U, 537A) poliovirus type 3 Leon strain.
XX
KW vaccine; polioviruses; poliomyelitis; virulence; immunise; inoculate.
XX

```

```

OS Human poliovirus 3; strain Leon.
XX AU9176128-A.
XX
XX
XX 15-OCT-1992.
XX
XX 29-APR-1991; 91AU-00076128.
XX
XX 10-APR-1991; 91GB-00007552.
XX
XX (ALMO/) ALMOND J W.
XX (MINO/) MINOR P D.
XX (MACA/) MACADAM A J.
XX (STON/) STONE D M.
XX
XX Macadam AJ, Minor PD, Stone DM, Almond JW;
XX WPI; 1992-399255/49.
XX
XX New attenuated poliovirus for vaccines - in which 5-non-coding region of
XX genome is 5 non-coding region of polio-virus type 3 Leon strain modified
XX by uracil and adenine etc.
XX
XX Claim 1; Page 12; 14pp; English.
XX
XX This is an attenuated poliovirus type 3 Leon strain in which the 5' non-
XX coding region of the genome is modified by substitution with U at posn.
XX 472, and A at posn. 537. The attenuated poliovirus may be used in a
XX vaccine against polioviruses. They may be administered orally, as a nasal
XX spray, or parenterally. A dose corresp. to the amt. admin. for a
XX conventional live virus vaccine, such as up to 10power6 TCID50 for a
XX sabin vaccine strain in the case of poliovirus may be admin. (Updated on
XX 24-OCT-2003 to standardise OS field)
XX
XX Sequence 7431 BP; 2148 A; 1738 C; 1749 G; 1796 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 7431;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20
DB 568 AAGGAACACGGACACCCAA 549

RESULT 83
AAQ22965/C
ID AAQ22965 standard; cDNA; 7432 BP.
XX
XX AAQ22965;
XX
XX 25-MAR-2003 (revised)
XX 14-JUL-1992 (first entry)
XX
XX True type 3 poliovirus vaccine strain cDNA.
XX
XX RNA virus; error reduction; ss.
XX
XX Poliovirus.
XX
XX Key Location/Qualifiers
XX CDS 743..7364
XX FT /*tag= b
XX mutation 2493
XX FT /*tag= a
XX FT /*note= "want to maintain C"
XX
XX WO9203538-A.
XX
XX 05-MAR-1992.
XX
XX 20-AUG-1991; 91WO-US005890.
XX

```

```

PR 20-AUG-1990; 90US-00569916.
PR 20-AUG-1990; 90US-00570000.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Racaniello V, Ta, Tatem JM, Weekslevy CL;
XX
XX WPI; 1992-096882/12.
XX P-PSDB; AAR22210.
XX
XX New vaccine against infectious polio-virus comprises RNA virus - for
XX producing RNA virus cDNA and viable RNA virus.
XX
XX Claim 7; Fig 6; 110pp; English.
XX
XX The cDNA sequence is that of a true RNA virus, i.e. the cDNA directs the
XX prodn. of a viable RNA virus which is phenotypically similar to the
XX source virus. Viral RNA was isolated from a virus pellet obtd. from a
XX culture of primary monkey kidney cells infected with an attenuated strain
XX 3 poliovirus. The RNA was sequenced and compared to the published
XX P3/Sabin cDNA sequence (Stanway et al., Proc. Natl. Acad. Sci. USA, 81;
XX 1539-43 (1984)). Two nucleotide differences were observed; at position
XX 2493 a T in the Stanway sequence was replaced by a C in the new sequence
XX and at position 6061 a C was replaced by a U(T). The viral DNA was then
XX used as a template for the synthesis of ds cDNA which was used to produce
XX a cDNA library in pUC9. A full length cDNA was determined from several
XX clones isolated from the library. On sequencing, three differences were
XX found in the cDNA, compared to the RNA sequence, at positions 198, 4466
XX and 6334. Site directed mutagenesis was used to correct the sequence at
XX each point. Fragments contg. the correct sequence were amplified by PCR
XX and then ligated to form a true P3/Sabin cDNA in a plasmid pVR318. On
XX sequencing, the plasmid was found to have a T at position 2493 instead of
XX a C. In order to change this, a SacI/HindIII fragment spanning a
XX nucleotides 1895-4241 from pVR318 was removed and replaced with a
XX corresp. fragment from a subclone pLJ3-271. The resulting ligation prod.
XX pLJED3, represents a true full length type 3 polio- virus vaccine strain
XX cDNA. The RNA viruses are used in vaccines against polio. The screening
XX method can be used during amplification of the source virus for vaccine
XX prodn. to ensure maintenance of C at position 2493 in the viral genome
XX i.e. increasing the attenuation. The new prod. overcomes the problem of
XX errors introduced during replication of ss RNA, which is much higher than
XX for ds DNA. See also AAQ22966,7. (Updated on 25-MAR-2003 to correct PA
XX field.)
XX
XX Sequence 7432 BP; 2148 A; 1743 C; 1738 G; 1803 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 7432;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20
DB 568 AAGGAACACGGACACCCAA 549

RESULT 84
AAN20042/C
ID AAN20042 standard; cDNA; 7440 BP.
XX
XX AAN20042;
XX
XX 28-OCT-2003 (revised)
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 05-AUG-1992 (first entry)
XX
XX Sequence of a full-length cDNA copy of the poliovirus genome in plasmid
XX pVR106.
XX
XX Poliovirus; picornavirus; vaccine; antigen; immunogen; ss.
XX
XX Homo sapiens; poliovirus.
XX

```

```
PH Key Location/Qualifiers
FT CDS 743..949
FT /*tag= a
FT /product= "p4"
FT CDS 950..1765
FT /*tag= b
FT /product= "VP2"
FT CDS 1766..2479
FT /*tag= c
FT /product= "VP3"
FT CDS 2480..3385
FT /*tag= d
FT /product= "VP1"
FT CDS 3386..3832
FT /*tag= e
FT /product= "3b"
FT CDS 3833..4123
FT /*tag= f
FT /product= "5b"
FT CDS 4124..5110
FT /*tag= g
FT /product= "X"
FT CDS 5111..5371
FT /*tag= h
FT /product= "1b"
FT CDS 5372..5986
FT /*tag= i
FT /product= "VPg"
FT CDS 5987..7375
FT /*tag= j
FT /product= "4(p63)"
XX
XX W08203632-A.
XX
XX 28-OCT-1982.
XX
XX 20-APR-1981; 81US-00255879.
XX
XX 20-APR-1981; 81US-00255879.
XX 12-NOV-1981; 81US-00320525.
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Baltimore D, Racanietello VR;
XX
XX WPI; 1982-95059E/44.
XX P-PSDB; AAP20037.
XX
XX Prodn. of CDNA representing viral RNA sequences - by transcription,
XX insertion into vector and host cell transformation.
XX
XX Example; Table 1, pages 25-31; 50pp; English.
XX
XX Plasmid pVR106 was produced by combining plasmids pVR104 and pVR105. It
XX contains a full-length cDNA copy of the poliovirus genome. E.coli HB101
XX contg. this plasmid has been registered as ATCC 31844. The full-length
XX poliovirus cDNA molecule is itself infectious and can be introduced into
XX cells and these cultured to produce RNA virus. Alternatively, the
XX infectious cDNA can be treated with mutagens and the altered material
XX used to infect cells so that attenuated viral RNA is prod. and this used
XX to make vaccines. For antibody prodn., cDNA capable of directing antigen
XX prodn. is selected and isolated and incorporated into cells which are
XX incubated to produce RNA antigen. (Updated on 25-MAR-2003 to correct PA
XX field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 28-OCT-
XX 2003 to standardise OS field)
XX
XX Sequence 7440 BP; 2205 A; 1734 C; 1716 G; 1785 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 1; Length 7440;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAGGAAACACGGACACCCAA 20
XX
XX
```

```
Db 565 AAGGAAACACGGACACCCAA 546
|||
RESULT 85
AAX26152/c
ID AAX26152 standard; DNA; 7441 BP.
XX
XX AAX26152;
AC
XX 21-MAY-1999 (first entry)
DT
XX
XX DNA sequence of human poliovirus 1.
XX
XX Replication-competent; Sabin type 1 poliovirus vector; cloning site;
XX 3C-protease cleavage site; mucosal vaccine; infectious disease; AIDS;
XX human immunodeficiency virus type 1; HIV-1; small pox; poliomyelitis;
XX Hepatitis C; acquired immunodeficiency syndrome; Mahoney vector; viral;
XX poliovirus; ss.
XX
XX Poliovirus.
XX
XX W09907859-A1.
FN
XX
XX 18-FEB-1999.
PD
XX
XX 07-AUG-1998; 98WO-KR000242.
PF
XX
XX 07-AUG-1997; 97KR-00037812.
XX
XX (ALTW-) ALTWELL BIOTECH INC.
PA
XX
XX Bae YS, Jung HR;
PI
XX
XX WPI; 1999-167434/14.
DR
XX
XX New replication-competent recombinant Sabin type 1 poliovirus vector -
XX useful for developing mucosal vaccines against HIV-type 1, small pox,
XX poliomyelitis and hepatitis C.
XX
XX Disclosure; Page 51-55; 64pp; English.
XX
XX The invention relates to a replication-competent recombinant Sabin type 1
XX poliovirus vector encoding a multiple cloning site and 3C-protease
XX cleavage site between the two end N-terminal residues. This comprises a
XX vector containing an exogenous vaccine gene at the multiple cloning site.
XX A method of production of both vectors is also provided. The recombinant
XX vectors are useful for developing various mucosal vaccines against a
XX number of infectious diseases, including human immunodeficiency virus
XX type 1 (HIV-1) (which causes acquired immunodeficiency syndrome (AIDS)),
XX small pox, poliomyelitis and Hepatitis C. The poliovirus-mediated mucosal
XX vaccine vectors overcome the disadvantages exhibited by Mahoney vectors
XX by being safe to humans, replicable (having equal replication ability to
XX that of the wild type) vectors, where the introduced vaccine genes are
XX stably maintained during viral passages
XX
XX Sequence 7441 BP; 2210 A; 1730 C; 1715 G; 1786 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 7441;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAGGAAACACGGACACCCAA 20
XX
XX 565 AAGGAAACACGGACACCCAA 546
|||
RESULT 86
ACC43138/c
ID ACC43138 standard; DNA; 7873 BP.
XX
XX ACC43138;
AC
XX
```

```
DT 17-JUN-2003 (first entry)
XX Nucleotide sequence of gene expression vector pGFPstopneo.
DE Gene expression vector; beta-galactosidase; luciferase; pGFPstopneo; ss.
KW Gene expression vector; beta-galactosidase; luciferase; pGFPstopneo; ss.
XX Synthetic.
OS WO2003014361-A1.
XX 20-FEB-2003.
XX 31-JUL-2002; 2002WO-EP008520.
XX 02-AUG-2001; 2001EP-00118632.
XX (ALTA-) ALTANA PHARMA AG.
XX Hauser H, Mueller PP, Schaefer KP, Steinhilber W;
XX WPI; 2003-268203/26.
XX New recombinant gene expression vector, useful for producing a host cell
PT clone highly expressing a gene of interest, comprises a promoter
PT sequence, gene of interest, translational stop signal and a selectable
PT marker gene.
XX
XX Example 1; Fig 12; 52pp; English.
XX The specification describes a recombinant gene expression vector, which
CC comprises a promoter sequence; a gene of interest encoding beta-
CC galactosidase; a TGA translational stop signal; and translationally
CC linked to the gene of interest a selectable marker gene encoding
CC luciferase. The recombinant gene expression vector is useful for
CC producing a host cell clone expressing a gene of interest. The vector is
CC also useful for the selection of transformed host cells that express a
CC gene of interest. The present sequence represents pGFPstopneo. It was
CC used during construction of vectors of the invention
XX
XX Sequence 7873 BP; 1939 A; 2060 C; 2053 G; 1821 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 7873;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGGAACACGACACCCAA 20
DB 3286 AAGGAACACGACACCCAA 3267
RESULT 87
ADP74702/c
ID ADP74702 standard; DNA; 7925 BP.
XX ADP74702;
XX 26-AUG-2004 (first entry)
XX Novel bicistronic retroviral vector related vector #4.
XX immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
KW severe combined immune deficiency syndrome; protein expression;
KW antisense; ds; gene.
XX Synthetic.
OS Unidentified.
XX
XX Key Location/Qualifiers
FH LTR 162..674
FT /*tag= a
FT /standard name= "5'-LTR"
FT 5'UTR 675..1572
FT /*tag= b
```

```
FT CDS 1573..2700
FT /*tag= c
FT /product= "HSV-TK"
FT misc_RNA 2711..3335
FT /*tag= d
FT /standard_name= "IRES"
FT CDS 3383..4183
FT /*tag= e
FT /product= "neo"
FT LTR 4478..5067
FT /*tag= f
FT /standard_name= "3'-LTR"
XX
XX EP1428886-A1.
XX 16-JUN-2004.
XX 09-DEC-2002; 2002EP-00027555.
XX 09-DEC-2002; 2002EP-00027555.
XX (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;
XX WPI; 2004-452367/43.
XX
XX Bicistronic retroviral vector, useful in gene therapy, particularly of
PT graft versus host disease, contains components of both murine embryonic
PT stem cell and myeloproliferative sarcoma viruses.
XX
XX Disclosure; Page 66-68; 91pp; German.
XX
XX The present invention relates to a new bicistronic retroviral vector.
CC These are used for (over)expression of proteins, suppressing expression
CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
CC suppress a dominant-negative phenotype, also infectious viral particles
CC that contain the vectors, in gene therapy, particularly for control of
CC guest versus host disease, especially where haematopoietic cells are
CC transduced with the vector or where T cells are transduced, for adoptive
CC immunotherapy, but also for treating severe combined immune deficiency
CC syndrome and for expression cloning of genes. The present sequence is a
CC vector sequence shown in the exemplification of the invention.
XX
XX Sequence 7925 BP; 1714 A; 2242 C; 2135 G; 1834 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 12; Length 7925;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGGAACACGACACCCAA 20
DB 3273 AAGGAACACGACACCCAA 3254
RESULT 88
ACC43139/c
ID ACC43139 standard; DNA; 7943 BP.
XX ACC43139;
XX 17-JUN-2003 (first entry)
XX Nucleotide sequence of gene expression vector pGFPstopneoSECIS.
XX Gene expression vector; beta-galactosidase; luciferase; pGFPstopneoSECIS;
KW ss.
XX Synthetic.
XX WO2003014361-A1.
XX 20-FEB-2003.
PD
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XX 31-JUL-2002; 2002WO-EP008520.
PF
XX
XX 02-AUG-2001; 2001EP-00118632.
PR
XX
XX (ALTA-) ALTANA PHARMA AG.
PA
XX
XX Hauser H, Mueller PP, Schaefer KP, Steinhilber W;
PI
XX WPI; 2003-268203/26.
DR
XX
XX New recombinant gene expression vector, useful for producing a host cell
XX clone highly expressing a gene of interest, comprises a promoter
XX sequence, gene of interest, translational stop signal and a selectable
XX marker gene.
XX
XX Example 4; Fig 13; 52pp; English.
XX
XX The specification describes a recombinant gene expression vector, which
XX comprises a promoter sequence; a gene of interest encoding beta-
XX galactosidase; a TGA translational stop signal; and translationally
XX linked to the gene of interest a selectable marker gene encoding
XX luciferase. The recombinant gene expression vector is useful for
XX producing a host cell clone expressing a gene of interest. The vector is
XX also useful for the selection of transformed host cells that express a
XX gene of interest. The present sequence represents pGFPstopneoSEClS. It
XX was used during construction of vectors of the invention
XX
XX Sequence 7943 BP; 1958 A; 2074 C; 2074 G; 1837 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 8; Length 7943;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 3286 AAGGAACACGGACACCCAA 3267

RESULT 89
ID AAV18096/C
XX
XX AAV18096 standard; DNA; 8298 BP.
AC AAV18096;
XX
XX 04-AUG-1998 (first entry)
XX
XX pMCLDHAP tricistronic vector for the expression of hmAb45-TNF alpha.
XX
XX Circular; antibody-cytokine fusion protein; tricistronic vector;
XX TNF alpha; IL-2; IRES; internal ribosome entry site; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX promoter 1..904
XX /tag= a
XX /note= "CMV promoter with an upstream MPSV enhancer"
XX intron 905..976
XX /tag= b
XX /number= Intron 1
XX sig_peptide 977..1018
XX /tag= c
XX /note= "Partial leader sequence"
XX 5'UTR 1019..1106
XX /tag= d
XX /note= "5'UTR from poliovirus"
XX CDS 1107..1433
XX /tag= e
XX /product= "Light chain hmAb425, variable region"
XX sig_peptide 1107..1115
XX /tag= f
XX /note= "Rest of the leader sequence"
XX

```

```

FT intron 1260..2581
FT /tag= k
FT /number= 3
FT intron 1434..1595
FT /tag= g
FT /number= Intron 2
FT CDS 1596..1913
FT /tag= h
FT /product= "Light chain hmAb425, constant region"
FT 5'UTR 1914..2028
FT /tag= i
FT /note= "5' UTR from poliovirus"
FT RBS 2029..2159
FT /tag= j
FT /note= "Poliovirus derived internal ribosome entry site"
FT CDS 2582..4537
FT /tag= l
FT /note= "Heavy chain hmAb425 fused to TNF alpha"
FT misc_feature 4555..5279
FT /tag= m
FT /note= "Comprises of a 5' UTR from poliovirus, an
FT internal ribosome entry site and intron 4"
FT CDS 5280..5876
FT /tag= n
FT /product= "Puromycin acetyl transferase"
FT /note= "Selection marker"
FT polyA_signal 5929..6181
FT /tag= o
FT /standard_name= "SV40 PolyA"
XX
XX WO9811241-A1.
XX
XX 19-MAR-1998.
PD
XX
XX 02-SEP-1997; 97WO-EP004765.
PF
XX
XX 16-SEP-1996; 96EP-00114820.
PR
XX
XX 30-SEP-1996; 96EP-00115635.
PR
XX
XX (MERE ) MERCK PATENT GMBH.
PA
XX
XX Von Hoegen I, Burge C, Bruemmer W, Dunker R, Rieke E, Welge T;
XX Hauser H, Mielke C;
PI
XX
XX WPI; 1998-207400/18.
DR
XX
XX P-PSDS; AAW48647, AAW48648, AAW48649, AAW48650, AAW48651.
DR
XX
XX Oligo:cistronic expression vector - useful for production of, e.g.
XX MAb425/TNF--a or MAb425/IL-2 antibody fusion protein.
PT
XX
XX Claim 11; Fig 15; 89pp; English.
PS
XX
XX The present sequence represents a new pMCLDHAP tricistronic vector for
XX the expression of an antibody-cytokine fusion protein, hmAb425-TNF alpha.
XX hmAb425-TNF alpha comprises of the TNF alpha fused to the C-terminus of
XX the heavy chain of humanized by the IL-2 sequence. The TNF alpha
XX sequence can be substituted by the IL-2 sequence. The hmAb425 has
XX specificity for the human EGF receptor. The vector also contains a strong
XX promoter/enhancer unit, a selection marker gene and at least two
XX poliovirus derived internal ribosomal entry site (IRES) sequences. The
XX vector can be expressed in mammalian host cells for the production of
XX heteromeric fusion proteins. This expression system is claimed to produce
XX the heteromeric proteins in high yields
XX
XX Sequence 8298 BP; 1974 A; 2364 C; 2134 G; 1826 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 2; Length 8298;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 5140 AAGGAACACGGACACCCAA 5121

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RESULT 90
ABK86535/c
ID ABK86535 standard; DNA; 10448 BP.
XX - AC ABK86535;
XX
DT 07-AUG-2003 (revised)
DT 30-AUG-2002 (first entry)
XX
XX
DE BIAV based retroviral vector PONY8-BIC.
XX
XX Parkinson's disease; gene therapy; retroviral vector; ds; cyclic; EIAV;
KW neuroprotective; antiparkinsonian; NOI; IRES; lentiviral particle;
KW nucleotide site of interest; Internal Ribosome Entry Site; PONY8-BIC;
KW tyrosine hydroxylase; GTP-cyclohydrolase 1; bicistronic cassette;
KW Aromatic Amino Acid Dopa Decarboxylase; triscistronic cassette;
KW Vesicular Monoamine Transporter 2; neurodegenerative disease.
XX
XX
OS Equine infectious anemia virus.
OS Human cytomegalovirus.
OS Escherichia coli.
OS Aequorea victoria.
OS Homo sapiens.
OS Synthetic.
XX
XX WO200229065-A2.
XX
XX 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-GB004433.
XX
XX 06-OCT-2000; 2000GB-00024550.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Kingsman AJ, Mazarakis ND, Martin-Rendon E, Azzouz M, Rohll J;
XX WPI; 2002-507885/54.
XX
XX A novel retroviral vector genome is useful in the treatment of
XX Parkinson's disease.
XX
XX
XX Example 8; Page 67-69; 106pp; English.
XX
XX The invention relates to a retroviral vector genome (G1) comprising two
XX or more NOIs (nucleotide sites of interest), operably linked by one or
XX more Internal Ribosome Entry Site(s) (IRES). Also included are a vector
XX system (S1) comprising (G1), production (M1) of a lentiviral particle, a
XX viral particle (P1) produced by (M1) or by (S1), a pharmaceutical
XX composition comprising (G1), (S1) or (P1), a bicistronic cassette
XX comprising a nucleotide sequence which encodes: a) tyrosine hydroxylase
XX and a nucleotide sequence that encodes GTP-cyclohydrolase 1 operably
XX linked by one or more IRES(s); or b) Aromatic Amino Acid Dopa
XX Decarboxylase and a nucleotide sequence which encodes Vesicular Monoamine
XX Transporter 2 operably linked by one or more IRES(s); a triscistronic
XX cassette comprising a nucleotide sequence which encodes tyrosine
XX hydroxylase, a nucleotide sequence that encodes GTP-cyclohydrolase 1 and
XX a nucleotide sequence which encodes Aromatic Amino Acid Dopa
XX Decarboxylase, operably linked by one or more IRES(s) and a cell that has
XX been transduced with (S1). G1, the vector system (S1), and the viral
XX particle (P1) can all be used to treat and/or prevent (by gene therapy) a
XX neurodegenerative disease, especially Parkinson's disease in a subject,
XX and also in the manufacture of a pharmaceutical composition to treat the
XX above mentioned disease. Treatment with vectors capable of delivering
XX e.g., Tyrosine hydroxylase, GTP-cyclohydrolase 1, Aromatic Amino Acid
XX Dopa Decarboxylase and Vesicular Monoamine Transporter 2, are useful for
XX the last stages of treatment for sufferers of Parkinson's disease where
XX they do not respond significantly to L-dopa treatment by prior art
XX methodologies. The present sequence is retroviral vector of the
XX invention, PONY8-BIC, comprising elements of the EIAV (Equine infectious
XX anaemia virus) genome, human cytomegalovirus sequences, a plasmid

CC backbone, a green fluorescent protein sequence and the bicistronic
CC cassette. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 10448 BP; 2780 A; 2431 C; 2611 G; 2626 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 10448;
Best Local Similarity 100.0%; Pred.No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAACACGACACCCAA 20
|||||
DB 1541 AAGGAACACGACACCCAA 1522

RESULT 91
ADO07660/c
ID ADO07660 standard; DNA; 10633 BP.
XX
XX ADO07660;
AC ADO07660;
XX
DT 15-JUL-2004 (first entry)
XX
XX Viral vector shuttle (CMV)IL12(IRES)4-1BBL.
DE
XX
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene.
XX
XX Synthetic.
OS Unidentified.
XX
XX WO2004035799-A2.
XX
XX 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-EP011252.
XX
XX 11-OCT-2002; 2002DE-01048141.
XX
XX (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
XX Waehler R, Schmieders F;
XX
XX WPI; 2004-357221/33.
XX
XX Viral vector that expresses single-chain interleukin-12 and costimulator,
XX useful for treatment of tumors, viral infections, e.g. human
XX immunodeficiency virus, and prion diseases.
XX
XX Disclosure; Fig 25; 129pp; German.
XX
XX The present invention relates to a viral vector that includes a nucleic
XX acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
XX protein. Viral vectors and virus particles derived from them are useful
XX for treatment of tumors, infectious diseases (e.g. HIV, hepatitis A, B
XX or C, cytomegalovirus or human papilloma virus), or prion diseases. The
XX present sequence is a viral vector shuttle sequence used in the
XX exemplification of the invention.
XX
XX Sequence 10633 BP; 2627 A; 2749 C; 2779 G; 2427 T; 0 U; 51 Other;
Query Match 100.0%; Score 20; DB 12; Length 10633;
Best Local Similarity 100.0%; Pred.No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAACACGACACCCAA 20
|||||
DB 3244 AAGGAACACGACACCCAA 3225

RESULT 92
ABK86536/c
ID ABK86536 standard; DNA; 11058 BP.

```
XX AC ABK86536;
XX DT 07-AUG-2003 (revised)
XX DT 30-AUG-2002 (first entry)
XX DE EIAV based retroviral vector PONY8-TRIC.
XX KW Parkinson's disease; gene therapy; retroviral vector; ds; cyclic; EIAV;
XX KW neuroprotective; antiparkinsonian; NOI; IRES; lentiviral particle;
XX KW nucleotide site of interest; Internal Ribosome Entry Site; PONY8-TRIC;
XX KW tyrosine hydroxylase; GTP-cyclohydrolase 1; bicistronic cassette;
XX KW Aromatic Amino Acid Dopa Decarboxylase; tricistronic cassette;
XX KW Vesicular Monoamine Transporter 2; neurodegenerative disease.
XX XX
XX OS Equine infectious anemia virus.
XX OS Human cytomegalovirus.
XX OS Escherichia coli.
XX OS Aequorea victoria.
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX FN WO200229065-A2.
XX XX
XX PD 11-APR-2002.
XX XX
XX PF 05-OCT-2001; 2001WO-GB004433.
XX XX
XX PR 06-OCT-2000; 2000GB-00024550.
XX XX
XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX XX
XX PI Kingsman AJ, Mazarakis ND, Martin-Rendon E, Azzouz M, Rohll J;
XX XX
XX DR WPI; 2002-507885/54.
XX XX
XX PT A novel retroviral vector genome is useful in the treatment of
XX PT Parkinson's disease.
XX FS
XX FS Example 8; Page 70-72; 106pp; English.
XX CC
XX CC The invention relates to a retroviral vector genome (G1) comprising two
XX CC or more NOIs (nucleotide sites of interest), operably linked by one or
XX CC more Internal Ribosome Entry Site(s) (IRES). Also included are a vector
XX CC system (S1) comprising (G1), production (M1) of a lentiviral particle, a
XX CC viral particle (P1) produced by (M1) or by (S1), a pharmaceutical
XX CC composition comprising (G1), (S1) or (P1), a bicistronic cassette
XX CC comprising a nucleotide sequence which encodes: a) tyrosine hydroxylase
XX CC and a nucleotide sequence that encodes GTP-cyclohydrolase 1 operably
XX CC linked by one or more IRES(s); or b) Aromatic Amino Acid Dopa
XX CC Decarboxylase and a nucleotide sequence which encodes Vesicular Monoamine
XX CC Transporter 2 operably linked by one or more IRES(s), a tricistronic
XX CC cassette comprising a nucleotide sequence which encodes tyrosine
XX CC hydroxylase, a nucleotide sequence that encodes GTP-cyclohydrolase 1 and
XX CC a nucleotide sequence which encodes Aromatic Amino Acid Dopa
XX CC Decarboxylase, operably linked by one or more IRES(s) and a cell that has
XX CC been transduced with (S1). G1, the vector system (S1), and the viral
XX CC particle (P1) can all be used to treat and/or prevent (by gene therapy) a
XX CC neurodegenerative disease, especially Parkinson's disease in a subject,
XX CC and also in the manufacture of a pharmaceutical composition to treat the
XX CC above mentioned disease. Treatment with vectors capable of delivering
XX CC e.g., Tyrosine hydroxylase, GTP-cyclohydrolase 1, Aromatic Amino Acid
XX CC Dopa Decarboxylase and Vesicular Monoamine Transporter 2, are useful for
XX CC the last stages of treatment for sufferers of Parkinson's disease where
XX CC they do not respond significantly to L-dopa treatment by prior art
XX CC methodologies. The present sequence is retroviral vector of the
XX CC invention, PONY8-TRIC comprising elements of the EIAV (Equine infectious
XX CC anaemia virus) genome, human cytomegalovirus sequences, a plasmid
XX CC backbone, a green fluorescent protein sequence and the tricistronic
XX CC cassette. (Updated on 07-AUG-2003 to correct OS field.)
XX SQ
XX Sequence 11058 BP; 2875 A; 2647 C; 2813 G; 2723 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 11058;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 3813 AAGGAAACACGGACACCCAA 3794
|||||
RESULT 93
AAV12373/c
ID AAV12373 standard; DNA; 11326 BP.
XX AC AAV12373;
XX DT 17-OCT-2003 (revised)
XX DT 03-JUL-1998 (first entry)
XX DE Chimeric protease NS3/poliiovirus gene NS3 delta-C-PV1.
XX KW Chimeric; Hepatitis C Virus; HCV; poliovirus; liver cirrhosis;
XX KW NS3 protease gene; NSSA/5B; hepatocellular carcinoma; anti-HCV drug; ss.
XX OS Hepatitis C virus.
XX OS Poliovirus.
XX OS Chimeric.
XX XX
XX FN WO9800548-A1.
XX XX
XX PD 08-JAN-1998.
XX XX
XX PF 25-JUN-1997; 97WO-KR000120.
XX XX
XX PR 28-JUN-1996; 96KR-00024910.
XX XX
XX PA (GLDS ) LG CHEM CO LTD.
XX PA (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
XX XX
XX PI Jang SK, Hahn BS;
XX XX
XX DR WPI; 1998-086973/08.
XX XX
XX PT Recombinant gene encoding hepatitis C surrogate virus - comprises
XX PT picornavirus and hepatitis C virus protease NS3 genes and hepatitis C
XX PT virus protease NS3 target sites, useful for drug screening.
XX FS
XX FS Claim 1; Fig 6A-6E; 36pp; English.
XX CC
XX CC The present chimeric sequence comprises of a Hepatitis C Virus (HCV)
XX CC protease NS3 gene and its target site NSSA/5B gene inserted into the open
XX CC reading frame of the poliovirus gene. HCV is the major etiologic agent of
XX CC non-A, non-B hepatitis, and has been implicated in liver cirrhosis and
XX CC hepatocellular carcinoma. The invention provides a hepatitis C surrogate
XX CC virus comprising of the recombinant gene described. Upon expression, the
XX CC HCV NS3 protease would cleave its target site to become independent of
XX CC the poliovirus polyprotein. HCV NS3 protease contained within the
XX CC surrogate is a good therapeutic target molecule for the development of
XX CC anti-HCV drugs, since its activity is considered essential for viral
XX CC proliferation. The surrogate virus is claimed to be useful than the
XX CC existing in vitro systems for HCV culture for screening anti-HCV drugs
XX CC and testing for their efficacy. It is also considered to be useful for
XX CC studying HCV genes in viral replication. (Updated on 17-OCT-2003 to
XX CC standardise OS field)
XX SQ
XX Sequence 11326 BP; 3169 A; 2751 C; 2737 G; 2669 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 11326;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 565 AAGGAAACACGGACACCCAA 546
|||||
```

```
RESULT 94
ADO07659/c
ID ADO07659 standard; DNA; 11746 BP.
XX
XX
AC ADO07659;
XX
XX
DT 15-JUL-2004 (first entry)
XX
XX
DE Viral vector shuttle (CMV) IL12 (IRES) 4-1BBL (IRES) IL-2.
XX
XX cytotatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene.
XX
XX Synthetic.
OS Unidentified.
XX
XX WO2004035799-A2.
FN
XX
XX 29-APR-2004.
PD
XX
XX 10-OCT-2003; 2003WO-EP011252.
PF
XX
XX 11-OCT-2002; 2002DE-01048141.
PR
XX
XX (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
PA
XX
XX Waehler R, Schnieders F;
PI
XX WPI; 2004-357221/33.
DR
XX
XX Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
XX Disclosure; Fig 24; 129pp; German.
PS
XX
XX The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumors, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a viral vector shuttle sequence used in the
CC exemplification of the invention.
XX
XX SQ Sequence 11746 BP; 2920 A; 3037 C; 3055 G; 2683 T; 0 U; 51 Other;
XX
XX Query Match 100.0%; Score 20; DB 12; Length 11746;
XX Best Local Similarity 100.0%; Pred. No. 14;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAGGAACACGGACACCCAA 20
XX 3244 AAGGAACACGGACACCCAA 3225
XX
XX RESULT 95
ADO07662/c
ID ADO07662 standard; DNA; 38246 BP.
XX
XX
AC ADO07662;
XX
XX
DT 15-JUL-2004 (first entry)
XX
XX Viral vector pAd-3.
DE
XX
XX cytotatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene.
XX
XX Synthetic.
OS
```

```
OS Unidentified.
XX WO2004035799-A2.
XX
XX 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-EP011252.
XX
XX 11-OCT-2002; 2002DE-01048141.
XX
XX (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
XX Waehler R, Schnieders F;
XX
XX WPI; 2004-357221/33.
XX
XX Viral vector that expresses single-chain interleukin-12 and costimulator,
XX useful for treatment of tumors, viral infections, e.g. human
XX immunodeficiency virus, and prion diseases.
XX
XX Disclosure; Fig 27; 129pp; German.
XX
XX The present invention relates to a viral vector that includes a nucleic
XX acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
XX protein. Viral vectors and virus particles derived from them are useful
XX for treatment of tumors, infectious diseases (e.g. HIV, hepatitis A, B
XX or C, cytomegalovirus or human papilloma virus), or prion diseases. The
XX present sequence is a viral vector used in the exemplification of the
XX invention.
XX
XX SQ Sequence 38246 BP; 8959 A; 10813 C; 10384 G; 8043 T; 0 U; 47 Other;
XX
XX Query Match 100.0%; Score 20; DB 12; Length 38246;
XX Best Local Similarity 100.0%; Pred. No. 15;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAGGAACACGGACACCCAA 20
XX 6097 AAGGAACACGGACACCCAA 6078
XX
XX RESULT 96
ADK66744/c
ID ADK66744 standard; DNA; 62 BP.
XX
XX
XX AC ADK66744;
XX
XX
XX DT 06-MAY-2004 (first entry)
XX
XX
XX DE Picornaviridae DNA 5'-untranslated region specific probe.
XX
XX Gene expression; gene polymorphism; cross-species hybridisation; probe;
XX ss.
XX
XX OS Picornaviridae.
XX
XX PN US2003211526-A1.
XX
XX PD 13-NOV-2003.
XX
XX PF 14-FEB-2003; 2003US-00366823.
XX
XX PR 15-FEB-2002; 2002US-0357541P.
XX
XX
XX (JUAN/) JUANG J.
XX (HSIU/) HSIUNG C A.
XX (LINC/) LIN C.
XX
XX Juang J, Hsiung CA, Lin C;
XX
XX WPI; 2004-059849/06.
XX
XX Collection of at least four nucleic acid probes for analysis of gene
```

PT expression and of gene polymorphisms, comprises each probe including
PT segment and entirety of which hybridizes under low stringency conditions
PT to genes of two species.

XX Example; SEQ ID NO 5; 11pp; English.

XX The present invention relates to a collection of at least four nucleic
CC acid probes, each including a segment, the entirety of which hybridizes
CC under low stringency conditions to at least a first gene of first species
CC and a second gene of second species, where the hybridising probes
CC correspond to different genes of the two species and the genes are
CC orthologous to each other. The invention is useful for analysis of gene
CC expression and of gene polymorphisms. The probes are designed for cross-
CC species hybridisation, e.g. by identification of conserved segments among
CC orthologous genes. The present sequence is Picornaviridae DNA 5'-
CC untranslated region (UTR) specific probe. This sequence is used in the
CC exemplification of the invention.

XX Sequence 62 BP; 9 A; 11 C; 15 G; 20 T; 0 U; 7 Other;

Query Match 100.0%; Score 20; DB 12; Length 62;
Best Local Similarity 95.0%; Pred. No. 15;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20
||:|||||
Db 57 AAKGAACACGGACACCCAA 38

RESULT 97

AE007516/c
ID AEC07516 standard; DNA; 62 BP.

XX AC AEC07516;

XX 20-OCT-2005 (first entry)

XX Picornaviridae 5'UTR degenerate probe, SEQ ID NO:5.

XX DNA detection; hybridization; 5'-UTR; probe; ss.

XX Picornaviridae.

XX TW200303921-A.

XX 16-SEP-2003.

XX 14-FEB-2003; 2003TW-00103058.

XX 15-FEB-2002; 2002US-00357541.

XX (NAHE-) NAT HEALTH RES INST.

XX Juang J, Shiung J, Lin J;

XX WPI; 2005-579874/59.

XX Trans-species nucleic acid probe - for a probe collection having at least
PT four nucleic acid probes.

XX Example; SEQ ID NO 5; 46pp; Chinese.

XX The invention relates to a collection of at least four nucleic acid
CC probes comprising a segment able to hybridize to orthologous genes from
CC at least two different species. In the embodiments of the invention, the
CC probe segment is at least 60% identical to orthologous genes from two
CC different species. The present sequence represents a degenerate probe
CC used to detect 5' untranslated region (5'UTR) sequences from viruses of
CC the Picornaviridae family.

XX Sequence 62 BP; 9 A; 11 C; 15 G; 20 T; 0 U; 7 Other;

Query Match 100.0%; Score 20; DB 14; Length 62;

Best Local Similarity 95.0%; Pred. No. 15;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20
||:|||||
Db 57 AAKGAACACGGACACCCAA 38

RESULT 98

ACD26711/c
ID ACD26711 standard; DNA; 28 BP.

XX AC ACD26711;

XX 11-SEP-2003 (first entry)

XX Enterovirus detection method associated primer #11.

XX Enterovirus detection; primer; ss.

XX Enterovirus.

XX CN1366066-A.

XX 28-AUG-2002.

XX 15-JAN-2001; 2001CN-00100622.

XX 15-JAN-2001; 2001CN-00100622.

XX (JING-) JINGYU BIOLOGIC SCI TECHNOLOGY IND CO LT.

XX Li G, Bai Q, Zeng Y;

XX WPI; 2003-230558/23.

XX Process, primer and probe for detecting and discriminating enterovirus.

XX Claim 5; Page 2; 33pp; Chinese.

XX The invention describes the application of nucleotide primer to detecting
CC enterovirus. The detection method and the reagent kit are disclosed. This
CC sequence represents an enterovirus detection method associated primer

XX Sequence 28 BP; 2 A; 4 C; 6 G; 15 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 8; Length 28;

Best Local Similarity 95.0%; Pred. No. 22;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20
||:|||||
Db 24 AAKGAACACGGACACCCAA 5

RESULT 99

ADU47464/c
ID ADU47464 standard; DNA; 28 BP.

XX AC ADU47464;

XX 27-JAN-2005 (first entry)

XX p3 probe used to detect enterovirus type 71 (EV71) in a sample.

XX Detection; enterovirus type 71; probe; ss.

XX Enterovirus.

XX US6818397-B1.

XX 16-NOV-2004.

```

PP 28-NOV-2000; 2000US-00724678.
XX
PR 28-NOV-2000; 2000US-00724678.
XX
PA (CHIP-) CHIP BIOTECHNOLOGY INC.
XX
PI Lee K, Bair C, Tseng Y, Wang Y, Wang S;
XX
XX WPI; 2004-793563/78.
DR
XX
XX New kit comprising a pair of oligonucleotide primers for nucleic acid
XX amplification, useful in detecting and differentiating an enterovirus in
XX a sample.
XX
PS Claim 1; SEQ ID NO 11; 14pp; English.
XX
XX The invention provides a method and a kit for detecting and
XX differentiating an enterovirus type 71 (EV71) in a sample. The method
XX involves contacting nucleic acids in the sample with a pair of primers to
XX form an amplification product; contacting the amplification product with
XX at least one synthetic nucleotide sequence fixed on a solid substrate and
XX detecting hybridisation. The present sequence is a probe used to detect
XX and differentiate enterovirus type 71 (EV71) in a sample.
XX
SQ Sequence 28 BP; 2 A; 4 C; 6 G; 15 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 95.0%; Pred. No. 22;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACGACCCAA 20
DB 24 AAGGAACACGACGACCCAA 5

RESULT 100
ID ADW75017/C
XX ADW75017 standard; DNA; 70 BP.
XX
XX ADW75017;
XX
XX 07-APR-2005 (first entry)
XX
XX Human rhinovirus probe PBRH_00006.
XX
XX probe; ss; biochip; DNA chip; microorganism detection; diagnosis;
XX infection; adenovirus infection; coronavirus infection;
XX respiratory disease; Chlamydia pneumoniae infection;
XX SARS coronavirus infection; treponema pallidum infection; sialodentitis;
XX rubella virus infection; rhinovirus infection; influenza virus infection;
XX respiratory syncytial virus infection; mycoplasma infection;
XX parainfluenza virus infection; HIV infection; HIV1 infection;
XX measles virus infection; hepatitis B virus infection;
XX hepatitis A virus infection; hepatitis D virus infection;
XX hepatitis E virus infection; hepatitis G virus infection;
XX herpesvirus infection.
XX
XX Human rhinovirus sp.
XX
XX WO2005005658-A1.
XX
XX 20-JAN-2005.
XX
XX 14-JUL-2003; 2003WO-CN0000561.
XX
XX 14-JUL-2003; 2003WO-CN0000561.
XX
XX (CAP1-) CAPITAL BIOCHIP CO LTD.
XX
XX (UYQ1) UNIV QINGHUA.
XX
XX Li Z, Tao S, Cheng J;
XX

```

WPI; 2005-122431/13.

New chip for assaying for a coronavirus causing the severe acute respiratory syndrome (SARS-CoV) and a non-SARS-CoV infectious organism comprising a support and oligonucleotide probes.

Disclosure; Page 34; 122pp; English.

This invention describes a novel chip used to detect a coronavirus causing the severe acute respiratory syndrome (SARS-CoV) and a non-SARS-CoV infectious organism. The chip comprises an oligonucleotide probe complementary to a nucleotide sequence of SARS-CoV or non-SARS-CoV infectious organism causing SARS-like symptoms which located within a conserved region of the viral genome. The conserved region of SARS-CoV genome is a region located within replicase 1A or 1B gene or the nucleocapsid gene of SARS-CoV. The structural protein coding gene of SARS-CoV genome is a gene encoding the spike glycoprotein, the small envelope protein or nucleocapsid gene. The chip also comprises at least one of an immobilization control probe labeled and not participating in any hybridization reaction when a sample containing or suspected of containing SARS-CoV or a non-SARS-CoV infectious organism. The detection method also includes multiplex PCR using primers which amplify nucleotide sequences from an influenza A and B virus, a human metapneumovirus, human adenovirus and human coronavirus 229E or OC43. The presence of the SARS-CoV is determined when a positive hybridization signal is detected using at least one of two oligonucleotide probes complementary to two different nucleotide sequences located within replicase 1A or 1B, spike glycoprotein or nucleocapsid genes of the SARS-CoV, a positive signal is detected from the immobilization control probe, a positive hybridization signal is detected using the positive control probe and there is no hybridization signal using the negative control probe. Detecting a positive hybridization signal using at least one of the two oligonucleotide probes while not detecting a positive hybridization signal using the probe complementary to a nucleotide sequence located within the spike glycoprotein gene of the SARS-CoV indicates mutation of the SARS-CoV. The non-SARS-CoV infectious organism causing SARS-like symptoms is a human coronavirus 229E or OC43, human enteric coronavirus, influenza A or B virus, parainfluenza virus 1, 2, 3 or 4, respiratory syncytial virus, human metapneumovirus, rhinovirus, adenovirus, mycoplasma pneumoniae, Chlamydia pneumoniae, measles virus or rubella virus. Non-SARS-CoV infectious organisms capable of damaging an infectious host's immune system include hepatitis A, B, C, D, E or G virus, a transfusion transmitting virus (TTV), a human immunodeficiency virus 1 (HIV1), a human cytomegalovirus (HCMV), an Epstein-Barr virus (EBV) or Treponema pallidum, avian infectious bronchitis virus, avian infectious laryngotracheitis virus, murine hepatitis virus, equine coronavirus, canine coronavirus, feline coronavirus, porcine epidemic diarrhoea virus, porcine transmissible gastroenteritis virus, bovine coronavirus, feline infectious peritonitis virus, rat coronavirus, neonatal calf diarrhoea coronavirus, porcine haemagglutinating encephalomyelitis virus of rat. The methods and compositions of the invention are useful in amplifying and detecting SARS-CoV nucleotide sequences, in particular for diagnosing early-stage SARS patients (infected less than one to three days) and determining whether a subject is infected by SARS-CoV and/or a non-SARS-CoV infectious organism causing SARS-like symptoms. This sequence represents a probe used in the method of the invention.

Sequence 70 BP; 11 A; 12 C; 20 G; 27 T; 0 U; 0 Other;

Query Match 95.0%; Score 19; DB 14; Length 70;

Best Local Similarity 100.0%; Pred. No. 29;

Matches -19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAACACGACGACCCAA 20

DB 52 AGGAACACGACGACCCAA 34

Search completed: March 9, 2006, 00:30:11
Job time : 214.388 secs

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:12:30 ; Search time 1570.68 Seconds
(without alignments)
595.756 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaacacggacacccaa 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_ges1:*
10: gb_ges2:*
11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	603	1	AL728550
2	18.4	92.0	676	7	CK751566
3	18.4	92.0	845	4	CNS0FP9W
4	18.4	92.0	908	4	CNS0FVC0
5	18.4	92.0	962	11	CNS0JBCU
6	18.4	92.0	1042	3	BQ056756
7	18.4	92.0	1230	2	BG752980
8	18	90.0	924	3	BM359242
9	17.4	87.0	458	6	CB359607
10	17.4	87.0	520	9	AZ078930
11	17.4	87.0	689	10	CW118506
12	17.4	87.0	717	7	CK028165
13	17.4	87.0	729	10	AG479585
14	17.4	87.0	750	7	CF998205
15	17.4	87.0	770	11	CNS03817
16	17.4	87.0	785	7	CV480587
17	17.4	87.0	794	2	BG985751
18	17.4	87.0	794	7	CV486670
19	17.4	87.0	798	7	CK026895
20	17.4	87.0	800	7	CV126404
21	17.4	87.0	819	10	CW117728
22	17.4	87.0	819	10	CW117728

23	17.4	87.0	848	7	CN835108
24	17.4	87.0	891	10	CW718544
25	17.4	87.0	905	10	CW717765
26	17.4	87.0	961	7	CK412195
27	17.4	87.0	963	3	BM415978
28	17.4	87.0	1121	10	CG745203
29	17.4	87.0	1134	7	CK027487
30	17	85.0	683	10	CZ679560
31	17	85.0	712	9	BZ020345
32	17	85.0	751	9	BM693975
33	16.8	84.0	108	10	CW176116
34	16.8	84.0	209	6	CD290195
35	16.8	84.0	210	6	CD319193
36	16.8	84.0	351	8	DN493639
37	16.8	84.0	363	10	CW585488
38	16.8	84.0	370	1	AI618550
39	16.8	84.0	391	3	BP813540
40	16.8	84.0	397	3	BP664023
41	16.8	84.0	412	6	CA730096
42	16.8	84.0	427	5	BZ237703
43	16.8	84.0	444	10	AG224508
44	16.8	84.0	447	3	BP616001
45	16.8	84.0	475	5	BO803856
46	16.8	84.0	484	6	CA728920
47	16.8	84.0	485	10	CW445890
48	16.8	84.0	514	5	BZ229997
49	16.8	84.0	519	5	CA013161
50	16.8	84.0	525	6	CF352554
51	16.8	84.0	544	6	CA637743
52	16.8	84.0	546	2	BG727965
53	16.8	84.0	559	9	AQ293334
54	16.8	84.0	580	2	BB621815
55	16.8	84.0	607	11	DE001557
56	16.8	84.0	608	10	CL773304
57	16.8	84.0	628	10	CG099060
58	16.8	84.0	632	7	CN206088
59	16.8	84.0	637	5	BZ052244
60	16.8	84.0	643	10	CL768700
61	16.8	84.0	656	6	CD893867
62	16.8	84.0	661	10	CG046335
63	16.8	84.0	666	9	BZ274036
64	16.8	84.0	673	8	CA682423
65	16.8	84.0	678	5	BZ476293
66	16.8	84.0	683	9	BZ510687
67	16.8	84.0	686	10	AG311675
68	16.8	84.0	709	10	AG514370
69	16.8	84.0	715	10	AG442384
70	16.8	84.0	729	8	DT057597
71	16.8	84.0	735	8	DT060396
72	16.8	84.0	737	10	AG429016
73	16.8	84.0	742	4	CNS0FV62
74	16.8	84.0	755	9	AQ740823
75	16.8	84.0	763	8	DT060112
76	16.8	84.0	780	6	CB247499
77	16.8	84.0	794	8	DT057062
78	16.8	84.0	822	8	CV944482
79	16.8	84.0	829	2	BP254545
80	16.8	84.0	872	6	CD303542
81	16.8	84.0	899	5	BQ674913
82	16.8	84.0	908	10	CZ511376
83	16.8	84.0	916	10	CZ5117024
84	16.8	84.0	918	6	CA789059
85	16.8	84.0	919	2	BF029135
86	16.8	84.0	930	9	CC694001
87	16.8	84.0	935	2	BE881640
88	16.8	84.0	950	5	BZ015367
89	16.8	84.0	953	5	BZ011794
90	16.8	84.0	959	2	BG335613
91	16.8	84.0	1031	2	BP532081
92	16.8	84.0	1032	10	CL111503
93	16.8	84.0	1071	2	BF337949
94	16.8	84.0	1097	10	CL049473
95	16.8	84.0	1123	9	CC276125

CN835108	AGENCOURT
CW718544	MARC 1010
CW717765	MARC 1009
CK412195	AUF IPHGX
BM415978	OP21060 M
CG745203	P038-1-B1
CK027487	AGENCOURT
CZ679560	OM_Ba023
BZ020345	oeht04a08
BM693975	BOMT227TF
CW176116	104 588 1
CD290195	StrFu538
CD319193	StrFu538
DN493639	G079P41.5
CW585488	OA_ABA011
AI618550	zewP0061
BP813540	BP813540
BP664023	BP664023
CA730096	wipic.pk0
AG224508	Lotus cor
BP616001	BP616001
BO803856	WHE2842 H
CA728920	wilic.pk0
CW445890	fsbb001f1
BZ229997	603947773
CA013161	HT07J07F
CF352554	lac30c03
CA637743	wrein.pk0
BG727965	fp08e03.x
AQ293334	HS_2266_B
BB621815	BB621815
DE001557	Branchios
CL773304	OR_BBA008
CG099060	PUTHL20TD
CN206088	Tor6515 G
BZ052244	HD09102r
CL768700	OR_BBA014
CD893867	G118.124L
CG046335	PUIFW42TB
BZ274036	CH230-403
CA682423	Ydf10h05
BZ476293	603471630
BZ510687	BOMQH50TF
AG311675	Mus muscu
AG514370	Mus muscu
AG442384	Mus muscu
DT057597	AGENCOURT
DT060396	AGENCOURT
AG429016	Mus muscu
CR693646	Tetraodon
AQ740823	HS_5508_A
DT060112	AGENCOURT
CB247499	UI-M-F10-
DT057062	AGENCOURT
CV944482	PU014G10
BP254545	HVSMEF000
CD303542	AGENCOURT
BQ674913	AGENCOURT
CZ511376	GMW2-49L8
CZ5117024	GMW2-49L8
CA789059	AGENCOURT
BF029135	601764643
CC694001	OGVAR91TV
BE881640	601490060
BZ015367	AGENCOURT
BZ011794	AGENCOURT
BG335613	602404233
BP532081	602073196
CL111503	ISB1-55G5
BF337949	602035776
CL049473	CH216-69P
CC276125	CH261-128

C 96	16.8	84.0	1251	9	B2576789	msh2_5104	169	15.8	79.0	284	10	CZ594840	CZ594840
C 97	16.8	84.0	1338	4	CNS0G3AI		170	15.8	79.0	286	1	AV052597	AV052597
C 98	16.8	84.0	1490	4	CNS0G3XN		171	15.8	79.0	286	1	AV021413	AV021413
C 99	16.8	84.0	1541	4	CNS0G3YF		172	15.8	79.0	314	6	CB684607	CB684607
C 100	16.8	84.0	1559	4	CNS0GLAC		173	15.8	79.0	315	2	CB576337	CB576337
C 101	16.8	84.0	1577	4	CNS0GLDM		174	15.8	79.0	316	2	BB237888	BB237888
C 102	16.8	84.0	1585	4	CNS0G3LR		175	15.8	79.0	329	1	AA098537	AA098537
C 103	16.8	84.0	1813	2	BF144191		176	15.8	79.0	331	8	D60927	D60927
C 104	16.8	84.0	3872	4	AK031828		177	15.8	79.0	340	9	AQ948615	AQ948615
C 105	16.4	82.0	391	9	BH432447		178	15.8	79.0	341	10	CW765705	CW765705
C 106	16.4	82.0	451	9	AZ065501		179	15.8	79.0	343	3	BQ168857	BQ168857
C 107	16.4	82.0	453	7	CK564864	rswpb0_01	180	15.8	79.0	348	1	AA894125	AA894125
C 108	16.4	82.0	496	9	AQ985003		181	15.8	79.0	352	4	AK206687	AK206687
C 109	16.4	82.0	503	3	B1387931		182	15.8	79.0	355	1	A1170242	A1170242
C 110	16.4	82.0	524	9	AZ025615		183	15.8	79.0	362	5	C15565	C15565
C 111	16.4	82.0	531	9	AQ633537		184	15.8	79.0	366	5	C15565	C15565
C 112	16.4	82.0	542	9	AQ508060		185	15.8	79.0	369	2	BG072477	BG072477
C 113	16.4	82.0	562	2	BF904033		186	15.8	79.0	371	9	BZ229210	BZ229210
C 114	16.4	82.0	566	9	AZ036472		187	15.8	79.0	375	10	CW118176	CW118176
C 115	16.4	82.0	583	9	AQ544174		188	15.8	79.0	376	8	D60883	D60883
C 116	16.4	82.0	600	5	BH236595		189	15.8	79.0	381	1	A1598789	A1598789
C 117	16.4	82.0	616	1	AV726635		190	15.8	79.0	384	5	BY689987	BY689987
C 118	16.4	82.0	653	9	BH1998		191	15.8	79.0	387	8	D80679	D80679
C 119	16.4	82.0	668	8	DN637308	UMC-bcl_0	192	15.8	79.0	389	7	CV043810	CV043810
C 120	16.4	82.0	674	9	AQ051998		193	15.8	79.0	397	5	BY001982	BY001982
C 121	16.4	82.0	682	7	CK515348		194	15.8	79.0	401	2	BE177238	BE177238
C 122	16.4	82.0	710	9	BH951435		195	15.8	79.0	404	5	BY610270	BY610270
C 123	16.4	82.0	730	9	BZ124104	CH230-489	196	15.8	79.0	407	2	BE137277	BE137277
C 124	16.4	82.0	751	11	CR823818		197	15.8	79.0	407	6	CB979169	CB979169
C 125	16.4	82.0	783	11	CR828043		198	15.8	79.0	408	7	CN304454	CN304454
C 126	16.4	82.0	795	9	BZ604205		199	15.8	79.0	410	9	AQ404432	AQ404432
C 127	16.4	82.0	839	8	CK777270	UI-EH-HG2	200	15.8	79.0	411	10	CW107557	CW107557
C 128	16.4	82.0	875	8	DR547552		201	15.8	79.0	417	2	BG010402	BG010402
C 129	16.4	82.0	916	10	CU128207		202	15.8	79.0	418	2	BG010401	BG010401
C 130	16.4	82.0	930	2	BF316245	601899764	203	15.8	79.0	421	5	BY631755	BY631755
C 131	16.4	82.0	938	2	BF312828	601896967	204	15.8	79.0	422	11	DE085040	DE085040
C 132	16.4	82.0	1080	10	CW931528	EDCC843TF	205	15.8	79.0	429	10	CZ669751	CZ669751
C 133	16.4	82.0	1210	8	DN688614	CGX59-H06	206	15.8	79.0	430	2	BG606657	BG606657
C 134	16.4	82.0	1507	1	AL932973		207	15.8	79.0	431	6	CD731564	CD731564
C 135	16	80.0	134	3	BF061196		208	15.8	79.0	433	9	AQ892575	AQ892575
C 136	16	80.0	188	8	T42425		209	15.8	79.0	436	2	BF547491	BF547491
C 137	16	80.0	361	9	CG601279		210	15.8	79.0	439	1	AW823378	AW823378
C 138	16	80.0	416	5	BY635171		211	15.8	79.0	442	7	CN956808	CN956808
C 139	16	80.0	459	9	CE101574		212	15.8	79.0	447	9	AZ072114	AZ072114
C 140	16	80.0	622	3	BN046383		213	15.8	79.0	450	9	AZ879853	AZ879853
C 141	16	80.0	664	7	CV221612	Le_mx0_50	214	15.8	79.0	459	9	BH772510	BH772510
C 142	16	80.0	714	2	BF583519		215	15.8	79.0	464	6	CD475142	CD475142
C 143	16	80.0	716	7	CO050810	Le_mx0_19	216	15.8	79.0	466	2	BG015617	BG015617
C 144	16	80.0	747	2	BF676532		217	15.8	79.0	466	2	BG015759	BG015759
C 145	16	80.0	863	7	CK936037		218	15.8	79.0	467	2	BB776876	BB776876
C 146	16	80.0	867	10	CL079034		219	15.8	79.0	468	9	CE202769	CE202769
C 147	16	80.0	919	5	BX435422		220	15.8	79.0	470	10	CE822376	CE822376
C 148	16	80.0	927	7	CK934596		221	15.8	79.0	476	9	BH296102	BH296102
C 149	16	80.0	985	5	BX411195		222	15.8	79.0	476	10	CE682954	CE682954
C 150	16	80.0	1052	5	BH412566	603155136	223	15.8	79.0	483	9	AZ454435	AZ454435
C 151	16	80.0	1101	10	CNS0DH11		224	15.8	79.0	484	1	AW435409	AW435409
C 152	16	80.0	1509	8	DN723376		225	15.8	79.0	494	2	BF418582	BF418582
C 153	16	80.0	1545	7	CK403600		226	15.8	79.0	498	5	BX519475	BX519475
C 154	15.8	79.0	73	7	CK725626	SWML3CAW	227	15.8	79.0	525	7	CN041963	CN041963
C 155	15.8	79.0	145	9	CV068770	f2_new_ch	228	15.8	79.0	526	2	BE850866	BE850866
C 156	15.8	79.0	150	9	AZ053463		229	15.8	79.0	526	9	AQ660324	AQ660324
C 157	15.8	79.0	156	6	CB979101		230	15.8	79.0	528	2	BE198402	BE198402
C 158	15.8	79.0	161	3	BQ361776		231	15.8	79.0	539	10	CW408585	CW408585
C 159	15.8	79.0	214	1	A1170319		232	15.8	79.0	540	9	AZ561040	AZ561040
C 160	15.8	79.0	221	1	A1136451		233	15.8	79.0	540	9	AQ507216	AQ507216
C 161	15.8	79.0	235	1	BB100454		234	15.8	79.0	542	8	DN867810	DN867810
C 162	15.8	79.0	236	8	D80694		235	15.8	79.0	543	3	BM506856	BM506856
C 163	15.8	79.0	253	1	A1013680		236	15.8	79.0	544	9	AZ559864	AZ559864
C 164	15.8	79.0	253	3	EM422604		237	15.8	79.0	545	9	CC896516	CC896516
C 165	15.8	79.0	261	1	AV373306		238	15.8	79.0	550	7	CN033182	CN033182
C 166	15.8	79.0	277	1	AV210353		239	15.8	79.0	550	7	CO748634	CO748634
C 167	15.8	79.0	279	1	AJ778950		240	15.8	79.0	552	6	CF341045	CF341045
C 168	15.8	79.0	281	2	BF849741	IL5-EN008	241	15.8	79.0	553	11	CR107466	CR107466

C 242	15.8	79.0	554	6	CD210985	HS1_58.D0
C 243	15.8	79.0	563	6	CB547866	AMGNUC:N
C 244	15.8	79.0	564	9	BS8842	CIT-HSP-201
C 245	15.8	79.0	566	1	AG962387	Drosophila
C 246	15.8	79.0	568	1	AUI59437	AUI59437
C 247	15.8	79.0	571	1	A1111294	SWOVAMCAQ
C 248	15.8	79.0	573	3	BI961817	MONOI_7.A
C 249	15.8	79.0	573	10	CW758775	OG_BBA006
C 250	15.8	79.0	573	10	CW764566	OG_BBA007
C 251	15.8	79.0	575	9	CC488592	CH240_320
C 252	15.8	79.0	577	3	BI834934	603088808
C 253	15.8	79.0	580	7	CF885358	tric081xd
C 254	15.8	79.0	580	9	AZ034756	RPCI-23-2
C 255	15.8	79.0	586	10	AG977843	Drosophila
C 256	15.8	79.0	587	6	CF622727	ih43e04.x
C 257	15.8	79.0	590	10	CL538864	OB_BA004
C 258	15.8	79.0	591	11	CR101159	Reverse s
C 259	15.8	79.0	592	9	BZ870876	CH240_226
C 260	15.8	79.0	593	10	CW165929	104_574_1
C 261	15.8	79.0	594	3	BM651695	170006873
C 262	15.8	79.0	596	8	DR947456	EST113899
C 263	15.8	79.0	599	7	CM041994	nm_36h.f1
C 264	15.8	79.0	600	5	BO416153	GA_Ed010
C 265	15.8	79.0	600	5	BU457823	60375861
C 266	15.8	79.0	603	9	AQ387125	RPCI11-14
C 267	15.8	79.0	604	5	BO783330	UI-R-PFO-
C 268	15.8	79.0	606	6	CD740184	4028969_1
C 269	15.8	79.0	607	10	CW213232	104_644_1
C 270	15.8	79.0	608	10	CW213304	Forward s
C 271	15.8	79.0	615	10	EX959231	Forward s
C 272	15.8	79.0	626	5	BM683351	EX959231
C 273	15.8	79.0	626	9	BZ143662	EX959231
C 274	15.8	79.0	629	10	CW213231	104_644_1
C 275	15.8	79.0	629	10	CW435965	fb5b001f1
C 276	15.8	79.0	632	9	AQ644444	RPCI93-EC
C 277	15.8	79.0	633	9	CW763950	OG_BBA007
C 278	15.8	79.0	634	2	BI295909	UI-R-DKO-
C 279	15.8	79.0	635	6	CA966114	CdL03a11
C 280	15.8	79.0	638	10	CW063252	104_308_1
C 281	15.8	79.0	640	2	BF538777	602050705
C 282	15.8	79.0	640	3	BM440217	pg2rin.pk0
C 283	15.8	79.0	640	10	CW092513	104_455_1
C 284	15.8	79.0	642	10	CE815541	tigr-gss-
C 285	15.8	79.0	647	9	AZ367385	1M0117G04
C 286	15.8	79.0	648	10	CL843379	ET13709.D
C 287	15.8	79.0	649	10	CL859570	OR_CBA009
C 288	15.8	79.0	651	10	CW406991	fb5b001f1
C 289	15.8	79.0	654	9	AZ086758	RPCI-23-4
C 290	15.8	79.0	656	1	AM027103	AM027103
C 291	15.8	79.0	660	7	CW504864	71437.1.M
C 292	15.8	79.0	660	10	CW664103	OG_BBA001
C 293	15.8	79.0	664	1	AV658301	AV658301
C 294	15.8	79.0	669	5	BM446460	BM446460
C 295	15.8	79.0	671	3	BI387900	BF226_002
C 296	15.8	79.0	672	6	CF361053	827360.MA
C 297	15.8	79.0	674	1	AW914884	EST346188
C 298	15.8	79.0	676	7	CN304450	170004252
C 299	15.8	79.0	676	10	CE378039	tigr-gss-
C 300	15.8	79.0	677	6	CB421329	594989.MA
C 301	15.8	79.0	681	7	CN734929	25RDENM.U
C 302	15.8	79.0	681	8	CM660197	POI019C0
C 303	15.8	79.0	681	10	CZ491861	OA_BBA013
C 304	15.8	79.0	682	3	BI695522	603347477
C 305	15.8	79.0	692	7	CK842307	UI-R-AD0-
C 306	15.8	79.0	694	5	BM446261	BM446261
C 307	15.8	79.0	694	9	CC519770	CH240_366
C 308	15.8	79.0	695	10	CW203965	104_631_1
C 309	15.8	79.0	696	6	CB422283	595373.MA
C 310	15.8	79.0	697	7	CN788698	4123060.B
C 311	15.8	79.0	697	8	CK772410	UI-EH-HG0
C 312	15.8	79.0	697	9	AZ869893	2M0182109
C 313	15.8	79.0	700	7	CN842112	AGENCOURT
C 314	15.8	79.0	704	5	BY702935	BY702935
C 315	15.8	79.0	706	9	BZ990015	PUBK029TD
C 316	15.8	79.0	707	10	CW408584	fb5b001f1
C 317	15.8	79.0	709	5	BU349121	603524415
C 318	15.8	79.0	709	5	EX467744	EX467744
C 319	15.8	79.0	713	10	CW235675	104_691_1
C 320	15.8	79.0	717	6	CA504021	UI-R-FJ0-
C 321	15.8	79.0	720	10	CNS000FE	AL090920
C 322	15.8	79.0	720	10	CNS000FE	Arabidops
C 323	15.8	79.0	737	8	CM660004	POI016G1
C 324	15.8	79.0	738	8	CN043178	v11_P45.n
C 325	15.8	79.0	738	8	DN870210	nad05b03
C 326	15.8	79.0	739	5	BU598431	AGENCOURT
C 327	15.8	79.0	743	11	CR134716	Forward s
C 328	15.8	79.0	744	9	BI188697	036_P_01-
C 329	15.8	79.0	744	11	CNS07SNM	AL625636
C 330	15.8	79.0	747	5	BU334634	T7_end of
C 331	15.8	79.0	750	9	BZ672480	603496920
C 332	15.8	79.0	752	5	BZ666985	BUD266985
C 333	15.8	79.0	755	10	AG572296	603817877
C 334	15.8	79.0	757	2	BG497439	Mus muscu
C 335	15.8	79.0	759	7	CV126842	602538774
C 336	15.8	79.0	765	6	CD100163	AGENCOURT
C 337	15.8	79.0	765	7	CO120323	GR_Eb023
C 338	15.8	79.0	771	5	BU432376	603220605
C 339	15.8	79.0	771	9	CC915049	C088613ba
C 340	15.8	79.0	774	2	BI261132	602967651
C 341	15.8	79.0	776	6	CB335725	CR042909
C 342	15.8	79.0	777	11	CR042909	Forward s
C 343	15.8	79.0	780	9	CC963638	BOIRB46TR
C 344	15.8	79.0	783	6	CB573559	AGENCOURT
C 345	15.8	79.0	791	10	CZ134998	OA_BBA002
C 346	15.8	79.0	796	9	BZ810168	BZ810168
C 347	15.8	79.0	805	1	AL525208	PUGAX03TB
C 348	15.8	79.0	807	10	AG446231	AL525208
C 349	15.8	79.0	808	2	BF278041	Mus muscu
C 350	15.8	79.0	810	2	BG494062	GA_Eb003
C 351	15.8	79.0	819	10	EX176133	602542362
C 352	15.8	79.0	820	6	CB663429	Danio rer
C 353	15.8	79.0	821	11	CR147047	OSJNE08G
C 354	15.8	79.0	823	11	CR197183	Forward s
C 355	15.8	79.0	827	7	CO120324	GR_Eb023
C 356	15.8	79.0	828	10	CG015394	ZUB678TV
C 357	15.8	79.0	830	2	BF209067	601872946
C 358	15.8	79.0	833	10	CG448216	OGTBF56TV
C 359	15.8	79.0	843	7	CK243139	EST726776
C 360	15.8	79.0	849	9	AQ741350	HS_5570.B
C 361	15.8	79.0	850	2	BG678112	602625866
C 362	15.8	79.0	850	8	DN981327	SV6_36C02
C 363	15.8	79.0	851	2	BI152566	602918423
C 364	15.8	79.0	851	10	CNS01SE9	AL165114
C 365	15.8	79.0	862	6	CD519427	Tetraodon
C 366	15.8	79.0	865	7	CK396760	AGENCOURT
C 367	15.8	79.0	882	7	CK246257	AGENCOURT
C 368	15.8	79.0	883	2	BG566405	EST729894
C 369	15.8	79.0	885	5	BU542166	602585201
C 370	15.8	79.0	886	9	CK243138	AGENCOURT
C 371	15.8	79.0	891	5	BX899502	GSSTC0176
C 372	15.8	79.0	891	8	DR949226	BX899502
C 373	15.8	79.0	894	7	CK271572	EST114076
C 374	15.8	79.0	896	8	DR732700	FGAS07862
C 375	15.8	79.0	898	10	CG133608	PJH21TID
C 376	15.8	79.0	904	2	BG192231	602806958
C 377	15.8	79.0	905	5	BU359063	BU359063
C 378	15.8	79.0	906	6	CF586659	AGENCOURT
C 379	15.8	79.0	917	2	BI255411	602978091
C 380	15.8	79.0	917	6	CD759635	AGENCOURT
C 381	15.8	79.0	923	10	CG284176	OGJ69TH
C 382	15.8	79.0	926	10	CG974398	MSEFT59TR
C 383	15.8	79.0	929	9	BI163074	CG974398
C 384	15.8	79.0	930	10	CZ502302	ENTTC04TF
C 385	15.8	79.0	930	10	AG159237	GMW2-4H14
C 386	15.8	79.0	932	9	CC302560	Pan trogl
C 387	15.8	79.0	932	11	CNS04H4X	CH261-73N
C 388	15.8	79.0	932	11	CNS04H4X	AL290490


```

/clone="BNOAA1002B08"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match          95.0%; Score 19; DB 1; Length 603;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCA 19
    |||||
Db 31 AAGGAAACACGACACCA 49
    |||||

RESULT 2
LOCUS          CK751666          676 bp      mRNA      linear      EST 09-JUN-2005
DEFINITION    atr02-9ms1-b08 Amborella trichopoda cDNA clone atr02-9ms1-b08
5', mRNA sequence.
ACCESSION     CK751666
VERSION       CK751666.1 GI:42642089
KEYWORDS      EST.
SOURCE        Amborella trichopoda
ORGANISM      Amborella trichopoda
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Basal Magnoliophyta; Amborellales;
              Amborellaceae; Amborella.
              1 (bases 1 to 676)
REFERENCE     1 depamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
AUTHORS       Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
              Leebens-Wack, J., Landherr, L., Ilut, D. and Wall, K.
              Generation of ESTs from early female flower buds of Amborella
              trichopoda
              Unpublished (2003)
JOURNAL
COMMENT       Contact: Claude depamphilis or James Leebens-Wack
              Mueller Laboratory
              Penn State University
              208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
              State University, University Park, PA 16802, USA
              Tel: 814 863 6413
              Fax: 814 865 9131
              Email: cw33@psu.edu or jhl10@psu.edu
              The sequence provided is trimmed of vector and low quality regions.
              Full sequence and original trace file are available from the Plant
              Genome Network website (http://pgn.cornell.edu)
              Plate: atr02-9ms1 row: b column: 08
              Seq primer: M13F.
              Location/Qualifiers
                1. .676
                  /organism="Amborella trichopoda"
                  /mol_type="mRNA"
                  /db_xref="PGN:atr02-9ms1-b08"
                  /db_xref="taxon:13333"
                  /clone="atr02-9ms1-b08"
                  /tissue_type="female flower buds"
                  /dev_stage="4mm buds"
                  /lab_host="SOLR"
                  /clone_lib="Atr02"
                  /note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
                  Site 2: XhoI; This is a directionally cloned,
                  non-normalized library. This library has been generated by
                  the Floral Genome Project (FGP). The Floral Genome Project
                  is funded by NSF's Plant Genome Research Program
                  (DBI-0115684). More information about the project can be
                  obtained at http://fgp.bio.psu.edu"

ORIGIN
Query Match          92.0%; Score 18.4; DB 7; Length 676;
Best Local Similarity 95.0%; Pred. No. 5.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/clone="BNOAA1002B08"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match          92.0%; Score 18.4; DB 4; Length 845;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCA 20
    |||||
Db 510 AAGGAAACACGACACCA 491
    |||||

RESULT 3
CNSOFFP9W/c
LOCUS          CNSOFFP9W          845 bp      mRNA      linear      HTC 05-JUL-2005
DEFINITION    Tetraodon nigroviridis full-length cDNA.
ACCESSION     CR682120
VERSION       CR682120.2 GI:56281159
KEYWORDS      HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
SOURCE        Tetraodon nigroviridis
ORGANISM      Tetraodon nigroviridis
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
              Tetraodontidae; Tetraodontidae; Tetraodon.
              1
REFERENCE     1 Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
AUTHORS       Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
              Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
              Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
              Castellano, S., Anhouard, V., Jubin, C., Castelli, V., Katinka, M.,
              Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De
              Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P.,
              Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J.,
              McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
              Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
              Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
              Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J.
              and Roest Crolius, H.
              Genome duplication in the teleost fish Tetraodon nigroviridis
              reveals the early vertebrate proto-karyotype
              Nature 431 (7011), 946-957 (2004)
JOURNAL
PUBMED        15496914
REFERENCE     2 (bases 1 to 845)
AUTHORS       Genoscope.
              Direct Submission
              Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -
              : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
              (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
              On Dec 3, 2004 this sequence version replaced gi:51180027.
              The sequences are based on single pass reads.
              More information available at
              http://www.genoscope.cns.fr/tetraodon.
              Location/Qualifiers
                1. .845
                  /organism="Tetraodon nigroviridis"
                  /mol_type="mRNA"
                  /db_xref="taxon:99883"
                  /tissue_type="Eyes"

ORIGIN
Query Match          92.0%; Score 18.4; DB 4; Length 845;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCA 20
    |||||
Db 510 AAGGAAACACGACACCA 491
    |||||

RESULT 4
CNSOFFVCO/c
LOCUS          CNSOFFVCO          908 bp      mRNA      linear      HTC 05-JUL-2005
DEFINITION    Tetraodon nigroviridis full-length cDNA.
ACCESSION     CR689972
VERSION       CR689972.2 GI:56284478
KEYWORDS      HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
SOURCE        Tetraodon nigroviridis
ORGANISM      Tetraodon nigroviridis

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraontoidea; Tetraodontidae; Tetraodon.

1
REFERENCE
AUTHORS
 Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N., Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C., Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N., Castellano, S., Anthonard, V., Jubin, C., Castelli, V., Katinka, M., Vacherie, B., Bismont, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P., Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C., Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J. and Roest Crolius, H.

TITLE
 Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype

JOURNAL
 Nature 431 (7011), 946-957 (2004)

REFERENCE
 2 (bases 1 to 908)
AUTHORS
 Genoscope.

TITLE
 Direct Submission

JOURNAL
 Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage - CP 5706 - 91057 EVRY cedex - FRANCE

COMMENT
 (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 On Dec 3, 2004 this sequence version replaced gi:51187879.
 The sequences are based on single pass reads.
 More information available at
 http://www.genoscope.cns.fr/tetraodon.

FEATURES
 source
 location/Qualifiers
 1..908
 /organism="Tetraodon nigroviridis"
 /mol_type="mRNA"
 /db_xref="taxon:99883"
 /tissue_type="Eyes"

ORIGIN
 Query Match 92.0%; Score 18.4; DB 4; Length 908;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACCCAA 20
 |||||
 Db 573 AAGGAACACGGACCCAA 554

RESULT 5
CNS03BCU/c
LOCUS
DEFINITION
 CNS03BCU Tetraodon nigroviridis genome survey sequence T7 end of clone 011J14 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION
 AL236343.1 GI:7895478

VERSION
 GSS; genome survey sequence.

KEYWORDS
 Tetraodon nigroviridis

SOURCE
 Tetraodon nigroviridis

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1
REFERENCE
AUTHORS
 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

TITLE
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL
 Nat. Genet. 25 (2), 235-238 (2000)

REFERENCE
 2
 10835645

Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

TITLE
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL
 Genome Res. 10 (7), 939-949 (2000)

REFERENCE
 3 (bases 1 to 962)
AUTHORS
 Genoscope.

TITLE
 Direct Submission

JOURNAL
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetraodon.

FEATURES
 source
 location/Qualifiers
 1..962
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="011J14"
 /clone_lib="G"
 /note="Genoscope sequence ID : COBG011DE07LP1 end : T7"

ORIGIN
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 Best Local Similarity 95.0%; Pred. No. 5.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACCCAA 20
 |||||
 Db 731 AAGGAACACGGACCCAA 712

RESULT 6
LOCUS
DEFINITION
 BQ056756 AGENCOURT_6940541 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5809184 5', mRNA sequence.

ACCESSION
 BQ056756

VERSION
 BQ056756.1 GI:19816096

KEYWORDS
 EST.

SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 (bases 1 to 1042)
AUTHORS
 NIH-MGC http://mgc.nci.nih.gov/.
TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
 Unpublished (1999)
COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: csapsb-r@mail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution by: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2054 row: 9 column: 09
 High quality sequence stop: 587.
 Location/Qualifiers
 1..1042
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5809184"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"

/clone lib="NIH_MGC_99"
 /note="Organ: lymph; Vector: POTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN
 Query Match 92.0%; Score 18.4; DB 3; Length 1042;
 Best Local Similarity 95.0%; Pred. No. 5.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
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 Db 841 AAGGAACACGACACCCAA 860
 |||||

RESULT 7
 BG752980/c
 LOCUS 602732438F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4876160 5',
 DEFINITION mRNA sequence.

ACCESSION BG752980

VERSION BG752980.1 GI:14063633

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.

REFERENCE

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LCM1758 row: k column: 09

High quality sequence start: 23

High quality sequence stop: 98.

Location/Qualifiers

1..1230

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4876160"

/tissue_type="normal pigmented retinal epithelium"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_43"

/note="Organ: eye; Vector: POTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dt priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 92.0%; Score 18.4; DB 2; Length 1230;

Best Local Similarity 95.0%; Pred. No. 5.4e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
 |||||
 Db 1123 AAGGAACACGACACCCAA 1104
 |||||

RESULT 8

BM359242/c

LOCUS 924 bp mRNA linear EST 09-JAN-2002

DEFINITION GA_Ba0018E15r Gossypium arboreum 7-10 dpa fiber library Gossypium

arboreum cDNA clone GA_Ba0018E15r, mRNA sequence.

ACCESSION BM359242

VERSION BM359242.1 GI:18099988

KEYWORDS EST.

SOURCE Gossypium arboreum

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

SpERMATOPHYTES; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium..

1 (bases 1 to 924)

Wing, R.A., Frisch, D., Yu, X., Main, D., Rambo, T., Simmons, J.,

Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution

of the cotton fiber

Unpublished (2000)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total High Quality bases = 150

Seq primer: TAATACGACTCACTATAGGG

High quality sequence start: 4

High quality sequence stop: 900.

Location/Qualifiers

1..924

/organism="Gossypium arboreum"

/mol_type="mRNA"

/strain="AKA"

/cultivar="8400"

/db_xref="taxon:29729"

/clone="GA_Ba0018E15r"

/tissue_type="Fibers isolated from bolls harvested 7-10

dpa"

/lab_host="E. coli"

/clone_lib="Gossypium arboreum 7-10 dpa fiber library"

/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 90.0%; Score 18; DB 3; Length 924;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

|||

Db 417 AAGGAACACGACACCC 400

|||

RESULT 9

CB359607

LOCUS 458 bp mRNA linear EST 10-NOV-2003

DEFINITION ZF001-P00027-DPB-F-D E08 GISEF001 Danio rerio cDNA clone

IMAGE:6901841 5' similar to (NM_002231) kangai 1, mRNA sequence.

ACCESSION CB359607

VERSION CB359607.1 GI:29003418

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 458)

AUTHORS Mathavan,S., Wei,C., Thoreau,H., Chia,J.M. and Ruan,Y.
 TITLE Genome Institute of Singapore, Zebrafish EST Collection
 JOURNAL Unpublished (2003)
 COMMENT Contact: Ruan Y

Cloning and Sequencing
 Genome Institute of Singapore
 60 Biopolis Street, #02-01, Genome, Singapore 138672

Tel: +65 6478 8073

Fax: +65 6478 9059

Email: ruanyj@gis.a-star.edu.sg

GIS-Clone ID: ZF001-P00027-PP_J16

PCR Primers

FORWARD: M13

BACKWARD: M13

Plate: ZF001-P00027-DPB-F-D

Seq primer: CCGCATACTGTATAGCA

High quality sequence stop: 458.

FEATURES
 source

Location/Qualifiers
 1. 458

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:6901841"

/tissue_type="Embryo"

/dev_stage="7 Different embryonic stages (From just

fertilized Embryos to 72 hours just hatched baby fish)"

/lab_host="DH10B"

/clone_lib="GISZF001"

/note="Vector: pDNR-LIB; Site_1: Sfi A (GGCATTACGGCC);

Site_2: Sfi B (GGCGCTCGGC); Priming method: Sfi-(dtr)30

Primed; Priming sequence: 5.ATTCTAGA GCGCAGGCGGCC

GACATG(T)30VN; directionally cloned.

Sfi A site GGCATTACGGCC; 5' linker/adaptor sequence:

5.AAGCAGTGTATCAACGAGAGTGCC; 3' cloning site: Sfi B

site GCGCGCTCGGC; 3' linker/adaptor sequence: same

as the priming sequence; Average insert size: 2kb; For

PCR insert analysis: Use M13 Forward and reverse primers;

Library Amplified Recombinants (inserts): 98; Library

complexity: Sxi06; Full-length construction (method):

SMART, a Clontech method; Library constructed by: S.

Mathavan, Chia-Lin Wei, and Yijun Ruan Genome Institute of

Singapore"

ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 458;

Best Local Similarity 94.7%; Pred. No. 1.5e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGAAACACGCGACACCA 19

|||||

Db 188 AAGAAACACGCGACACTCA 206

RESULT 10

AZ078930/c

LOCUS

DEFINITION RPCI-23-410F20-TV RPCI-23 Mus musculus genomic clone

RPCI-23-410F20, genomic survey sequence.

ACCESSION AZ078930

VERSION AZ078930.1 GI:7371829

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 520)

Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., de

Akinret,B., Levins,M., McGann,S., Teegaye,G., Geer,K., Krol,M., de

Jong,P. and Frazer,C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other_GSSs: RPCI-23-410F20.TJ

COMMENT

Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 410 row: F column: 20

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. 520

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-410F20"

/sex="Female"

/lab_host="DH10B"

/clone_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:

ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methylase. Size

selected DNA was cloned into the pBACe3.6 vector at the

ECORI sites. The ligation products were transformed into

ECORI sites. The ligation products were transformed into

DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 520;

Best Local Similarity 94.7%; Pred. No. 1.5e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGAAACACGCGACACCA 20

|||||

Db 79 AGGAAACACGCGACACCA 61

RESULT 11

CW718506/c

LOCUS

DEFINITION MARC 1010385 CHORI-240-397C5 Bos taurus genomic clone 1C6, genomic

survey sequence.

ACCESSION CW718506

VERSION CW718506.1 GI:55422216

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 682)

Smith,T.F.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Harhay,G.P.

SNP discovery in cattle based on low coverage sequencing of BAC

clones

Unpublished (2004)

Other_GSSs: MARC_1009233

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified with

cross match v0.990329.

Seq primer: GTAATACGACTCACTATAGG

```

Class: BAC subclone.
FEATURES             Location/Qualifiers
     source
     1..682
     /organism="Bos taurus"
     /mol_type="genomic DNA"
     /db_xref="taxon:9913"
     /clone="1C6"
     /sex="Male"
     /tissue_type="blood"
     /clone_lib="CHORI-240-397C5"
     /note="Vector: pBLUESCRIPT SK-; Site 1: BamHI; Site 2:
     BamHI; BAC DNA was digested with Sau3A. Fragments were
     sized to 800-1200 bases and subcloned into pBLUESCRIPT
     SK-."

ORIGIN
Query Match      87.0%; Score 17.4; DB 10; Length 682;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCCA 19
    |||||||
Db 300 AAGGAACACGACACCCCA 282

RESULT 12
Cw682736
LOCUS
DEFINITION
  OG_BB0039K22.r OG_BBA Oryza glaberrima genomic clone OG_BB0039K22
  3'- genomic survey sequence.
ACCESSION
Cw682736
VERSION
Cw682736.1 GI:55150750
KEYWORDS
GSS.
SOURCE
Oryza glaberrima (African rice)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Zingiberales; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 689)
Kim,H., Yu,Y., Wissotski,M., Byrne,M., Stum,D., Smart,D., Rao,K.,
Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C.
and Wing,R.
OMAP
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0039 row: K column: 22
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
FEATURES             Location/Qualifiers
     source
     1..689
     /organism="Oryza glaberrima"
     /mol_type="genomic DNA"
     /db_xref="taxon:4538"
     /clone="OG_BB0039K22"
     /tissue_type="young leaves"
     /lab_host="DH10B T1 phage resistant"
     /clone_lib="OG_BBA"
     /note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      87.0%; Score 17.4; DB 10; Length 689;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 AAGGAACACGACACCCCA 19
    |||||||
Db 506 AAGGAACACGACACCCCA 524

RESULT 13
Ck028165
LOCUS
DEFINITION
  AGENCOURT 16626291 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7052495
  5', mRNA sequence.
ACCESSION
Ck028165
VERSION
Ck028165.1 GI:38554089
KEYWORDS
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 717)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsbbs-re@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIA014826 row: k column: 21
High quality sequence stop: 686.
FEATURES             Location/Qualifiers
     source
     1..717
     /organism="Danio rerio"
     /mol_type="mRNA"
     /db_xref="taxon:7955"
     /clone="IMAGE:7052495"
     /tissue_type="whole body"
     /lab_host="DH10B"
     /clone_lib="NIH_ZGC_7"
     /note="Vector: pExpress; Site 1: NotI; Site 2: EcoRV;
     Bulk tissue was collected from a whole adult individual
     from the tuebingen strain. 1st strand cDNA was primed with
     a Not I - oligo(dT) primer, double-stranded cDNA was
     cloned into the Not I and EcoRV sites of pExpress-1.
     Library was size-selected for >1 kb fragments and
     normalized. A non-normalized version of this library is
     also available (NIH_ZGC_10). Library was constructed by
     Open Biosystems (Huntsville, AL)"

ORIGIN
Query Match      87.0%; Score 17.4; DB 7; Length 717;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCCA 19
    |||||||
Db 335 AAGGAACACGACACCCCA 353

RESULT 14
AG479585/c
LOCUS
DEFINITION
  AG479585 Mus musculus molossinus DNA, clone:MSMG01-373J11.T7, genomic survey
  sequence.
ACCESSION
AG479585
VERSION
AG479585.1 GI:48186815
KEYWORDS
GSS.

```

SOURCE
ORGANISM Mus musculus molossinus (Japanese wild mouse)
 Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and Shiroishi, T.
TITLE Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823
REFERENCE 2 (bases 1 to 729)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@psc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Tsukuba Institute, Bio Resource Center.
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
 Vector : pBACe3.6
 R.Site 1 : ECoRI.
 R.Site 2 : ECoRI.
FEATURES
source
 1..729
 Location/Qualifiers
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-373J11.T7"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
 Query Match 87.0%; Score 17.4; DB 10; Length 729;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCA 19
 |||||
Db 629 AAGGAAACACGACACCCA 611
 |||||

RESULT 15
LOCUS CF998205
DEFINITION AGENCOURT 16393924 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7038534 5', mRNA sequence.
ACCESSION CF998205
VERSION CF998205.1 GI:38519056
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 750)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Len Zon, Harvard
 cDNA Library Preparation: Open Biosystems
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM14790 row: f column: 04
 High quality sequence stop: 698.
FEATURES
source
 1..750
 Location/Qualifiers
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7038534"
 /tissue_type="whole body"
 /lab_host="DHI0B"
 /clone_lib="NIH_ZGC_7"
 /notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
 Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments and normalized. A non-normalized version of this library is also available (NIH_ZGC 10). Library was constructed by Open Biosystems (Huntsville, AL)"

ORIGIN
 Query Match 87.0%; Score 17.4; DB 7; Length 750;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCA 19
 |||||
Db 259 AAGGAAACACGACACTCA 277
 |||||

RESULT 16
LOCUS CNS03817/c
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 004G16 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL232036
VERSION AL232036.1 GI:7891040
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)

10899143
PUBMED 3 (bases 1 to 770)
REFERENCE: Genoscope.
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequençage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end and sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1..770
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="004G16"
/clone_lib="G"
/note="Genoscope sequence ID : COBG004BD08XE1
end : PUC-Ori"

ORIGIN
Query Match 87.0%; Score 17.4; DB 11; Length 770;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCA 19
Db 303 AAGGAAACACGGACACCCA 285
|||||
|||||

RESULT 17
CV480587/c
LOCUS AGENCOURT 33240879 NIH_ZGC_19 Danio rerio cDNA clone IMAGE:7452402
DEFINITION 3', mRNA sequence.
ACCESSION CV480587
VERSION CV480587.1 GI:53736629
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: William S. Talbot, Stanford University
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution by: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL15709 row: j column: 16
High quality sequence start: 8
High quality sequence stop: 673.
Location/Qualifiers
1..785
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7452402"
/tissue type="5 day old whole larvae"
/lab host="DH10B Tona"
/clone_lib="NIH_ZGC_19"
/note="Organ: mixed; Vector: pME18S-FL3; Site_1: DraIII;

Site 2: DraIII; 1st strand cDNA was primed with an
oligo(dT) primer
(GCGCGTGAAGCGCCTATGCGCTTTTTTTTTTTTTT);
double-stranded cDNA was ligated to a DraIII adaptor
(GGCUACUGG), digested and directionally cloned into
distinct DraIII sites of the pME18S-FL3. Library was size
selected for 1.0 kb, with an average insert size of 1.2 kb.
Library constructed by Yutaka Suzuki (University of Tokyo
Institute of Medical Science). Custom primers recommended
for sequencing: 5' end primer 5'-GGATGTGCTTTACTTCA-3'
and 3' end primer 5'-CGACCTGCAGCTCGACACA-3'. Note: This
is a Zebrafish Gene Collection (ZGC) library"

ORIGIN
Query Match 87.0%; Score 17.4; DB 7; Length 785;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCA 19
Db 77 AAGGAAACACGGACACTCA 59
|||||
|||||

RESULT 18
BG985751
LOCUS 2867 NICHD_Zebrafish_normalized_I Danio rerio cDNA clone 2867, mRNA
DEFINITION sequence.
ACCESSION BG985751
VERSION BG985751.1 GI:14389831
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 794)
AUTHORS Kudoh, T., Tsang, M., Hukriede, N.A., Chen, X., Dedekian, M.,
Clarke, C.J., Kiang, A., Schultz, S., Epstein, J.A., Toyama, R. and
David, I.B.
A gene expression screen in zebrafish embryogenesis
Genome Res. 11 (12), 1979-1987 (2001)
11731487
Contact: David IB
Laboratory of Molecular Genetics
National Institute of Child Health and Human Development, NIH
Bldg. 6B, Room 413, 9000 Rockville Pike, Bethesda, MD 20892 USA
Tel: 301 496 4448
Fax: 301 496 0243
Email: idavid@nih.gov
Seq primer: T3.
Location/Qualifiers
1..794
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="2867"
/dev stage="bud to 10 somite stage embryos"
/clone_lib="NICHD_Zebrafish_normalized_I"
/note="vector: pBluescript KS+; Site 1: NotI; Site 2:
Sali; RNA was reverse-transcribed to first strand cDNA
using SuperScriptII reverse-transcriptase and tagged
oligo-dT primer which contains several restriction sites
including a NotI site:
gactgtcttagatcgatcgacgagggcgccgttttttttttttt. Second
strand DNA was synthesized by E. coli DNA polymerase I in
combination with E. coli RNase H and E. coli DNA ligase.
Double stranded cDNA was ligated with Sali adaptor. These
cDNAs were cloned into the Sali/NotI site of pBluescript
KS+ and transformed into E. coli Electromax DH10B by
electroporation."

FEATURES
source
1..794
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="2867"
/dev stage="bud to 10 somite stage embryos"
/clone_lib="NICHD_Zebrafish_normalized_I"
/note="vector: pBluescript KS+; Site 1: NotI; Site 2:
Sali; RNA was reverse-transcribed to first strand cDNA
using SuperScriptII reverse-transcriptase and tagged
oligo-dT primer which contains several restriction sites
including a NotI site:
gactgtcttagatcgatcgacgagggcgccgttttttttttttt. Second
strand DNA was synthesized by E. coli DNA polymerase I in
combination with E. coli RNase H and E. coli DNA ligase.
Double stranded cDNA was ligated with Sali adaptor. These
cDNAs were cloned into the Sali/NotI site of pBluescript
KS+ and transformed into E. coli Electromax DH10B by
electroporation."

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 794;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCA 19
 |||||
 Db 460 AAGGAAACACGGACACTCA 478

RESULT 19

CV486670/c

LOCUS CV486670 794 bp mRNA linear EST 01-OCT-2004
 DEFINITION AGENCOURT 33240863 NIH_ZGC_19 Danio rerio cDNA clone IMAGE:7452401
 3', mRNA sequence.

ACCESSION CV486670.1 GI:53742712

VERSION EST.

KEYWORDS Danio rerio (zebrafish)

SOURCE ORGANISM

Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 794)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: William S. Talbot, Stanford University

cDNA Library Preparation: Dr. Sumio Sugano

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUM15709 row: j column: 15

High quality sequence start: 6

High quality sequence stop: 710.

FEATURES

source

Location/Qualifiers
 1..794
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7452401"
 /tissue_type="5 day old whole larvae"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_ZGC_19"
 /note="Organ: mixed; Vector: pME18S-FL3; Site 1: DraIII;
 Site 2: DraIII; 1st strand cDNA was primed with an
 oligo(dT) primer
 [GCGCTGAAGACGGCTATGTGGCTTTTTTTTTTTTTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 [GGCUACUG] digested and directionally cloned into
 distinct DraIII sites of the pME18S-FL3. Library was size
 selected for 1.0 kb, with an average insert size of ~1.2kb.
 Library constructed by Yutaka Suzuki (University of Tokyo
 Institute of Medical Science). Custom primers recommended
 for sequencing: 5' end primer 5'-GGATGTTGCTTTACTTCTA-3',
 and 3' end primer 5'-CGACTTGCAGCTCGACACA-3'. Note: This
 is a Zebrafish Gene Collection (ZGC) library"

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 794;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCA 19
 |||||
 Db 79 AAGGAAACACGGACACTCA 61

RESULT 20

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 798)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Len Zon, Harvard

cDNA Library Preparation: Open Biosystems

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUM14832 row: e column: 12

High quality sequence stop: 720.

Location/Qualifiers

1..798

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:7054646"

/tissue_type="whole body"

/lab_host="DH10B"

/clone_lib="NIH_ZGC_7"

/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;

Bulk tissue was collected from a whole adult individual

from the Tuebingen strain. 1st strand cDNA was primed with

a Not I - oligo(dT) primer, double-stranded cDNA was

cloned into the Not I and EcoRV sites of pExpress-1.

Library was size-selected for >1 kb fragments and

normalized. A non-normalized version of this library is

also available (NIH_ZGC 10). Library was constructed by

Open Biosystems (Huntsville, AL)"

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

RESULT 21

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

1 (bases 1 to 800)

NIH_ZGC_17 Danio rerio cDNA clone IMAGE:7416843

5', mRNA sequence.

CV126404

CV126404.1 GI:51861239

EST.

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 800)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Will Talbot
 cDNA Library Preparation: Dr. Yutaka Suzuki and Dr. Sumio Sugano
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM15633 row: e column: 01
 High quality sequence start: 16
 High quality sequence stop: 728.
 Location/Qualifiers
 1..800
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7416843"
 /tissue_type="Dissected hearts from 100 Zebrafish samples
 were pooled"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_ZGC_17"
 /note="Organ: heart; Vector: pME18S-FL3; Site 1: DraIII;
 Site 2: DraIII; 1st strand cDNA was primed with an
 oligo(dT) primer
 [CGCGCTGAAGACGCGCTATGCGCTTTTITTTTTTTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 (GGCUACUGG), digested and directionally cloned into
 distinct DraIII sites of the pME18S-FL3. Library was size
 selected for 1.0 kb, with a average insert size of ~1.2kb.
 Library constructed by Yutaka Suzuki (University of Tokyo
 Institute of Medical Science). Custom primers recommended
 for sequencing: 5' end primer 5'-GGATGTGCTTACTTCTA-3'
 and 3' end primer 5'-CGACTTCAGCTGAGCACA-3'. Note: This
 is a Zebrafish Gene Collection (ZGC) library"

Query Match 87.0%; Score 17.4; DB 7; Length 800;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCA 19
 |||||
 Db 664 AAGGAACACGACACTCA 682

RESULT 22
 Cw717728
 LOCUS
 DEFINITION MARC_1009233 CHORI-240-397C5 Bos taurus genomic clone 1C6, genomic
 survey sequence.
 ACCESSION Cw717728
 VERSION Cw717728.1 GI:55421438
 KEYWORDS GSS.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 819)
 Smith, T.P.L., Stone, R.T., Keele, J.W., Snelling, W.M. and Harhay, G.P.
 SNP discovery in cattle based on low coverage sequencing of BAC
 clones
 Unpublished (2004)
 Other_GSSs: MARC_1010385

Query Match 87.0%; Score 17.4; DB 10; Length 819;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCA 19
 |||||
 Db 646 AAGGAACACGACACCA 664

RESULT 23
 Cn835108
 LOCUS
 DEFINITION AGENCOURT 25055017 NIH_ZGC_4 Danio rerio cDNA clone IMAGE:7289204
 5', mRNA sequence.
 ACCESSION Cn835108
 VERSION Cn835108.1 GI:47940763
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 848)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: John Ngai, Univ of CA, Berkeley
 cDNA Library Preparation: Dr. Sumio Sugano
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM15301 row: f column: 18
 High quality sequence start: 21
 High quality sequence stop: 656.
 Location/Qualifiers
 1..848
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7289204"

Query Match 87.0%; Score 17.4; DB 10; Length 819;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCA 19
 |||||
 Db 646 AAGGAACACGACACCA 664

RESULT 23
 Cn835108
 LOCUS
 DEFINITION AGENCOURT 25055017 NIH_ZGC_4 Danio rerio cDNA clone IMAGE:7289204
 5', mRNA sequence.
 ACCESSION Cn835108
 VERSION Cn835108.1 GI:47940763
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 848)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: John Ngai, Univ of CA, Berkeley
 cDNA Library Preparation: Dr. Sumio Sugano
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM15301 row: f column: 18
 High quality sequence start: 21
 High quality sequence stop: 656.
 Location/Qualifiers
 1..848
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7289204"

CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smithemail.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Seq primer: AATTAAACCTCACTAAAGGG
 Class: BAC subclone.
 Location/Qualifiers
 1..819
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9913"
 /clone="1C6"
 /sex="Male"
 /tissue_type="Blood"
 /clone_lib="CHORI-240-397C5"
 /note="Vector: pBLUESCRIPT SK-; Site 1: BamHI; Site 2:
 BamHI; BAC DNA was digested with Sau3A. Fragments were
 sized to 800-1200 bases and subcloned into pBLUESCRIPT
 SK-."

ORIGIN
 Query Match 87.0%; Score 17.4; DB 10; Length 819;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCA 19
 |||||
 Db 646 AAGGAACACGACACCA 664

FEATURES
 source
 1..819
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9913"
 /clone="1C6"
 /sex="Male"
 /tissue_type="Blood"
 /clone_lib="CHORI-240-397C5"
 /note="Vector: pBLUESCRIPT SK-; Site 1: BamHI; Site 2:
 BamHI; BAC DNA was digested with Sau3A. Fragments were
 sized to 800-1200 bases and subcloned into pBLUESCRIPT
 SK-."

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/lab host="DH10B Tona"
/clone.lib="NIH ZGC 4"
/ncore="Organ: brain/CNS; Vector: PME18S-FL3; Site_1:
Dralll; Site_2: Dralll"

ORIGIN
Query Match      87.0%; Score 17.4; DB 7; Length 848;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCA 19
    |||||
Db 218 AAGGAAACACGGACACTCA 236

RESULT 24
CW718544/c
LOCUS
DEFINITION MARC_1010456 CHORI-240-397C5 Bos taurus genomic clone 1F5, genomic
survey sequence.
ACCESSION CW718544
VERSION CW718544.1 GI:55422254
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 891)
AUTHORS Smith,T.P.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Hathay,G.P.
TITLE SNP discovery in cattle based on low coverage sequencing of BAC
clones
JOURNAL Unpublished (2004)
COMMENT Other_GSSs: MARC_1009304
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Seq primer: GTAATACGACTCACTATAGGG
Class: BAC subclone.
FEATURES
Location/Qualifiers
source
1..891
/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="1F5"
/sex="Male"
/tissue_type="Blood"
/clone_lib="CHORI-240-397C5"
/notes="Vector: pBLUESCRIPT SK-; Site 1: BamHI; Site 2:
BamHI; BAC DNA was digested with Sau3A. Fragments were
sized to 800-1200 bases and subcloned into pBLUESCRIPT
SK-."
ORIGIN
Query Match      87.0%; Score 17.4; DB 10; Length 891;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCA 19
    |||||
Db 651 AAAGAAACACGGACACCCA 669

RESULT 26
CW412195/c
LOCUS
DEFINITION AUF_IpHdk 47 p20 Head kidney cDNA library Ictalurus punctatus cDNA
5' similar to Autosomal Highly Conserved Protein, mRNA sequence.
ACCESSION CW412195
VERSION CW412195.1 GI:40572779
KEYWORDS EST.
SOURCE Ictalurus punctatus (channel catfish)
ORGANISM Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
REFERENCE 1 (bases 1 to 961)
AUTHORS Liu,Z., Li,P., Liu,L., He,C., Kucuktas,H., Feng,J., Chen,L.,
Peatman,R., Baoprasertkul,P., Simmons,M., Muir,W., Grizzle,J.,
Dunham,R. and Brady,Y.
TITLE 30,000 new catfish ESTs: new resources for functional analysis of
genes involved in aquaculture performance traits
JOURNAL Unpublished (2004)
COMMENT Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell

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survey sequence.
ACCESSION CW717765
VERSION CW717765.1 GI:55421475
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 905)
AUTHORS Smith,T.P.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Hathay,G.P.
TITLE SNP discovery in cattle based on low coverage sequencing of BAC
clones
JOURNAL Unpublished (2004)
COMMENT Other_GSSs: MARC_1010456
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Seq primer: AATTACCTCACTATAAGGG
Class: BAC subclone.
FEATURES
Location/Qualifiers
source
1..905
/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="1F5"
/sex="Male"
/tissue_type="Blood"
/clone_lib="CHORI-240-397C5"
/notes="Vector: pBLUESCRIPT SK-; Site 1: BamHI; Site 2:
BamHI; BAC DNA was digested with Sau3A. Fragments were
sized to 800-1200 bases and subcloned into pBLUESCRIPT
SK-."
ORIGIN
Query Match      87.0%; Score 17.4; DB 10; Length 905;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCA 19
    |||||
Db 651 AAAGAAACACGGACACCCA 669

RESULT 26
CW412195/c
LOCUS
DEFINITION AUF_IpHdk 47 p20 Head kidney cDNA library Ictalurus punctatus cDNA
5' similar to Autosomal Highly Conserved Protein, mRNA sequence.
ACCESSION CW412195
VERSION CW412195.1 GI:40572779
KEYWORDS EST.
SOURCE Ictalurus punctatus (channel catfish)
ORGANISM Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
REFERENCE 1 (bases 1 to 961)
AUTHORS Liu,Z., Li,P., Liu,L., He,C., Kucuktas,H., Feng,J., Chen,L.,
Peatman,R., Baoprasertkul,P., Simmons,M., Muir,W., Grizzle,J.,
Dunham,R. and Brady,Y.
TITLE 30,000 new catfish ESTs: new resources for functional analysis of
genes involved in aquaculture performance traits
JOURNAL Unpublished (2004)
COMMENT Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell

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and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: 17.

FEATURES
    source
        Location/Qualifiers
            1..961
                /organism="Ictalurus punctatus"
                /mol_type="mRNA"
                /db_xref="taxon:7998"
                /clone_lib="Head kidney cDNA library"
                /note="Organ: Head kidney; Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
    Query Match      87.0%; Score 17.4; DB 7; Length 961;
    Best Local Similarity 94.7%; Pred. No. 1.6e+03;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACCGACACCCA 19
    |||||
Db 270 AAGGAACACCGACACCCA 252

RESULT 27
LOCUS BM415978 963 bp mRNA linear EST 28-JAN-2002
DEFINITION OP21060 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION BM415978
VERSION BM415978.1 GI:18382777
KEYWORDS EST.
SOURCE Globodera pallida
ORGANISM Globodera pallida
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE
    1 (bases 1 to 963)
    Heer, J., Sosinski, B., Pokrzywa, R.M., Wairy, A. and Opperman, C.
    Mixed Stage EST's from Globodera pallida, the potato cyst nematode
    Unpublished (2001)
    Contact: Opperman, C
    Center for the Biology of Nematode Parasitism
    NC State University; IACR-Rothamsted
    Campus Box 7616; Raleigh, NC 27695, USA
    Tel: 919.515.6699
    Fax: 919.515.9500
    Email: warthog@unity.ncsu.edu
    GT11-9PCN F A05 GT11-9_F_033.ab1.
    Location/Qualifiers
        1..963
            /organism="Globodera pallida"
            /mol_type="mRNA"
            /db_xref="taxon:36090"
            /clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"
            /note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."

FEATURES
    source
        Location/Qualifiers
            1..963
                /organism="Globodera pallida"
                /mol_type="mRNA"
                /db_xref="taxon:36090"
                /clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"
                /note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."

ORIGIN
    Query Match      87.0%; Score 17.4; DB 3; Length 963;
    Best Local Similarity 94.7%; Pred. No. 1.6e+03;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACCGACACCCA 19
    |||||
Db 572 AAGGTACACCGACACCCA 590

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RESULT 28
LOCUS CG745203 1121 bp DNA linear GSS 24-OCT-2003
DEFINITION P038-1-B12.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CG745203
VERSION CG745203.1 GI:37966129
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE
    1 (bases 1 to 1121)
    Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perbolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
    An integrated physical and genetic map of the nematode Pristionchus pacificus
    Mol. Genet. Genomics 269 (5), 715-722 (2003)
    12884007
    Contact: Sommer RJ
    Evolutionary Biology
    Max-Planck-Institute for Developmental Biology
    Spemannstr. 37-39, Tuebingen D-72076, Germany
    Tel: 00497071601371
    Fax: 00497071601498
    Email: ralf.sommer@tuebingen.mpg.de
    Class: BAC ends.
    Location/Qualifiers
        1..1121
            /organism="Pristionchus pacificus"
            /mol_type="genomic DNA"
            /strain="California"
            /db_xref="taxon:54126"
            /clone_lib="Ppa EcoRI BAC Library"
            /note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN
    Query Match      87.0%; Score 17.4; DB 10; Length 1121;
    Best Local Similarity 94.7%; Pred. No. 1.6e+03;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGAACACCGACACCCA 20
    |||||
Db 1098 AGGAACACCGACACCCA 1116

RESULT 29
LOCUS CK027487 1134 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_16624073 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7053855
ACCESSION CK027487
VERSION CK027487.1 GI:38553411
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE
    1 (bases 1 to 1134)
    NIH-MGC http://mgs.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Daniela S. Gerhard, Ph.D.
    Office of Cancer Genomics
    National Cancer Institute / NIH
    Bldg. 31 Rm10A07 Bethesda, MD 20892
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Len Zon, Harvard
    cDNA Library Preparation: Open Biosystems
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LRAM14830 row: d column: 13
 High quality sequence stop: 832.

FEATURES

source

1..1134
 Location/Qualifiers
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7053855"
 /tissue_type="whole body"
 /lab_host="DH10B"
 /clone_lib="NIH_ZGC_7"

/note="vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pExpress-1.
 Library was size-selected for >1 kb fragments and
 normalized. A non-normalized version of this library is
 also available (NIH_ZGC_10). Library was constructed by
 Open Biosystems (Huntsville, AL)"

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 1134;
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCA 19
 |||||
 DB 861 AAGGAAACACGGACACTCA 879

RESULT 30
 C2679560 683 bp DNA linear GSS 07-JUL-2005
 LOCUS OM_Ba0237005.r OM_Ba Oryza minuta genomic clone OM_Ba0237005 3',
 DEFINITION genomic survey sequence.
 C2679560
 VERSION GI:70291142
 C2679560.1
 SOURCE GSS.

ORGANISM Oryza minuta
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 683)
 AUTHORS Kim,H., Collura,K., Wasotski,M., Byrne,M., Stum,D., Smart,D.,
 Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
 Wang,R.

TITLE OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
 JOURNAL Unpublished (2005)
 COMMENT Contact: Rod A. Wing

Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 Plate: 0237 row: 0 column: 05
 Class: BAC ends.

FEATURES

source

1..683
 Location/Qualifiers
 /organism="Oryza minuta"
 /mol_type="genomic DNA"
 /db_xref="taxon:63629"
 /clone="OM_Ba0237005"
 /tissue_type="leaves"
 /lab_host="DH10B"
 /clone_lib="OM_Ba"
 /note="vector: pCUGIBAC1; Site 1: HindIII; Site 2:

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 683;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACACGGACACCCA 19
 |||||
 DB 653 GGAACACGGACACCCA 669

RESULT 31
 BZ020345/c 712 bp DNA linear GSS 08-OCT-2002
 LOCUS osh04a08.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION sequence.

ACCESSION BZ020345
 VERSION BZ020345.1 GI:23580078
 KEYWORDS GSS.
 SOURCE Brassica oleracea

ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 712)
 AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
 Nash,W., Rabinowicz,P.D. and Wilson,R.K.

TITLE Whole genome shotgun reads from Brassica oleracea
 JOURNAL Unpublished (2002)
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu

Plate: osh04 row: a column: 08
 Seq primer: -21UPPOT forward
 Class: shotgun

High quality sequence start: 28
 High quality sequence stop: 551.
 Location/Qualifiers
 1..712

FEATURES

source

/organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_lib="B.oleracea002"
 /note="vector: P0TW13; Whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear
 prep using Brassica oleracea TO1000DH3 buds provided by
 Thomas Osborn at the University of Wisconsin. Genomic
 DNA was provided by Pablo Rabinowicz (CSHL) and the
 shotgun library prepared at Washington University Genome
 Sequencing Center."

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 712;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAACACGGACACCC 18
 |||||
 DB 497 AGGAACACGGACACCC 481

RESULT 32
 BH693975

LOCUS BH693975 751 bp DNA linear GSS 19-FEB-2002
 DEFINITION BOMI227TF BO 2.3 KB Brassica oleracea genomic clone BOMI227,
 genomic survey sequence.

ACCESSION BH693975
 VERSION BH693975.1 GI:18764555
 KEYWORDS GSS.
 SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica;

REFERENCE AUTHORS

1 (bases 1 to 751)
Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

TITLE

Whole genome shotgun sequencing of *Brassica oleracea* and its application to gene discovery and annotation in Arabidopsis

JOURNAL PUBMED

Genome Res. 15 (4), 487-495 (2005)

COMMENT

Other GSSs: BOMIZ27TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

FEATURES source

Location/Qualifiers
1..751

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="T01000DH3"

/db_xref="taxon:3712"

/clone="BOMIZ27"

/note="Vector: pBOM2.3 kb"

/note="Vector: pBOM2.3 kb sheared genomic DNA inserted into pBOM1 using BstXI linkers"

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 AGGAACACGACACCC 18

Db

80 AGGAACACGACACCC 96

RESULT 33

LOCUS

CW176116 108 bp DNA linear GSS 29-OCT-2004
104 588 11158315 116 36578 066 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 11158315, genomic survey sequence.

ACCESSION

CW176116 GI:54868683

VERSION

GSS.

KEYWORDS

Sorghum bicolor (sorghum)

ORGANISM

Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

AUTHORS

1 (bases 1 to 108)
Bedell, J.A., Budiman, M.A., Nurnberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Huleman, H., Roe, B.A., Wiley, G., Korff, I.F., Rabinowitz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and Martienssen, R.A.

TITLE

Sorghum genome sequencing by methylation filtration

JOURNAL

PLoS Biol. 3 (1), e13 (2005)

PUBMED

15660154

COMMENT

Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 588 row: p column: 19
Seq primer: T3 Reverse

Class: methylation filtered

FEATURES source

High quality sequence stop: 108.

Location/Qualifiers

1..108

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/cultivar="ATx623"

/db_xref="taxon:4558"

/clone="11158315"

/clone_lib="Sorghum methylation filtered library (LibID: 104)"

/note="Organ: leaf; Vector: pBSCSK(-); Site: 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 108;
Best Local Similarity 90.0%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1 AAGGAACACGACACCAA 20

Db

81 AAGGAGACGACACCAA 100

RESULT 34

LOCUS

CD290195 209 bp mRNA linear EST 16-SEP-2003
StrPus38.003354 Sea urchin embryo 7hr cleavage stage cDNA library
MPMGp538 Strongylocentrotus purpuratus cDNA clone
CALTP538J242;MPI_538_2J24_3', mRNA sequence.

ACCESSION

CD290195

VERSION

CD290195.1 GI:34741272

KEYWORDS

EST.

SOURCE

Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.

REFERENCE

AUTHORS

1 (bases 1 to 209)
Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A., Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H.

TITLE

Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters

JOURNAL

Genome Res. 13 (12), 2736-2746 (2003)

COMMENT

Contact: Poustka AJ
Laboraty 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inhestr.63-73, D-14195 Berlin, Germany

Tel: +49 30 8413 1235

Fax: +49 30 8413 1128

Email: poustka@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONF) to reduce sequencing redundancy. According to the ONF procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONF cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA clones and filters are distributed via the Resource Center/Primary Database of the German Human Genome Project (<http://www.rzpd.de>)
PCR Primers
FORWARD: 5' CCCAGGCTTACACTTATGCTCCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTACCGCAGCTGCGAAGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5' GCTATTACCGCAGCTGCGAAGGGGATGTG 3' (M13FSP)
High quality sequence stop: 209.

FEATURES source

Location/Qualifiers
1..209

OA_ABA0117123 3', genomic survey sequence.

```

ACCESSION CW585488
VERSION CW585488.1 GI:54477247
KEYWORDS GSS.
SOURCE Oryza australiensis
ORGANISM Oryza australiensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 363)
AUTHORS Kim H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0117 row: I column: 23
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..363
/organism="Oryza australiensis"
/mol_type="genomic DNA"
/db_xref="taxon:4532"
/clone="OA_ABA0117123"
/tissue_type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OA_ABA"
/notes="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 363;
Best Local Similarity 90.0%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 129 AAGGAAATCGCGACACCCAA 110
|||||
RESULT 39
AI618550 370 bp mRNA linear EST 21-APR-1999
LOCUS zewp0061.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio
DEFINITION CDNA 5', mRNA sequence.
ACCESSION AI618550
VERSION AI618550.1 GI:4627717
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 370)
AUTHORS Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and
Liew, C.C.
TITLE Identification and Characterization of Expressed Sequence Tags from
an Embryonic Zebrafish Heart cDNA Library
JOURNAL Unpublished (1999)
COMMENT Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 61797750995

```

Email: cliw@rics.bwh.harvard.edu

```

PCR Primers
FORWARD: 5' GCCAAGCTCGAAATTAACCTCACTAAAGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTAAGGCG 3'
Seq primer: 5' GAAATTAACCTCACTAAAGG 3'.
FEATURES
source
Location/Qualifiers
1..370
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrf"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/notes="Organ: heart; Vector: Lambda ZAP Express; Site_1:
EcoRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector."
ORIGIN
Query Match 84.0%; Score 16.8; DB 1; Length 370;
Best Local Similarity 90.0%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 193 AAGGAAACACGACACCCAA 174
|||||
RESULT 39
BP813540/c 391 bp mRNA linear EST 15-FEB-2005
LOCUS BP813540
DEFINITION BP813540 RAF119 Arabidopsis thaliana cDNA clone RAFL22-06-L22 5',
mRNA sequence.
ACCESSION BP813540
VERSION BP813540.1 GI:59849619
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 391)
AUTHORS Seki, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K.,
Iida, K., Enju, A., Sakurai, T., Arakawa, T., Carninci, P., Fukuda, S.,
Iida, J., Kawai, J., Sasaki, D., Shiraki, T., Hayashizaki, Y. and
Shinozaki, K.
TITLE Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs
JOURNAL Unpublished (2005)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998, 2002). This clone is in a
modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.jp and
http://arge.gsc.riken.jp) for further details.
FEATURES
source
Location/Qualifiers
1..391
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL22-06-L22"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL19"
/notes="Site_1: BamHI; Site_2: SalI; Subtraction Library"

```

ORIGIN

Query Match 84.0%; Score 16.8; DB 3; Length 391;
 Best Local Similarity 90.0%; Pred. No. 2.8e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
 Db 346 AAGGAAACACGACACACCA 327

RESULT 40
 BP664023 397 bp mRNA linear EST 27-JUN-2004
 LOCUS BP664023 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-50-E09 3',
 DEFINITION mRNA sequence.

ACCESSION BP664023
 VERSION BP664023
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 397)
 AUTHORS Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
 Nakajima, M., Enju, A., Akiyama, K., Ono, Y., Muramatsu, M.,
 Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.

TITLE Functional annotation of a full-length Arabidopsis cDNA collection
 JOURNAL Science 296 (5565), 141-145 (2002)
 PUBMED 11910074

COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-3060

Email: msekio@r.riken.go.jp
 reversed clone; Please visit our web site
 (http://pfgweb.gsc.riken.go.jp/) for further details.

FEATURES

source

1..397

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="RAFL21-50-E09"

/lab_host="DH10B"

/clone_lib="RAFL21"

/note="Site 1: BamHI; Site 2: SalI; Subtraction Library.
 The sequence was obtained from samples subjected to
 various stress and plant hormones-treated"

ORIGIN

Query Match 84.0%; Score 16.8; DB 3; Length 397;
 Best Local Similarity 90.0%; Pred. No. 2.8e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
 Db 37 AAGGAAACACGACACACCA 56

RESULT 41
 CA730096 412 bp mRNA linear EST 26-NOV-2002
 LOCUS CA730096 wipic.pk002.e2 wipic Arabidopsis thaliana cDNA clone wipic.pk002.e2 5',
 DEFINITION end, mRNA sequence.

ACCESSION CA730096
 VERSION CA730096.1 GI:25452099
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Triticum.

1 (bases 1 to 412)

Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,

Miao, G., Caraher, N. and Hanafey, M.K.

DuPont Wheat cDNA Sequence

Unpublished (2002)

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: M13.

FEATURES

source

1..412

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone="wipic.pk002.e2"

/tissue_type="pistils"

/lab_host="DH10B"

/clone_lib="wipic"

/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:

XhoI; Wheat (Triticum aestivum, Hi Line) immature pistils"

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 412;
 Best Local Similarity 90.0%; Pred. No. 2.9e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

Db 141 AAGGAAACCGGACACCCAA 160

RESULT 42

BU237703/c

LOCUS BU237703

DEFINITION 603410683F1 CSEQCHN24 Gallus gallus CDNA clone CHEST327e22 5', mRNA

sequence.

ACCESSION BU237703

VERSION BU237703.1

KEYWORDS GI:25484495

SOURCE EST.

ORGANISM Gallus gallus (chicken)

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 427)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

12445392

COMMENT Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1..427

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, HiseX"

/db_xref="taxon:9031"

/clone="CHEST327e22"

/dev_stage="22"

/lab_host="DH10B"
/clone_lib="CSQCHN24"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 427;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 96 AAGGAAACACGACACCCAA 77

RESULT 43

AG224508/c
LOCUS AG224508 444 bp DNA linear GSS 19-JUL-2003
DEFINITION Lotus corniculatus var. japonicus DNA, clone: LjB10118_r, genomic survey sequence.

ACCESSION AG224508.1 GI:26534354
VERSION AG224508
KEYWORDS GSS.

SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)

ORGANISM Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

REFERENCE

1 Sato, S., Nakamura, Y. and Tabata, S.
Lotus japonicus BAC End sequences
JOURNAL Published Only in Database (2002)
2 (bases 1 to 444)
AUTHORS Sato, S.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)

FEATURES

source
1..444
/organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/variety="japonicus"
/db_xref="taxon:34305"
/clone="LjB10118_r"
/clone_lib="genomic BAC library"
/note="VECTOR: pBelOBAC11
synonym: Lotus japonicus"

ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 444;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 345 AAGTAAACACGGAACCCAA 326

RESULT 44

BP616001
LOCUS BP616001 447 bp mRNA linear EST 26-JUN-2004
DEFINITION BP616001 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-18-B08 3', mRNA sequence.

ACCESSION BP616001.1 GI:49267183
VERSION BP616001
KEYWORDS EST.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE

AUTHORS 1 (bases 1 to 447)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T., Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M., Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
TITLE Functional annotation of a full-length Arabidopsis cDNA collection
JOURNAL Science 296 (5565), 141-145 (2002)
PUBMED 11910074

COMMENT

Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060

Email: msek@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfgwweb.gsc.riken.go.jp/) for further details.

FEATURES

source
1..447
/location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clones="RAFL16-18-B08"
/lab_host="DH10B"
/clone_lib="RAFL16"
/note="Site_1: BamHI; Site_2: SalI; dark-grown"

ORIGIN

Query Match 84.0%; Score 16.8; DB 3; Length 447;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 37 AAGGAAACACGACACCCAA 56

RESULT 45

BQ803856
LOCUS BQ803856 475 bp mRNA linear EST 30-JUL-2002
DEFINITION WHE2842_H02_004ZS Triticum monococcum vernalized apex cDNA library Triticum monococcum cDNA clone WHE2842_H02_004, mRNA sequence.

ACCESSION BQ803856
VERSION BQ803856.1 GI:22018825
KEYWORDS EST.

SOURCE

ORGANISM Triticum monococcum
Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

REFERENCE

AUTHORS 1 (bases 1 to 475)
Anderson, O.D., Chao, S., Crossman, C., Dubcovsky, J., Echenique, V., Lazo, G.R., Pham, J., Rausch, C.J., Stamova, B., Wilson, C. and Woo, J.
TITLE The structure and function of the expressed portion of the wheat genomes - Vernalized apex cDNA library from Triticum monococcum unpublished (2002)
Contact: Olin Anderson

JOURNAL

COMMENT US Department of Agriculture, Agriculture Research Service, Pacific

West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510595773
Fax: 510595818

Email: andersn@gw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: SK primer.

Location/Qualifiers

FEATURES

source

1. .475
/organism="Triticum monococcum"
/mol_type="mRNA"
/cultivar="G3116"
/db_xref="taxon:4568"
/clone="WHE2842_H02_O04"
/tissue_type="Vernalized apex"
/dev_stage="One month old plants"
/lab_host="E. coli XL0LR"
/clone_lib="Triticum monococcum vernalized apex cDNA library"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; One-month old plants were subjected to vernalization treatment by placing them in the cold room at 6 C, under 15hr light/9hr dark condition. Total RNA was prepared from apex tissue extracted from plants with no cold treatment; and from plants with 2-week, 4-week and 6-week cold treatment separately. Equal amount of total RNA was pooled from all four samples, a cDNA library was made using pooled polyA RNA and cDNA clones were in vivo excised at the University of California, Davis (V. Echenique, B. Stamova, J. Dubcovsky). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 475;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 10 AAGAAACACGACACCCAA 29

RESULT 46

CA728920/c

LOCUS

DEFINITION wdilc.pk005.e10 wdilc Triticum aestivum cDNA clone wdilc.pk005.e10 5' end, mRNA sequence.

ACCESSION CA728920.1 GI:25450920

VERSION

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 484)

AUTHORS Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,

Miao,G., Caraher,N. and Hanafey,M.K.

TiDuPont Wheat cDNA Sequence

Unpublished (2002)

CONTACT: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: M13.

FEATURES

source

Location/Qualifiers

1. .484

Query Match

Best Local Similarity

84.0%; Score 16.8; DB 10; Length 485;

90.0%; Pred. No. 2.9e+03;

/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4568"
/clone="wdilc.pk005.e10"
/tissue_type="inflorescence"
/lab_host="DH10B"
/clone_lib="wdilc"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum, Hi Line) developing inflorescence +/- 4 cm"

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 484;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 219 AAGAAACACGACACCCAA 200

RESULT 47

CA745890/c

LOCUS

DEFINITION CW445890 485 bp DNA linear GSS 02-NOV-2004 fabb001f171e14f0 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone fabb001f171e14, genomic survey sequence.

ACCESSION CW445890

VERSION CW445890.1 GI:55193851

KEYWORDS

SOURCE

ORGANISM

Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 485)

AUTHORS

Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., Korf,I.F., McMenamy,J., Smith,M., Holsen,H., Roe,B.A., Wiley,G., Korf,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and Martienssen,R.A.

Sorghum genome sequencing by methylation filtration

PLoS Biol. 3 (1), e13 (2005)

PUBMED 15660154

COMMENT

Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: fabb001f171 row: e column: 14

Seq primer: f Forward

Class: methylation filtered

High quality sequence stop: 485.

FEATURES

source

1. .485

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/cultivar="ATx623"

/db_xref="taxon:4558"

/clone="fabb001f171e14"

/clone_lib="Sorghum methylation filtered library (LibID: 104)"

/note="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match

Best Local Similarity

84.0%; Score 16.8; DB 10; Length 485;

90.0%; Pred. No. 2.9e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCAA 20
 Db 342 AAGGAACACGGACACCAA 323

RESULT 48

BU229997
 LOCUS CA013161
 DEFINITION HT07J07: HT Hordeum vulgare subsp. vulgare cDNA clone CHEST903a19 5', mRNA

ACCESSION BU229997
 VERSION BU229997.1 GI:25470352
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 514)
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 PUBMED 12445392

COMMENT Contact: Simon Hubbard
 Department of Biomedical Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1OD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source
 1..514
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST903a19"
 /dev_stage="22"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN23"
 /note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 514;
 Best Local Similarity 90.0%; Pred. No. 2.9e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCAA 20
 Db 344 AAGGAACACGGACACCAA 363

RESULT 49

CA013161
 LOCUS HT07J07: HT Hordeum vulgare subsp. vulgare cDNA clone HT07J07
 DEFINITION HT07J07: HT Hordeum vulgare subsp. vulgare cDNA clone HT07J07

ACCESSION CA013161
 VERSION CA013161.1 GI:24290505
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Hordeum.

REFERENCE

AUTHORS Zhang, H., Potokina, E., Michalek, W., Weschke, W., Stein, N. and Graner, A.
 TITLE Barley ESTs from germinating seeds
 JOURNAL Unpublished (2002)
 COMMENT Contact: Stein Nils

Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595

Email: stein@ipk-gatersleben.de
 Insert Length: 519 Std Error: 0.00
 Plate: 7 row: J column: 7
 Seq primer: M13rev.

FEATURES

source
 1..519
 Location/Qualifiers
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Barke"
 /sub_species="vulgare"
 /db_xref="GABI:261687"
 /db_xref="taxon:112509"
 /clone="HT07J07"
 /tissue_type="endosperm early"
 /dev_stage="0-16 hours after imbibition"
 /lab_host="XL10-Gold"
 /clone_lib="HT"
 /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 519;
 Best Local Similarity 90.0%; Pred. No. 2.9e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCAA 20
 Db 125 AAGGAACACGGACACCAA 144

RESULT 50

CF352554
 LOCUS lac30C03.y1 SiEP Mus musculus cDNA 5', mRNA sequence.
 DEFINITION CF352554
 VERSION CF352554.1 GI:33956646
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 525)
 AUTHORS Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J.,
 Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J.,
 Ronko, I., Teagareishvili, R., Belaygorod, L., Grow, A., Maguire, L.,
 Waterston, R. and Wilson, R.

TITLE
JOURNAL
COMMENT
WashU Stem cell EST Project
Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
WashU, Human Genetics Division
Washington University School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 525.
Location/Qualifiers
source
1. 525
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="small intestinal epithelial progenitors"
/lab_host="DH5alpha Ultra Max cells (Invitrogen)"
/clone_lib="SIEP"
/note="Vector: pAMP1; The library was synthesized with
modified SMART primers with dntp at the end. After
treatment with UDG the cDNA was cloned in pAMP1 vector by
annealing."

ORIGIN
Query Match 84.0%; Score 16.8; DB 6; Length 525;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAACACGACACCCAA 20
Db 488 AAGGAACACGACACCCAA 507

RESULT 51
CA637743/c
LOCUS
DEFINITION
CA637743 544 bp mRNA linear EST 23-NOV-2002
wreln.pk0002.c4 wreln Triticum aestivum cDNA clone wreln.pk0002.c4
5' end, mRNA sequence.
CA637743
VERSION
CA637743.1 GI:25216039
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 544)
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.
Miouf Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
source
1..544
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wreln.pk0002.c4"
/tissue_type="root"
/clone_lib="wreln"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) root; normalized from
wre1 library"

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 544;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAACACGACACCCAA 20
Db 292 AATGAACACGACACCCAA 273

RESULT 52
BG727965/c
LOCUS
DEFINITION
BG727965 546 bp mRNA linear EST 09-MAY-2001
fp08e03.xl zebrafish gridded kidney Danio rerio cDNA clone
IMAGE:4729037 3' similar to TR:095624 095624 CPLA2 INTERACTING
PROTEIN. ;, mRNA sequence.

ACCESSION
BG727965
VERSION
BG727965.1 GI:14013040
KEYWORDS
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 546)

REFERENCE
AUTHORS
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, P., Marra, M.,
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
WashU Zebrafish EST Project 1998

TITLE
JOURNAL
COMMENT
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu

cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address:
www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzpd.de)

zebrafish identity (p-value greater than 1e-99) found to:
gi|2289384|gb|AA542449|AA542449 fa07a11.s1 Zebrafish ICRFzfls Danio
rerio cDNA
Seq primer: T7 from Gibco
High quality sequence stop: 353.
Location/Qualifiers
source
1..546
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4729037"
/sex="mixed"
/tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XL0LR"
/clone_lib="zebrafish gridded kidney"
/note="Organ: kidney; Vector: pBK-CMV; Site 1: EcoRI;
Site 2: XhoI; Oligo dt cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
zebrafish."

FEATURES

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 546;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAACACGACACCCAA 20

```

Db      518  AAGGAAGCGGCGACCCAA 499
|||||
RESULT 53
LOCUS   AQ293334
DEFINITION HS_2266_B2_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=10 Row=J, genomic survey sequence.
ACCESSION AQ293334
VERSION   AQ293334.1
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 559)
AUTHORS  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED   10449764
COMMENT   Contact: Mahairas GG, Wallace JC, Hood L
          High Throughput Sequencing Center
          University of Washington
          401 Queen Anne Avenue North, Seattle, WA 98109, USA
          Tel: (206) 616-3618
          Fax: (206) 616-3887
          Email: jwallace@u.washington.edu
          Sequence Tagged Connector
          Plate: 2266 row: J column: 10
          Class: BAC ends
          High quality sequence stop: 559.
FEATURES             source
     location/Qualifiers
         1..559
         /organism="Homo sapiens"
         /mol_type="genomic DNA"
         /db_xref="taxon:9606"
         /clone="Plate=2266 Col=10 Row=J"
         /sex="male"
         /clone_lib="CIT Approved Human Genomic Sperm Library D"
         /note="Organ: sperm; Vector: pBLOBAC11; BAC Clones in E-Coli DH10B"
ORIGIN
Query Match      84.0%; Score 16.8; DB 9; Length 559;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  AAGGAACCGGCGACCCAA 20
|||||
Db      527  AAGGGACACGGACCCAA 546
|||||
RESULT 54
LOCUS   BB621815
DEFINITION BB621815 RIKEN full-length enriched, adult male medulla oblongata Mus musculus cDNA clone 6330410L21 5', mRNA sequence.
ACCESSION BB621815
VERSION   BB621815.1
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 580)
AUTHORS  Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,

```

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Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Onno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
     location/Qualifiers
         1..580
         /organism="Mus musculus"
         /mol_type="mRNA"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="6330410L21"
         /sex="male"
         /tissue_type="medulla oblongata"
         /dev_stage="adult"
         /lab_host="DH10B"
         /clone_lib="RIKEN full-length enriched, adult male medulla oblongata"
         /note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATCTCGAGTTAATAATTAATATATATATTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGAGTTAATAATTAATATATATATATATATATTTTNN 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI"

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ORIGIN

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Query Match      84.0%; Score 16.8; DB 2; Length 580;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 396 AAGCAACACGACACCCAA 415

RESULT 55
LOCUS DE001557/c
DEFINITION Branchiostoma floridae DNA, clone: CH302-004F04.R, genomic survey
sequence.
ACCESSION DE001557
VERSION DE001557.1 GI:62243906
KEYWORDS GSS.
SOURCE Branchiostoma floridae (Florida lancelet)
ORGANISM Branchiostoma floridae
          Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
          Branchiostoma.
REFERENCE 1
AUTHORS Fujiyama A., Toyoda A., Hattori M. and Sakaki Y.
TITLE BAC end sequences of CH01-302 Amphioxus Library
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 607)
AUTHORS Fujiyama A.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2005) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: afujiyama@gsc.riken.jp, URL: http://hgp.gsc.riken.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pTAREAC2.1
R.Site 1 : ECORI
R.Site 2 : ECORI.
Location/Qualifiers
1. .607
/organism="Branchiostoma floridae"
/mol_type="genomic DNA"
/db_xref="taxon:7739"
/clone="CH302-004F04.R"
/sex="male"
/tissue type="sperm"
/clone_lib="CH010302 Amphioxus genomic BAC library"
/note="Common name: amphioxus"

ORIGIN
Query Match      84.0%; Score 16.8; DB 11; Length 607;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 32 AAGGAAACACGGACACTAAA 13

RESULT 56
LOCUS CL773304/c
DEFINITION OR_BB0086D16.r OR_BBa Oryza nivara genomic clone OR_BB0086D16 3',
genomic survey sequence.
ACCESSION CL773304
VERSION CL773304.1 GI:50847690
KEYWORDS GSS.
SOURCE Oryza nivara
          Oryza nivara
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Poaceae;

Query Match      84.0%; Score 16.8; DB 2; Length 580;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 396 AAGCAACACGACACCCAA 415

RESULT 55
LOCUS DE001557/c
DEFINITION Branchiostoma floridae DNA, clone: CH302-004F04.R, genomic survey
sequence.
ACCESSION DE001557
VERSION DE001557.1 GI:62243906
KEYWORDS GSS.
SOURCE Branchiostoma floridae (Florida lancelet)
ORGANISM Branchiostoma floridae
          Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
          Branchiostoma.
REFERENCE 1
AUTHORS Fujiyama A., Toyoda A., Hattori M. and Sakaki Y.
TITLE BAC end sequences of CH01-302 Amphioxus Library
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 607)
AUTHORS Fujiyama A.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2005) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: afujiyama@gsc.riken.jp, URL: http://hgp.gsc.riken.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pTAREAC2.1
R.Site 1 : ECORI
R.Site 2 : ECORI.
Location/Qualifiers
1. .607
/organism="Branchiostoma floridae"
/mol_type="genomic DNA"
/db_xref="taxon:7739"
/clone="CH302-004F04.R"
/sex="male"
/tissue type="sperm"
/clone_lib="CH010302 Amphioxus genomic BAC library"
/note="Common name: amphioxus"

ORIGIN
Query Match      84.0%; Score 16.8; DB 11; Length 607;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 32 AAGGAAACACGGACACTAAA 13

RESULT 56
LOCUS CL773304/c
DEFINITION OR_BB0086D16.r OR_BBa Oryza nivara genomic clone OR_BB0086D16 3',
genomic survey sequence.
ACCESSION CL773304
VERSION CL773304.1 GI:50847690
KEYWORDS GSS.
SOURCE Oryza nivara
          Oryza nivara
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Poaceae;

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REFERENCE 1 (bases 1 to 608)
AUTHORS Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
          Arizona Genomics Institute
          University of Arizona
          Forbes Building Room 303, Tucson, AZ 85721-0036, USA
          Tel: 520 626 9595
          Fax: 520 621 1259
          Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0086 row: D column: 16
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
1. .608
/organism="Oryza nivara"
/mol_type="genomic DNA"
/db_xref="taxon:4536"
/clone="OR_BB0086D16"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 608;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
   |||||
Db 129 AAGGAAATGCGACACCCAA 110

RESULT 57
LOCUS CG099060/c
DEFINITION PUIHL20TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMB7a0594C16,
genomic survey sequence.
ACCESSION CG099060
VERSION CG099060.1 GI:33981354
KEYWORDS GSS.
SOURCE Zea mays
          Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Poaceae;
          1 (bases 1 to 628)
          Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
          Resnick, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J. and
          Bennetzen, J.
          Maize Genomics Consortium
          Unpublished (2003)
          Other GSSs: PUIHL20TB
          Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TP
          Class: sheared ends.
          Location/Qualifiers
          1. .628
          /organism="Zea mays"
          /mol_type="genomic DNA"

REFERENCE 1 (bases 1 to 628)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUIHL20TB
          Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TP
          Class: sheared ends.
          Location/Qualifiers
          1. .628
          /organism="Zea mays"
          /mol_type="genomic DNA"

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/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA0584C16"
/clone_lib="ZM 0.6-1.0 kb"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 628;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAAC 20
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Db 80 AAGGAACGACGACGCCAAC 61

RESULT 58
CN206088
LOCUS Tor6515 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
DEFINITION Tor6515 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
ACCESSION CN206088
VERSION CN206088.1 GI:46902819
KEYWORDS EST.
SOURCE Tortula ruralis
ORGANISM Tortula ruralis
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
AUTHORS Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
TITLE 1 (bases 1 to 632)
JOURNAL Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauger, S.A. and Payton, P.R.
PUBMED The rehydration transcriptome of the desiccation-tolerant bryophyte
COMMENT BMC Genomics 5 (1), 89 (2004)
15546486
Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbr.ars.usda.gov
PCR Primers
FORWARD: GTTTCCAGTCACGAC
BACKWARD: CAGGAACAGCTATGAC.
Location/Qualifiers
1. 632
/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration library"
/note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
SalI; Site_2: NotI"

ORIGIN
Query Match      84.0%; Score 16.8; DB 7; Length 632;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAAC 20
    ||||| ||||| ||||| |||||
Db 605 AAGGAACGACGACGCCAAC 624

RESULT 59
BU992244
LOCUS BU992244 HD09102r HD Hordeum vulgare cDNA clone HD09102 5-PRIME, mRNA
DEFINITION BU992244 HD09102r HD Hordeum vulgare cDNA clone HD09102 5-PRIME, mRNA
ACCESSION BU992244
VERSION BU992244.1 GI:24243190
KEYWORDS EST.
SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 637)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 637 Std Error: 0.00
Plate: 9 row: 1 column: 2
Seq primer: M13rev.
Location/Qualifiers
1. 637
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Golden Promise"
/db_xref="GABI:242352"
/db_xref="taxon:4513"
/clone="HD09102"
/tissue type="callus"
/lab_host="Xa10-Gold"
/clone_lib="HD"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is 1
kb"

ORIGIN
Query Match      84.0%; Score 16.8; DB 5; Length 637;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAAC 20
    ||||| ||||| ||||| |||||
Db 123 AAGGAACGACGACGCCAAC 142

RESULT 60
CN206088
LOCUS CL768700/c
DEFINITION OR BBa0140P17.f OR BBa Oryza nivara genomic clone OR_BBa0140P17 5',
genomic survey sequence.
ACCESSION CL768700
VERSION CL768700.1 GI:50815109
KEYWORDS GSS.
SOURCE Oryza nivara
ORGANISM Oryza nivara
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 643)
Kim, H., Yu, Y., Stum, D., Vost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595

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QY 1 AAGGAAACACGGACACCAA 20


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JOURNAL      Genome Res. 14 (12), 2439-2447 (2004)
PUBMED       15574823
REFERENCE    2 (bases 1 to 709)
AUTHORS      Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE        Direct Submission
JOURNAL      Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT      Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY      : pBACe3.6
Vector       : EcoRI
R.Site 1    : EcoRI
R.Site 2    : EcoRI
FEATURES     Location/Qualifiers
source      1..709
            /organism="Mus musculus molossinus"
            /mol_type="genomic DNA"
            /sub_species="molossinus"
            /db_xref="taxon:57486"
            /clone="MSMg01-419D11.T7"
            /sex="male"
            /tissue_type="mixture of kidney and spleen"
            /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 709;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGGAACACGACACCCAA 20
    |||||
Db 69 AAGGAACCTGACACCCAA 88
    |||||

RESULT 69
AG442384/c
LOCUS       AG442384
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-324C12.T7, genomic survey
sequence.
ACCESSION   AG442384
VERSION     AG442384.1 GI:48085447
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
ORGANISM    Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriaki,K. and
            Shiroishi,T.
TITLE        Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
JOURNAL     Genome Res. 14 (12), 2439-2447 (2004)
PUBMED     15574823
REFERENCE   2 (bases 1 to 715)
AUTHORS     Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE        Direct Submission
JOURNAL     Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT      Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY      : pBACe3.6
Vector       : EcoRI
R.Site 1    : EcoRI
R.Site 2    : EcoRI
FEATURES     Location/Qualifiers
source      1..709
            /organism="Mus musculus molossinus"
            /mol_type="genomic DNA"
            /sub_species="molossinus"
            /db_xref="taxon:57486"
            /clone="MSMg01-419D11.T7"
            /sex="male"
            /tissue_type="mixture of kidney and spleen"
            /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 715;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGGAACACGACACCCAA 20
    |||||
Db 141 AAGGAACACGACACCCAA 122
    |||||

RESULT 70
DT057597/c
LOCUS       DT057597
DEFINITION AGENCOURT 55704374 NIH_ZGC_21 Danio rerio cDNA clone IMAGE:7919645
5', mRNA sequence.
ACCESSION   DT057597
VERSION     DT057597.1 GI:72356846
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 729)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT      Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Chung-Der Hsiao, Ming-Yi Chou and Pung-Pung
            Hwang
            CDNA Library Preparation: Dr. Yutaka Suzuki
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
            CDNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNL at:
            http://image.llnl.gov
            Plate: LLAM16325 row: g column: 03
            High quality sequence start: 24
            High quality sequence stop: 287.
FEATURES     Location/Qualifiers
source      1..729
            /organism="Danio rerio"
            /mol_type="mRNA"
            /db_xref="taxon:7955"

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/clone="IMAGE:7919645"
/tissue_type="40 pooled samples"
/lab_host="DH10B Tona"
/clone_lib="NIH_ZGC_21"
/notes="Organ: skin; Vector: pME18S-FL3; Site 1: DraIII;
Site 2: DraIII; 1st strand cDNA was primed with an
oligo(dT) primer
5'-GGCGTAGAGCGGCTATGGCTTTTTTTTTTTTTTT-3';
double-stranded cDNA was ligated to a DraIII adaptor
5'-GCCACUUGG-3', digested and directionally cloned into
distinct DraIII sites of the pME18S-FL3. Library was size
selected for ~1.0 kb, with a average insert size of ~1.2
kb and is not amplified. Library constructed by Yutaka
Suzuki (University of Tokyo Institute of Medical Science).
Custom primers recommended for sequencing: 5' end primer
5'-GGATGTTGCTTACTTCTA-3' and 3' end primer
5'-CCAGTCGAGCTCGACACA-3'. Reference for library
construction: Methods Mol Bio 221:73-91. Note: this is a
library."
(http://zgc.nci.nih.gov/) Zebrafish Gene Collection
library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 8; Length 729;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
|||||
Db 571 AAGGCCACACGACACCCAA 552

RESULT 71
DT060396/c
LOCUS DT060396 735 bp mRNA linear EST 11-AUG-2005
DEFINITION AGENCOURT 55719638 NICHD_XGC Fab Xenopus laevis cDNA clone
IMAGE:8072872 5', mRNA sequence.
ACCESSION DT060396
VERSION DT060396.1 GI:72359645
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1..(bases 1 to 735)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM17351 row: c column: 14
High quality sequence stop: 719.
FEATURES
source
1..735
Location/Qualifiers
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:8072872"
/lab_host="DH10B Tona"
/clone_lib="NICHD_XGC Fab"
/notes="Organ: fat body; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; cDNA was primed using oligo-dT primer:
5'-pGACTAGTCTAGATCGGCGCGCC(T)25-3' and cloned into

```

```

the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb
resulted in an average insert size of 1.8kb. This is a
primary library (normalized library is NICHD_XGC FabN) and
was constructed by Express Genomics (Frederick, MD). Note:
this is a (http://xgc.nci.nih.gov/) Xenopus Gene
Collection library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 8; Length 735;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
|||||
Db 159 AAGGAACACGACACCCAA 140

RESULT 72
AG429016
LOCUS AG429016 737 bp DNA linear GSS 21-DEC-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-303G16.T7, genomic survey
sequence.
ACCESSION AG429016
VERSION AG429016.1 GI:48072079
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE 1
AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823
REFERENCE 2 (bases 1 to 737)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
1-7-22 Shuhiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045; Japan
(E-mail:hattori@gsc.riken.jp, URL:http://bgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACE3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
source
1..737
Location/Qualifiers
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-303G16.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 737;

```

Best Local Similarity 90.0%; Pred. No. 3e+03; Mismatches 0; Indels 2; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 535 AAGGAAACACGACACCCAA 554

RESULT 73
CNS0FY62/c
LOCUS
DEFINITION Tetraodon nigroviridis full-length cDNA.
ACCESSION CR693646
VERSION CR693646.2 GI:56286064
KEYWORDS HTc; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS
Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N., Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicaud, S., Jaffe, P., Fisher, S., Lutfalla, G., Dossat, C., Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N., Castellano, S., Anhouard, V., Jubin, C., Castelli, V., Katinka, M., Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P., Guzey, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., Zody, M.C., McSwain, P., Boeak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C., Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J., and Roest Crollius, H.
Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype
Nature 431 (7011), 946-957 (2004)

15496914
REFERENCE 2 (bases 1 to 742)
Genoscope.
Direct Submission
Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage - 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 3, 2004 this sequence version replaced gi:51191553.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
Location/Qualifiers
1..742
/organism="Tetraodon nigroviridis"
/mol_type="mRNA"
/db_xref="taxon:99883"
/tissue_type="Eyes"

ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 742;
Best Local Similarity 90.0%; Pred. No. 3e+03; Mismatches 0; Indels 2; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 407 AAGGAAACACGACACCCAA 388

RESULT 74
AQ740823/c
LOCUS
DEFINITION HS_5508_A2_F10_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1084 Col=20 Row=K, genomic survey sequence.
ACCESSION AQ740823
VERSION AQ740823.1 GI:5518345

KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 756)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
COMMENT
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1084 row: K column: 20
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 756.
FEATURES
Location/Qualifiers
1..756
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1084 Col=20 Row=K"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 756;
Best Local Similarity 90.0%; Pred. No. 3e+03; Mismatches 0; Indels 2; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 309 AAGGAAACACGACACCCCTA 290

RESULT 75
DT060112/c
LOCUS
DEFINITION AGENCOURT_55787745 NICHHD_XGC_FaEN Xenopus laevis cDNA clone IMAGE:8074943 5', mRNA sequence.
ACCESSION DT060112
VERSION DT060112.1 GI:72359361
KEYWORDS EST.
SOURCE
ORGANISM Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE
AUTHORS
1 (bases 1 to 763)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.

```

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM17356 row: i column: 21
High quality sequence start: 52
High quality sequence stop: 656.

FEATURES
    source
    1. .763
    /organism="Xenopus laevis"
    /mol_type="mRNA"
    /db_xref="taxon:8355"
    /clone="IMAGE:8074943"
    /lab_host="DH10B TORa"
    /clone_lib="NICHHD_XGC_FaBN"
    /note="Organ: fat body; Vector: pExpress-1; Site_1: EcoRV;
    Site 2: NotI; cDNA was primed using oligo-dT primer:
    5'-pGACTAGTCTAGATCGAGCGCGGCC(T)25-3' and cloned into
    the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb
    resulted in an average insert size of 1.5kb, and Cot value
    of 7. This is a normalized library (primary library is
    NICHHD_XGC FaB) and was constructed by Express Genomics
    (Frederick, MD). Note: this is a
    http://xgc.nci.nih.gov/ Xenopus Gene Collection library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 8; Length 763;
Best Local Similarity 90.0%; Pred. NO. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAAC 20
    |||||
Db 210 AAGGAACACGACGCCAAC 191

RESULT 76
CB247499/c
LOCUS
DEFINITION
UI-M-F10-cdz-j-16-0-UI-r1 NIH BMAP_F10 Mus musculus cDNA clone
IMAGE:6836561 5', mRNA sequence.
CB247499
VERSION
CB247499.1 GI:28369143
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 780)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
    Location/Qualifiers
    1. .780

FEATURES
    source
    1. .780
    /organism="Xenopus laevis"
    /mol_type="mRNA"
    /db_xref="taxon:8355"
    /clone="IMAGE:8075729"

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM17356 row: i column: 21
High quality sequence start: 52
High quality sequence stop: 656.

FEATURES
    source
    1. .763
    /organism="Xenopus laevis"
    /mol_type="mRNA"
    /db_xref="taxon:8355"
    /clone="IMAGE:8074943"
    /lab_host="DH10B TORa"
    /clone_lib="NICHHD_XGC_FaBN"
    /note="Organ: fat body; Vector: pExpress-1; Site_1: EcoRV;
    Site 2: NotI; cDNA was primed using oligo-dT primer:
    5'-pGACTAGTCTAGATCGAGCGCGGCC(T)25-3' and cloned into
    the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb
    resulted in an average insert size of 1.5kb, and Cot value
    of 7. This is a normalized library (primary library is
    NICHHD_XGC FaB) and was constructed by Express Genomics
    (Frederick, MD). Note: this is a
    http://xgc.nci.nih.gov/ Xenopus Gene Collection library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 6; Length 780;
Best Local Similarity 90.0%; Pred. NO. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAAC 20
    |||||
Db 750 AAGGAACACGACGCCAAC 731

RESULT 77
DT057062/c
LOCUS
DEFINITION
AGENCOURT 55788803 NICHHD_XGC_FaBN Xenopus laevis cDNA clone
IMAGE:18075729 3', mRNA sequence.
DT057062
VERSION
DT057062.1 GI:72356311
KEYWORDS
EST.
SOURCE
Xenopus laevis (African clawed frog)
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 794)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Daniela S. Gerhardt, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM17358 row: j column: 15
High quality sequence start: 42
High quality sequence stop: 671.

FEATURES
    source
    1. .794
    /organism="Xenopus laevis"
    /mol_type="mRNA"
    /db_xref="taxon:8355"
    /clone="IMAGE:8075729"

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/lab_host="DHL08 Tona"
 /clone_lib="NICHD_XGC_FaBN"
 /note="Organ: fat body; Vector: pExpress-1; Site 1: EcoRV;
 Site 2: NotI; cDNA was primed using oligo-dT primer:
 5'-pGACTAGTCTTACATCGGCGCGCC(T)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb
 resulted in an average insert size of 1.5kb, and Cot value
 of 7. This is a normalized library (primary library is
 NICHD_XGC_FaB) and was constructed by Express Genomics
 (Frederick, MD). Note: this is a (
 http://xgc.nci.nih.gov/) Xenopus Gene Collection library."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 794;
 Best Local Similarity 90.0%; Pred. No. 3e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGACGCCCA 20
 |||||
 DB 140 AAGGAACACGACGCCCA 121

RESULT 78

CV944482/c
 LOCUS
 DEFINITION P014G10 mycelium, subtracted infection mimic Phytophthora
 infestans cDNA, mRNA sequence.
 ACCESSION CV944482
 VERSION
 KEYWORDS EST
 SOURCE Phytophthora infestans (potato late blight agent)
 ORGANISM Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 Phytophthora.

REFERENCE

1 (bases 1 to 822)
 AUTHORS Randall,T., Dwyer,R.A., Huitena,E., Beyer,K., Cvitanich,C.,
 Kelkar,H., Pong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
 Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
 Windas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
 Mauch,P., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
 Lam,S.T. and Judelson,H.S.
 TITLE Large-scale gene discovery in the oomycete Phytophthora infestans
 reveals likely components of phytopathogenicity shared with true
 fungi

JOURNAL

PUBLISHED Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)

COMMENT

Contact: Judelson HS
 Department of Plant Pathology
 University of California
 Webber Hall, Riverside, CA 92521, USA
 Tel: 909 787 4199
 Fax: 909 787 4294
 Email: howard.judelson@ucr.edu.

FEATURES

source

1..822
 /organism="Phytophthora infestans"
 /mol_type="mRNA"
 /strain="88069"
 /db_xref="taxon:4787"
 /sex="M"
 /clone_lib="mycelium, subtracted infection mimic"
 /note="Vector: pSPORT1"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 822;
 Best Local Similarity 90.0%; Pred. No. 3e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGACGCCCA 20
 |||||
 DB 57 ACGGAACACGACGCCCA 38

RESULT 79

LOCUS

BF254545
 DEFINITION HVSMEF0004F07f Hordeum vulgare seedling root EST library HVCDA0007
 clone HVSMEF0004F07f, mRNA sequence.
 ACCESSION BF254545
 VERSION
 KEYWORDS EST
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 829)
 Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
 Fenton,R.D., Oates,R. and Main,D.

TITLE

Development of a genetically and physically anchored EST resource
 for barley genomics: Morex unstressed seedling root cDNA library
 Unpublished (2001)

JOURNAL

COMMENT On Nov 16, 2000 this sequence version replaced gi:11183650.

COMMENT

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hq bases = 465

Seq primer: AATTACCCCTCACTAAAGGG

High quality sequence stop: 659.

FEATURES

source

1..829
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Morex"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="HVSMEF0004F07f"
 /tissue_type="Seedling root"
 /lab_host="TUC121"
 /clone_lib="Hordeum vulgare seedling root EST library
 HVCDA0007 (Bt isolated and unstressed)"
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and ceftaxime in covered
 crystallization dishes. Five-day old seedling roots were
 then harvested, total RNA was prepared, poly(A) RNA was
 purified, one primary unamplified cDNA library was made,
 and 1 million pfu were in vivo excised to give pBluescript
 SK(-) cDNA phagemids. these steps were performed in the TJ
 Close laboratory at the University of California,
 Riverside (Choi, Close, Fenton). Phagemids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
 Oates, Rambo, Main). The sequence has been trimmed to
 remove vector sequence and contains a minimum of 100 bases
 of phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html)"

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 829;
 Best Local Similarity 90.0%; Pred. No. 3e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||
Db 762 AAGGAACACGACACCCAA 781

RESULT 80

CD303542/C

LOCUS

DEFINITION AGNCOURT_14236123 NICHD_XGC Brn1 Xenopus laevis cDNA clone

IMAGE:6956191 5', mRNA sequence.

ACCESSION

CD303542

VERSION

CD303542.1

GI:31083408

KEYWORDS

EST.

SOURCE

ORGANISM

Xenopus laevis

(African clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 872)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement:

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14582 row: 0 column: 06

High quality sequence start: 38

High quality sequence stop: 558.

Location/Qualifiers

1..872

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:6956191"

/dev_stage="adult"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NICHD XGC Brn1"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5 kb. Constructed by Life

Technologies. Note: This is a Xenopus Gene Collection

(XGC) library."

ORIGIN

Query Match

Best Local Similarity

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

|||||

Db 194 AAGGAACACGACACCCAA 175

RESULT 81

BO674913

LOCUS

DEFINITION

AGNCOURT_8062638 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6211356

5', mRNA sequence.

ACCESSION

BO674913

VERSION

BO674913.1

GI:21785747

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

1000

```

/organism="Glycine max"
/mol_type="genomic DNA"
/db_xref="taxon:3847"
/clone_lib="GMW2"
/notes="Glycine max BAC library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 908;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGACCCCAA 20
    |||||
Db 112 AAGGAACACGACGACCCCAA 93

RESULT 83
CZ517024/c
LOCUS      CZ517024      916 bp      DNA      linear      GSS 11-MAY-2005
DEFINITION GMW2-49L8a.g2 GMW2 Glycine max genomic, genomic survey sequence.
ACCESSION  CZ517024
VERSION     CZ517024.1 GI:63242451
KEYWORDS   GSS.
SOURCE     Glycine max (soybean)
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE  1 (bases 1 to 916)
AUTHORS   Nuberger,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
            Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H.,
            Clifton,S.W. and Stacey,G.
            BAC end sequences from Glycine max Williams 82 cultivar genome
            Unpublished (2005)
            Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..916
                     /organism="Glycine max"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3847"
                     /clone_lib="GMW2"
                     /note="Glycine max BAC library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 916;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGACCCCAA 20
    |||||
Db 125 AAGGAACACGACGACCCCAA 106

RESULT 84
CA789059/c
LOCUS      CA789059      918 bp      mRNA      linear      EST 04-DEC-2002
DEFINITION AGNCOURT_10304322 NICHG XGC_001 Xenopus laevis cDNA clone
            IMAGE:5084447 5', mRNA sequence.
ACCESSION  CA789059
VERSION     CA789059.1 GI:26033729
KEYWORDS   EST.
SOURCE     Xenopus laevis (African clawed frog)
ORGANISM   Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE  1 (bases 1 to 918)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL    Tumor Gene Index
COMMENT    Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapsb@mail.nih.gov
            Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov.
            Plate: LLNL1226 row: a column: 24
            High quality sequence start: 19
            High quality sequence stop: 732.
            Location/Qualifiers
                1..918
                /organism="Xenopus laevis"
                /mol_type="mRNA"
                /db_xref="taxon:8355"
                /clone="IMAGE:5084447"
                /tissue_type="oocytes"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NICHG XGC_001"
                /notes="vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
                Cloned unidirectionally. Primer: Oligo dt. Average insert
                size 2.2 kb. Constructed by Life Technologies."

ORIGIN
Query Match      84.0%; Score 16.8; DB 6; Length 918;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGACCCCAA 20
    |||||
Db 284 AAGGAACACGACGACCCCAA 265

RESULT 85
BF029135
LOCUS      BF029135      919 bp      mRNA      linear      EST 10-OCT-2000
DEFINITION 601764643F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996683 5',
            mRNA sequence.
ACCESSION  BF029135
VERSION     BF029135.1 GI:10736847
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 919)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapsb@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: CLONTECH Laboratories, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: L1CM849 row: f column: 12
            High quality sequence stop: 487.
            Location/Qualifiers
                1..919
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3996683"
                /tissue_type="carcinoma, cell line"
                /lab_host="DH10B (T1 phage-resistant)"

```

/clone lib="NIH_MGC_53"
 /site="Organ: bladder; Vector: pDNR-LIB (Clontech);
 Site_1: Sfil (ggcgctcgcc); Site_2: Sfil
 (ggcattagcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGCC-3' and
 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCGGCACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.55
 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 919;
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 767 AAGGAACACGAGGTACCCAA 786

RESULT 86

LOCUS CC694001/c 330 bp DNA linear GSS 19-JUN-2003
 DEFINITION OGVAR91TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMWBMA0491014,
 genomic survey sequence.

ACCESSION CC694001

VERSION CC694001.1 GI:32098777

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 330)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

AUTHORS

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.

TITLE

Consortium for Maize Genomics

JOURNAL

Unpublished (2002)

COMMENT

Other_GSSs: OGVAR91TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

1..930

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMWBMA0491014"

/clone lib="ZM_0.7_1.5_KB"

/note="Vector: pBC5K-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 930;
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 397 AAGGAACACGACACCCAA 378

RESULT 87

LOCUS BE881640/c

DEFINITION 601490060F1_NIH_MGC_69_Homo_sapiens_cDNA_clone_IMAGE:3892287_5',
 mRNA sequence.

ACCESSION BE881640

VERSION BE881640.1 GI:10330416

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiinae; Homo.

REFERENCE

1 (bases 1 to 935)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM9678 row: h column: 16

High quality sequence stop: 679.

FEATURES

source

1..935

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3892287"

/tissue type="large cell carcinoma, undifferentiated"

/lab host="DH10B (phage-resistant)"

/clone lib="NIH_MGC_69"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.1 kb. Library constructed by Life

Technologies."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 935;

Best Local Similarity 90.0%; Pred. No. 3.1e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 762 AAGGATCCGACACCCAA 743

RESULT 88

LOCUS BU915367/c

DEFINITION AGENCOURT_10493183_NICHD_XGC_001_Xenopus_laevis_cDNA_clone
 IMAGE:6642041_5', mRNA sequence.

ACCESSION BU915367

VERSION BU915367.1 GI:24097281

KEYWORDS EST.

SOURCE Xenopus laevis

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 950)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14226 row: m column: 17
High quality sequence stop: 700.

Location/Qualifiers
1. .950

FEATURES

source
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6642041"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC OOI"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."

ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 950;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||
Db 706 AAGGAACACGACCCCAA 687

RESULT 89

BU911794

LOCUS

DEFINITION AGENCOURT 10463379 NICHD XGC OOI Xenopus laevis cDNA clone
IMAGE:6637855 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.llnl.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14215 row: o column: 07
High quality sequence stop: 597.

FEATURES

source
Location/Qualifiers
1. .953
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6637855"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC OOI"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."

ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 953;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||
Db 900 AAGGAACACGAAACCCAA 919

RESULT 90

BG335613

LOCUS

DEFINITION BG335613 959 bp mRNA linear EST 27-FEB-2001
602404233F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541840 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 959)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHCMI221 row: a column: 09

High quality sequence stop: 373.

FEATURES

source

Location/Qualifiers
1. .959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4541840"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 959;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||
Db 926 AAGGAACACGACCCCAA 945

RESULT 91

BF532081

LOCUS

DEFINITION BF532081 1031 bp mRNA linear EST 11-DEC-2000
602073196F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4210415 5',
mRNA sequence.

ACCESSION

VERSION

BF532081.1 GI:11619547

```

KEYWORDS      EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 1031)
AUTHORS        NIH-MGC http://mgi.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgabbs-remail.nih.gov
               Tissue Procurement: Jeffrey E. Green, M.D.
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM9777 row: 0 column: 24
               High quality sequence stop: 595.

FEATURES       source
               1..1031
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="FVB/N"
               /db_xref="taxon:10090"
               /clones="IMAGE:4210415"
               /lab_host="DH10B (T1 phage-resistant)"
               /clone_lib="NCI CGAP L19"
               /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
               Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
               Average insert size 1.9 kb. Constructed by Life
               Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 2; Length 1031;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
        |||||
Db      920 AAGGAACACGGAAACCAA 939

RESULT 92
CL111503
LOCUS      CL111503      1032 bp      DNA      linear      GSS 05-JAN-2004
DEFINITION ISB1-55G5 Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-55G5,
genomic survey sequence.
ACCESSION  CL111503
VERSION     CL111503.1 GI:40605138
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
               Xenopodinae; Xenopus; Silurana.
REFERENCE   1 (bases 1 to 1032)
AUTHORS     Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
               Mardis, E., and Wilson, R.
TITLE       A physical map of the xenopus tropicalis genome
JOURNAL     Unpublished (2003)
COMMENT     Contact: Richard K Wilson
               Genome Sequencing Center
               Washington University School of Medicine
               Email: submissions@wustl.edu
               Insert Length: 75000 Std Error: 0.00
               Seq primer: Sp6 ATTAGTGACACTATAG
               Class: BAC ends
               High quality sequence start: 5
               High quality sequence stop: 756.

FEATURES       Location/Qualifiers
               1..1031
               /organism="Xenopus tropicalis"
               /mol_type="genomic DNA"
               /db_xref="taxon:8364"
               /clone_lib="ISB1-55G5"
               /notes="Vector: pBelOBAC11; ISB-1 Xenopus tropicalis BAC
               Library Segment 1"

ORIGIN
Query Match      84.0%; Score 16.8; DB 2; Length 1032;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
        |||||
Db      813 AAGGAACACGTGACACCCAA 832

RESULT 93
BF337949
LOCUS      BF337949      1071 bp      mRNA      linear      EST 22-NOV-2000
DEFINITION 602035776F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183723
5', mRNA sequence.
ACCESSION  BF337949
VERSION     BF337949.1 GI:11284335
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE   1 (bases 1 to 1071)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
               Email: cgabbs-remail.nih.gov
               Tissue Procurement: David N. Louis, M.D.
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM9500 row: 9 column: 20
               High quality sequence start: 4
               High quality sequence stop: 438.

FEATURES       Location/Qualifiers
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               /db_xref="taxon:9606"
               /clone="IMAGE:4183723"
               /tissue_type="glioblastoma with EGFR amplification"
               /lab_host="DH10B (T1 phage-resistant)"
               /clone_lib="NCI CGAP_Brn64"
               /notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
               Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
               Average insert size 1.57 kb. Constructed by Life
               Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 2; Length 1071;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
        |||||
Db      867 ACGGAACACGGACACCCAA 886

RESULT 94

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CL049473
 LOCUS
 DEFINITION CH216-69P17_Sp6.1 CH216 Xenopus tropicalis genomic clone
 CH216-69P17 genomic survey sequence.
 ACCESSION
 VERSION CL049473
 KEYWORDS
 SOURCE CL049473.1 GI:40505386
 ORGANISM
 Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 REFERENCE
 AUTHORS 1 (bases 1 to 1097)
 TITLE Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
 A physical map of the xenopus tropicalis genome
 JOURNAL Unpublished (2003)
 COMMENT Contact: Richard K Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Insert Length: 175000 Std Error: 0.00
 Seq primer: Sp6 ATTAGTGACACTATAG
 Class: BAC ends
 High quality sequence start: 223
 High quality sequence stop: 392.
 Location/Qualifiers
 1..1097
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 /mol_type="Genomic DNA"
 /strain="Nigerian frog"
 /db_xref="taxon:8364"
 /clone="CH216-69P17"
 /sex="male"
 /cell_line="Stock 248 F7A2, inbred N7"
 /clone_lib="CH216"
 /notes="vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
 BAC library"
 ORIGIN
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 Best Local Similarity 90.00; Pred. No. 3.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAGGAAACACGGACACCCAA 20
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 114 AAGCAACACGGACACCA 133
 Db
 RESULT 95
 CC276125
 LOCUS
 DEFINITION CH261-128F17_Sp6.1 CH261 Gallus gallus genomic clone CH261-128F17,
 genomic survey sequence.
 ACCESSION
 VERSION CC276125
 KEYWORDS
 SOURCE CC276125.1 GI:30634975
 ORGANISM
 Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE
 AUTHORS 1 (bases 1 to 1123)
 TITLE Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
 Warren, W., Graves, T., Mardis, E. and Wilson, R.
 Gallus gallus BAC End Reads
 JOURNAL Unpublished (2003)
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Insert Length: 182000 Std Error: 0.00.
 Seq primer: Sp6 ATTAGTGACACTATAG

JOURNAL Nature 431 (7011), 946-957 (2004)
PUBMED 15496914
REFERENCE 2 (bases 1 to 1541)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT On Dec 3, 2004 this sequence version replaced gi:51143763.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.

FEATURES
source
1. .1541
/organism="Tetraodon nigroviridis"
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/db_xref="taxon:99883"
/tissue_type="Liver"

ORIGIN
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Best Local Similarity 90.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGGAACACGGACACCCAA 20
|||||
DB 1222 AAGGAACACGGACACCCAA 1203

RESULT 100
CNS0G1AC/c
LOCUS CNS0G1AC 1559 bp mRNA linear HTC 05-JUL-2005
DEFINITION Tetraodon nigroviridis full-length cDNA.
ACCESSION CR697688
VERSION CR697688.2 GI:56350687
KEYWORDS HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
Jailon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M.,
Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De
Berardinis, V., Cruaud, C., Duprat, S., Bottier, P., Coutanceau, J.P.,
Goury, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J.,
McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.
and Roest Crollius, H.
Genome duplication in the teleost fish Tetraodon nigroviridis
reveals the early vertebrate proto-karyotype

TITLE
JOURNAL Nature 431 (7011), 946-957 (2004)
PUBMED 15496914
REFERENCE 2 (bases 1 to 1559)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT On Dec 3, 2004 this sequence version replaced gi:51195597.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.

FEATURES
source
1. .1559
/organism="Tetraodon nigroviridis"

ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 1541;
Best Local Similarity 90.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGGAACACGGACACCCAA 20
|||||
DB 1222 AAGGAACACGGACACCCAA 1203

REFERENCE
AUTHORS
Jailon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M.,
Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De
Berardinis, V., Cruaud, C., Duprat, S., Bottier, P., Coutanceau, J.P.,
Goury, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J.,
McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.
and Roest Crollius, H.
Genome duplication in the teleost fish Tetraodon nigroviridis
reveals the early vertebrate proto-karyotype

TITLE
JOURNAL Nature 431 (7011), 946-957 (2004)
PUBMED 15496914
REFERENCE 2 (bases 1 to 1559)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT On Dec 3, 2004 this sequence version replaced gi:51195597.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.

FEATURES
source
1. .1559
/organism="Tetraodon nigroviridis"

ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 1559;
Best Local Similarity 90.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGGAACACGGACACCCAA 20
|||||
DB 1241 AAGGAACACGGACACCCAA 1222

Search completed: March 9, 2006, 02:45:43
Job time : 1603.68 secs

/mol_type="mRNA"
/db_xref="taxon:99883"
/tissue_type="Eyes"

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 9, 2006, 00:09:45 ; Search time 1055.34 Seconds
(without alignments)
1346.567 Million cell updates/sec

Title: US-10-829-474-4
Perfect score: 25
Sequence: 1 tccgctgcagagttgccggttacga 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

- GenEmbl.*
1: gb.ba.*
2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.hcg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	25	100.0	73	13	AY189930 Human ent
C 2	25	100.0	73	13	AY189933 Human ent
C 3	25	100.0	83	13	ESU55870 Enterovirus
C 4	25	100.0	100	13	ESU55868 Enterovirus
C 5	25	100.0	109	13	DQ220993 Human ech
C 6	25	100.0	109	13	EU008071 Enterovirus
C 7	25	100.0	109	13	EU008072 Enterovirus
C 8	25	100.0	112	13	AY189929 Human ent
C 9	25	100.0	115	13	AY189179 Human ent
C 10	25	100.0	116	13	AY189158 Human ent
C 11	25	100.0	116	13	AY189159 Human ent
C 12	25	100.0	116	13	AY189160 Human ent
C 13	25	100.0	116	13	AY189161 Human ent
C 14	25	100.0	116	13	AY189162 Human ent
C 15	25	100.0	116	13	AY189163 Human ent
C 16	25	100.0	116	13	AY189164 Human ent
C 17	25	100.0	116	13	AY189166 Human ent
C 18	25	100.0	116	13	AY189167 Human ent

116	13	AY189169	Human ent
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116	13	AY189171	Human ent
116	13	AY189173	Human ent
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116	13	AY189201	Human ent
116	13	AY189202	Human ent
116	13	AY189206	Human ent
116	13	AY189215	Human ent
117	13	AB183003	Human ent
117	13	AY189205	Human ent
154	13	AF314005	Enterovir
162	13	AY626235	Human cox
162	13	AY626236	Human cox
172	13	HEN312088	Human ent
177	13	ESP295207	Echovirus
185	13	AF521433	Human ech
185	13	AF521436	Human ech
185	13	AF521447	Human ech
185	13	AF521449	Human ech
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185	13	AF521461	Human ech
185	13	AF521474	Human ech
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185	13	AF521477	Human ech
185	13	AF521478	Human ech
185	13	AF521483	Human ech
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185	13	AF521492	Human ech
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185	13	AF521515	Human ech
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185	13	AF521525	Human ech
185	13	AF521538	Human ech
185	13	AF521539	Human ech
185	13	AF521542	Human ech
185	13	AF521543	Human cox
185	13	AF521546	Human ech
185	13	AF521547	Human ech
185	13	AF521548	Human ech
186	13	AF521454	Human ech
186	13	AF521479	Human ech
186	13	AY343038	Human ech
187	13	AY343032	Human ech
188	13	AF521468	Human ech
188	13	AY342837	Human ech
188	13	AY342838	Human ech
188	13	AY342840	Human cox
188	13	AY342841	Human cox
188	13	AY342843	Human cox
188	13	AY342844	Human cox

C 92	25	100.0	188	13	AY342846	AY342846 Human ech	C 165	25	100.0	297	13	CVU30925	U30925 Coxackievi
C 93	25	100.0	188	13	AY342854	AY342854 Human ech	C 166	25	100.0	297	13	CVU30928	U30928 Coxackievi
C 94	25	100.0	188	13	AY342856	AY342856 Human ech	C 167	25	100.0	297	13	ELU11705	U11705 Echovirus 1
C 95	25	100.0	188	13	AY342857	AY342857 Human ech	C 168	25	100.0	297	13	E6U11709	U11709 Echovirus 6
C 96	25	100.0	188	13	AY342858	AY342858 Human ech	C 169	25	100.0	298	13	CBU31213	U31213 Coxackievi
C 97	25	100.0	188	13	AY342859	AY342859 Human ech	C 170	25	100.0	298	13	CVU30922	U30922 Coxackievi
C 98	25	100.0	188	13	AY342860	AY342860 Human ech	C 171	25	100.0	298	13	CVU30926	U30926 Coxackievi
C 99	25	100.0	188	13	AY342862	AY342862 Human ech	C 172	25	100.0	299	13	CBU31212	U31212 Coxackievi
C 100	25	100.0	188	13	AY342864	AY342864 Human ech	C 173	25	100.0	314	13	ECV7345	AJ007345 Echovirus
C 101	25	100.0	188	13	AY342865	AY342865 Human ech	C 174	25	100.0	316	13	ECV7335	AJ007335 Echovirus
C 102	25	100.0	188	13	AY342874	AY342874 Human ech	C 175	25	100.0	316	13	ECV7336	AJ007336 Echovirus
C 103	25	100.0	188	13	AY342881	AY342881 Human ech	C 176	25	100.0	316	13	ECV7337	AJ007337 Echovirus
C 104	25	100.0	188	13	AY342882	AY342882 Human ech	C 177	25	100.0	316	13	ECV7338	AJ007338 Echovirus
C 105	25	100.0	188	13	AY342888	AY342888 Human ech	C 178	25	100.0	316	13	ECV7339	AJ007339 Echovirus
C 106	25	100.0	188	13	AY342891	AY342891 Human ech	C 179	25	100.0	316	13	ECV7341	AJ007341 Echovirus
C 107	25	100.0	188	13	AY342892	AY342892 Human ech	C 180	25	100.0	316	13	ECV7342	AJ007342 Echovirus
C 108	25	100.0	188	13	AY342916	AY342916 Human ech	C 181	25	100.0	316	13	ECV7343	AJ007343 Echovirus
C 109	25	100.0	188	13	AY342922	AY342922 Human ech	C 182	25	100.0	316	13	ECV7344	AJ007344 Echovirus
C 110	25	100.0	188	13	AY342927	AY342927 Human ech	C 183	25	100.0	317	13	ECV7340	AJ007340 Echovirus
C 111	25	100.0	188	13	AY342944	AY342944 Human ech	C 184	25	100.0	317	13	ECV7346	AJ007346 Echovirus
C 112	25	100.0	188	13	AY342945	AY342945 Human ech	C 185	25	100.0	319	13	HEC579634	AJ579634 Human ech
C 113	25	100.0	188	13	AY342946	AY342946 Human ech	C 186	25	100.0	319	13	HEC579640	AJ579640 Human ech
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C 115	25	100.0	188	13	AY342953	AY342953 Human ech	C 188	25	100.0	340	6	CQ964034	CQ964034 Sequence
C 116	25	100.0	188	13	AY342960	AY342960 Human ech	C 189	25	100.0	358	13	AY899051	AY899051 Human ech
C 117	25	100.0	188	13	AY342961	AY342961 Human ech	C 190	25	100.0	359	13	AY603031	AY603031 Human ech
C 118	25	100.0	188	13	AY342963	AY342963 Human ech	C 191	25	100.0	359	13	AY898965	AY898965 Human ech
C 119	25	100.0	188	13	AY342965	AY342965 Human ech	C 192	25	100.0	359	13	AY898966	AY898966 Human ech
C 120	25	100.0	188	13	AY342966	AY342966 Human ech	C 193	25	100.0	359	13	AY898967	AY898967 Human ech
C 121	25	100.0	188	13	AY342999	AY342999 Human ech	C 194	25	100.0	359	13	AY898968	AY898968 Human ech
C 122	25	100.0	188	13	AY343004	AY343004 Human ech	C 195	25	100.0	359	13	AY898969	AY898969 Human ech
C 123	25	100.0	188	13	AY343006	AY343006 Human ech	C 196	25	100.0	359	13	AY898970	AY898970 Human ech
C 124	25	100.0	188	13	AY343008	AY343008 Human ech	C 197	25	100.0	359	13	AY898972	AY898972 Human ech
C 125	25	100.0	188	13	AY343011	AY343011 Human ech	C 198	25	100.0	359	13	AY898973	AY898973 Human ech
C 126	25	100.0	188	13	AY343012	AY343012 Human ech	C 199	25	100.0	359	13	AY898976	AY898976 Human ech
C 127	25	100.0	188	13	AY343015	AY343015 Human ech	C 200	25	100.0	359	13	AY898977	AY898977 Human ech
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C 394	25	100.0	497	13	HEC295183	AJ295183 Human ech
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C 453	25	100.0	703	13	AF225473	Coxsackie
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C 465	25	100.0	894	13	CXAMYQJ	M74567 Coxsackievi
C 466	25	100.0	939	13	AB162756	Human cox
C 467	25	100.0	1029	13	AB1626206	Human cox
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DEFINITION	partial sequence.					
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VERSION	AY189930.1	GI:28395429				
KEYWORDS	Human enterovirus B					
SOURCE	Human enterovirus B					
ORGANISM	Human enterovirus B					
REFERENCE	1 (bases 1 to 73)					
AUTHORS	Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.					
TITLE	Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA					
JOURNAL	J. Infect. Dis. 187 (10), 1562-1570 (2003)					
PUBMED	12721936					
REFERENCE	2 (bases 1 to 73)					
AUTHORS	Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.					
TITLE	Direct Submission					
JOURNAL	Submitted (03-DEC-2002) Virology Division, University of New South Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia					

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VERSION
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KEYWORDS
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  Viruses; ssRNA positive-strand viruses, no DNA stage;
  Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 73)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
  J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
  12721936
PUBMED
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REFERENCE
  2 (bases 1 to 73)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (03-DEC-2002) Virology Division, University of New South
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VERSION
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  Viruses; ssRNA positive-strand viruses, no DNA stage;
  Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 83)
  Muir,P., Nicholson,F., Spencer,G.T., Ajetumobi,J.F., Starkey,W.G.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
  Khan,M., Archard,L.C., Cairns,N.J., Anderson,V.E.R., Leigh,P.N.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
  Muir,P.
  Direct Submission
  Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
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  Muir,P., Nicholson,F., Spencer,G.T., Ajetumobi,J.F., Starkey,W.G.,
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  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
  Khan,M., Archard,L.C., Cairns,N.J., Anderson,V.E.R., Leigh,P.N.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
  Muir,P.
  Direct Submission
  Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
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  Muir,P., Nicholson,F., Spencer,G.T., Ajetumobi,J.F., Starkey,W.G.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
  Khan,M., Archard,L.C., Cairns,N.J., Anderson,V.E.R., Leigh,P.N.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
  Muir,P.
  Direct Submission
  Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
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ACCESSION DQ029093
VERSION DQ029093.1 GI:66473301
KEYWORDS
SOURCE Human echovirus 11
ORGANISM Human echovirus 11
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 109)
N'Saibia,S. and Aouni,M.
N'Saibia,S., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
Nucleotide sequences of the IRES domains IV and V of natural
isolates ECHO virus type 11 with different replicative capacities
phenotypes
JOURNAL Unpublished (2005)
PUBMED
REFERENCE 2 (bases 1 to 109)
AUTHORS Garbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
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DEFINITION Enterovirus 71 prototype BrCr 5' untranslated region.
ACCESSION U00871
VERSION U00871.1 GI:405114
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE Zheng,Z.M., He,P.J., Caueffield,D., Neumann,M., Specter,S.,
Enterovirus 71 isolated from China is serologically similar to the
prototype E71 BrCr strain but differs in the 5'-noncoding region
JOURNAL J. Med. Virol. 47 (2), 161-167 (1995)
PUBMED 8830120
REFERENCE 2 (bases 1 to 109)
AUTHORS Bankowski,M.J.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1993) Bankowski M.J., Diagnostic Services, Inc.,
Clinical Virology & Molecular Medicine, 340 Goodlette Road South,
Naples, FL 33940, USA
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Db 67 TCCGCTGCAGAGTTGCCCGTTACGA 43

RESULT 8
AY189929/c
LOCUS AY189929 112 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/47/97 5' untranslated region,
partial sequence.
ACCESSION AY189929
VERSION AY189929.1 GI:28395428
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 112)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Virology Division, University of New South
Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,

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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 9
AY189179/c
LOCUS             AY189179             115 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/100/98 5' UTR, partial sequence.
ACCESSION        AY189179
VERSION          AY189179.1 GI:28274402
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 115)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
  J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
  PUBLISHED      12721936
REFERENCE
  2 (bases 1 to 115)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (29-NOV-2002) Virology Division, South Eastern Area
  Laboratory Services, University of New South Wales/Prince of Wales
  Hospital, High Street, Randwick, NSW 2031, Australia
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 10
AY189158/c
LOCUS             AY189158             116 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/01/97 5' UTR, partial sequence.
ACCESSION        AY189158
VERSION          AY189158.1 GI:28274381
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
  J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
  PUBLISHED      12721936
REFERENCE
  2 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (29-NOV-2002) Virology Division, South Eastern Area
  Laboratory Services, University of New South Wales/Prince of Wales
  Hospital, High Street, Randwick, NSW 2031, Australia
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 11
AY189159/c
LOCUS             AY189159             116 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/02/97 5' UTR, partial sequence.
ACCESSION        AY189159
VERSION          AY189159.1 GI:28274382
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
  J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
  PUBLISHED      12721936
REFERENCE
  2 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (29-NOV-2002) Virology Division, South Eastern Area
  Laboratory Services, University of New South Wales/Prince of Wales
  Hospital, High Street, Randwick, NSW 2031, Australia
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 12
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LOCUS             AY189160             116 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.
ACCESSION        AY189160
VERSION          AY189160.1 GI:28274383
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
  J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
  PUBLISHED      12721936
REFERENCE
  2 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (29-NOV-2002) Virology Division, South Eastern Area
  Laboratory Services, University of New South Wales/Prince of Wales
  Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50
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TITLE             Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
                  Diabetes Associated with Enterovirus RNA
JOURNAL           J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBLISHED        12721936
REFERENCE
  2 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (29-NOV-2002) Virology Division, South Eastern Area
  Laboratory Services, University of New South Wales/Prince of Wales
  Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 11
AY189159/c
LOCUS             AY189159             116 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/02/97 5' UTR, partial sequence.
ACCESSION        AY189159
VERSION          AY189159.1 GI:28274382
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
  J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
  PUBLISHED      12721936
REFERENCE
  2 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (29-NOV-2002) Virology Division, South Eastern Area
  Laboratory Services, University of New South Wales/Prince of Wales
  Hospital, High Street, Randwick, NSW 2031, Australia
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 12
AY189160/c
LOCUS             AY189160             116 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.
ACCESSION        AY189160
VERSION          AY189160.1 GI:28274383
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
  J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
  PUBLISHED      12721936
REFERENCE
  2 (bases 1 to 116)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (29-NOV-2002) Virology Division, South Eastern Area
  Laboratory Services, University of New South Wales/Prince of Wales
  Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50
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ACCESSION AY189160
VERSION AY189160.1 GI:28274383
KEYWORDS Human enterovirus B
SOURCE Human enterovirus B
ORGANISM Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)

JOURNAL 12721936
PUBMED 12721936

REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia

FEATURES
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 13
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LOCUS Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
DEFINITION Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
ACCESSION AY189161
VERSION AY189161.1 GI:28274384
KEYWORDS Human enterovirus 71
SOURCE Human enterovirus 71
ORGANISM Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)

JOURNAL 12721936
PUBMED 12721936

REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 14
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LOCUS Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
DEFINITION Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
ACCESSION AY189162
VERSION AY189162.1 GI:28274385
KEYWORDS Human enterovirus B
SOURCE Human enterovirus B
ORGANISM Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)

JOURNAL 12721936
PUBMED 12721936

REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia

FEATURES
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 15
AY189163/c
LOCUS Human enterovirus B isolate NSW/16/97 5' UTR, partial sequence.
DEFINITION Human enterovirus B isolate NSW/16/97 5' UTR, partial sequence.
ACCESSION AY189163
VERSION AY189163.1 GI:28274386
KEYWORDS Human enterovirus B
SOURCE Human enterovirus B
ORGANISM Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)

JOURNAL 12721936
PUBMED 12721936

REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia

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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 16
AY189164/c
LOCUS AY189164 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/17/97 5' UTR, partial sequence.
ACCESSION AY189164
VERSION AY189164.1 GI:28274387
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 17
AY189166/c
LOCUS AY189166 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus NSW/23/97 5' UTR, partial sequence.
ACCESSION AY189166
VERSION AY189166.1 GI:28274389
KEYWORDS
SOURCE Human enterovirus NSW/23/97
ORGANISM Human enterovirus NSW/23/97
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936

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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 18
AY189167/c
LOCUS AY189167 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/25/97 5' UTR, partial sequence.
ACCESSION AY189167
VERSION AY189167.1 GI:28274390
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 19
AY189169/c
LOCUS AY189169 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/45/97 5' UTR, partial sequence.
ACCESSION AY189169
VERSION AY189169.1 GI:28274392
KEYWORDS
SOURCE Human enterovirus B

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REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 18
AY189167/c
LOCUS AY189167 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/25/97 5' UTR, partial sequence.
ACCESSION AY189167
VERSION AY189167.1 GI:28274390
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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RESULT 19
AY189169/c
LOCUS AY189169 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/45/97 5' UTR, partial sequence.
ACCESSION AY189169
VERSION AY189169.1 GI:28274392
KEYWORDS
SOURCE Human enterovirus B

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ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE
2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 20
AY189170/c
LOCUS Human enterovirus B isolate NSW/48/97 5' UTR, partial sequence.
DEFINITION
ACCESSION AY189170
VERSION AY189170.1 GI:28274393
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE
2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 21
AY189171/c
LOCUS Human enterovirus B isolate NSW/60/97 5' UTR, partial sequence.
DEFINITION
ACCESSION AY189171
VERSION AY189171.1 GI:28274394
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE
2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 22
AY189173/c
LOCUS Human enterovirus B isolate NSW/73/97 5' UTR, partial sequence.
DEFINITION
ACCESSION AY189173
VERSION AY189173.1 GI:28274396
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE
2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 23
AY189174/c
LOCUS AY189174 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/76/97 5' UTR, partial sequence.
ACCESSION AY189174
VERSION AY189174.1 GI:28274397
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 24
AY189175/c
LOCUS AY189175 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/82/97 5' UTR, partial sequence.
ACCESSION AY189175
VERSION AY189175.1 GI:28274398
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia

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Best Local Similarity 100.0%; Pred. No. 0.32;
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 25
AY189176/c
LOCUS AY189176 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/83/97 5' UTR, partial sequence.
ACCESSION AY189176
VERSION AY189176.1 GI:28274399
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia

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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 26
AY189180/c
LOCUS AY189180 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/111/98 5' UTR, partial sequence.
ACCESSION AY189180
VERSION AY189180.1 GI:28274403
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.

TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia
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Matches 25; Conservative 0;
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50
RESULT 27
AY189183/c
LOCUS Human enterovirus B isolate NSW/141/98 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/141/98 5' UTR, partial sequence.
ACCESSION AY189183
VERSION AY189183.1 GI:28274406
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES Location/Qualifiers
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Matches 25; Conservative 0;
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50
RESULT 28
AY189184/c
LOCUS Human enterovirus B isolate NSW/143/98 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/143/98 5' UTR, partial sequence.

AY189184
AY189184.1 GI:28274407
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50
RESULT 29
AY189186/c
LOCUS Human enterovirus B isolate NSW/147/98 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/147/98 5' UTR, partial sequence.
ACCESSION AY189186
VERSION AY189186.1 GI:28274409
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES Location/Qualifiers
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/mol_type="genomic RNA"
/isolate="NSW/147/98"
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Matches 25; Conservative 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 30
AY189187/c
LOCUS AY189187 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/149/98 5' UTR, partial sequence.
ACCESSION AY189187
VERSION AY189187.1 GI:28274410
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 31
AY189191/c
LOCUS AY189191 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/156/98 5' UTR, partial sequence.
ACCESSION AY189191
VERSION AY189191.1 GI:28274414
KEYWORDS
SOURCE
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
LOCATION/Qualifiers
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QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 32
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LOCUS AY189192 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/157/98 5' UTR, partial sequence.
ACCESSION AY189192
VERSION AY189192.1 GI:28274415
KEYWORDS
SOURCE
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.32;
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 33
AY189195/c
LOCUS AY189195 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/166/98 5' UTR, partial sequence.
ACCESSION AY189195
VERSION AY189195.1 GI:28274418
KEYWORDS
SOURCE
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
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PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 34
AY189196/c
LOCUS AY189196 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/169/98 5' UTR, partial sequence.
ACCESSION AY189196
VERSION AY189196.1 GI:28274419
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 35
AY189198/c
LOCUS AY189198 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/180/98 5' UTR, partial sequence.
ACCESSION AY189198

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VERSION AY189198.1 GI:28274421
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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        /organism="Human enterovirus 71"
        /mol_type="genomic RNA"
        /isolate="NSW/180/98"
        /db_xref="taxon:39054"
        /note="Human enterovirus 71"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 36
AY189199/c
LOCUS AY189199 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/182/98 5' UTR, partial sequence.
ACCESSION AY189199
VERSION AY189199.1 GI:28274422
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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J. Infect. Dis. 187 (10), 1562-1570 (2003)
1271936
REFERENCE
PUBMED
AUTHORS
TITLE
JOURNAL
SUBMITTED (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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Location/Qualifiers
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/organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/338/99"
/db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
|||||
Db 74 TCCGCTGCAGAGTTCGCCGTTACGA 50

RESULT 41
AB183003/c
LOCUS
DEFINITION
Human enterovirus 71 genomic RNA, 5' UTR, partial sequence,
isolate: 2279/EV71/Hyogo/2003.
ACCESSION
AB183003
VERSION
AB183003.1 GI:49614920
KEYWORDS
Human enterovirus 71
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 Fujimoto,T., Yoshida,S., Munemura,T., Yoshida,H., Chikahira,M. and
Nishio,O.
TITLE
Enterovirus 71 sequence detected from cerebrospinal fluid
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 117)
AUTHORS
Fujimoto,T., Munemura,T. and Chikahira,M.
TITLE
Direct Submission
JOURNAL
Submitted (30-JUN-2004) Tauguto Fujimoto, Hyogo Prefectural
Institute of Public Health and Environmental Sciences, Infectious
Disease Research Division; 2-1-29, Arata-Cho, Hyogo-Ku, Kobe, Hyogo
652-0032, Japan (E-mail:Tauguto_Fujimoto@pref.hyogo.jp,
URL:http://www.iphes.pref.hyogo.jp/, Tel:81-78-511-6640(ex.236),
Fax:81-78-531-7080)
FEATURES
source
Location/Qualifiers
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/organism="Human enterovirus 71"
/mol_type="genomic RNA"
/isolate="2279/EV71/Hyogo/2003"
/specification source="cerebrospinal fluid"
/specific host="human"
/db_xref="taxon:39054"
/country="Japan:Hyogo"
<1..>117
5'UTR
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
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Db 75 TCCGCTGCAGAGTTCGCCGTTACGA 51

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RESULT 42
AY189205/c
LOCUS
DEFINITION
Human enterovirus B isolate NSW/204/99 5' UTR, partial sequence.
ACCESSION
AY189205
VERSION
AY189205.1 GI:28274428
KEYWORDS
Human enterovirus B
SOURCE
Human enterovirus B
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 117)
AUTHORS
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
12721936
PUBMED
REFERENCE
2 (bases 1 to 117)
AUTHORS
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE
Direct Submission
JOURNAL
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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/organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/204/99"
/db_xref="taxon:138949"
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Query Match 100.0%; Score 25; DB 13; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
|||||
Db 74 TCCGCTGCAGAGTTCGCCGTTACGA 50

RESULT 43
AF314005/c
LOCUS
DEFINITION
Enterovirus 5656/SIN/002209 5' UTR, partial sequence.
ACCESSION
AF314005
VERSION
AF314005.2 GI:13111668
KEYWORDS
Enterovirus 5656/SIN/002209
SOURCE
Enterovirus 5656/SIN/002209
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 154)
AUTHORS
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
TITLE
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
JOURNAL
12149336
PUBMED
REFERENCE
2 (bases 1 to 154)
AUTHORS
Singh,S., Chow,V.T.K. and Poh,C.L.
TITLE
Direct Submission
JOURNAL
Submitted (18-OCT-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
REFERENCE
3 (bases 1 to 154)
AUTHORS
Singh,S., Chow,V.T.K. and Poh,C.L.
TITLE
Direct Submission
JOURNAL
Submitted (23-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
REMARK
Sequence update by submitter
COMMENT
On Feb 23, 2001 this sequence version replaced gi:12667228.
FEATURES
Location/Qualifiers

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/organism="Enterovirus 5656/SIN/002209"
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/strain="5656/SIN/002209"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 92 TCCGCTGCAGAGTTGCCCGTTACGA 68
RESULT 44
AY626235/c
LOCUS AY626235 162 bp RNA linear VRL 15-JUN-2004
DEFINITION Human coxsackievirus B3 isolate subject 6 5' UTR.
ACCESSION AY626235
VERSION AY626235.1 GI:48526363
KEYWORDS
SOURCE Human coxsackievirus B3
ORGANISM Human coxsackievirus B3
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 162)
AUTHORS Lednicky, J.A. and Ohr, J.S.
TITLE Coxsackievirus B in myocardium tissue
JOURNAL Unpublished
AUTHORS Lednicky, J.A. and Ohr, J.S.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2004) Pathology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA
FEATURES
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1. .162
/organism="Human coxsackievirus B3"
/mol_type="genomic RNA"
/isolate="subject 6"
/isolation_source="myocardium tissue from patient that
died of myocarditis"
/db_xref="taxon:12072"
/country="USA"
/note="Enterovirus"
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5'UTR
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
RESULT 45
AY626236/c
LOCUS AY626236 162 bp RNA linear VRL 15-JUN-2004
DEFINITION Human coxsackievirus B3 isolate subject 9 5' UTR.
ACCESSION AY626236
VERSION AY626236.1 GI:48526364
KEYWORDS
SOURCE Human coxsackievirus B3
ORGANISM Human coxsackievirus B3
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 162)
AUTHORS Lednicky, J.A. and Ohr, J.S.
TITLE 5' untranslated region (5' UTR) of Human coxsackievirus B in
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myocardium tissue of subject 9
Unpublished
REFERENCE 2 (bases 1 to 162)
AUTHORS Lednicky, J.A. and Ohr, J.S.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2004) Pathology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA
FEATURES
Location/Qualifiers
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1. .162
/organism="Human coxsackievirus B3"
/mol_type="genomic RNA"
/isolate="subject 9"
/isolation_source="myocardium tissue from patient that
died of myocarditis"
/db_xref="taxon:12072"
/country="USA"
/note="Enterovirus"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
RESULT 46
HEN312088/c
LOCUS HEN312088 172 bp RNA linear VRL 02-JUL-2003
DEFINITION Human enterovirus 71 partial 5'UTR, strain /di/Roma98.
ACCESSION AJ312088
VERSION AJ312088.1 GI:16555706
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1
AUTHORS Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and
Fadda, G.
TITLE Molecular identification and typing of enteroviruses isolated from
clinical specimens
JOURNAL J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
PUBMED 12454151
REFERENCE 2 (bases 1 to 172)
AUTHORS Muscillo, M.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
00161, Italy
FEATURES
Location/Qualifiers
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1. .172
/organism="Human enterovirus 71"
/virion
/mol_type="genomic RNA"
/strain="/di/Roma98"
/isolate="IT98-5114"
/db_xref="taxon:39054"
/lab_hosts="vero cell cultures"
/note="throat swab from child with aseptic meningitis,
identified by immunofluorescence assay"
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5'UTR
ORIGIN
Query Match 100.0%; Score 25; DB 13; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 90 TCCGCTGCAGAGTTGCCCGTTACGA 66
RESULT 47
ESP295207 177 bp RNA linear VRL 15-MAY-2001
LOCUS Echovirus sp. genomic RNA for partial 5'UTR, isolate ATCC VR-322.
DEFINITION
ACCESSION AJ295207
VERSION AJ295207.1 GI:14140008
KEYWORDS
SOURCE Echovirus sp.
ORGANISM Echovirus sp.
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Muscillo,M., La Rosa,G., Marianelli,C., Capobianchi,M.R.,
          Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and
          Ticca,F.
TITLE A phylogenetic analysis of the two echovirus 30 isolated in Rome
          (Italy) in 1997 from an outbreak of aseptic meningitis associated
          with swimming pools
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 177)
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
          Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
          00161, Italy
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          /strain="Bastiani"
          /isolate="ATCC VR-322"
          /db_xref="taxon:145390"
          /note="isolated from fecal specimen of 10-year-old boy
          with symptoms of headache, stiff neck, fever"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 88 TCCGCTGCAGAGTTGCCCGTTACGA 112
          |||||
RESULT 48
AF521433/c AF521433 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-14 5' UTR, partial sequence.
DEFINITION
ACCESSION AF521433
VERSION AF521433.1 GI:31790775
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
          Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
          an outbreak of aseptic meningitis in Belgium during the summer of
          2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
          Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
          Virology, Department of Microbiology and Immunology, Rega Institute
          for Medical Research, University of Leuven, Minderbroedersstraat
          10, Leuven BE-3000, Belgium
FEATURES
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          /isolation_source="patient 2 - zipcode Belgium 3001"
          /db_xref="taxon:41846"
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
          |||||
RESULT 49
AF521436/c AF521436 185 bp RNA linear VRL 17-JUN-2003
LOCUS Human echovirus 30 isolate BE00-2 5' UTR, partial sequence.
DEFINITION
ACCESSION AF521436
VERSION AF521436.1 GI:31790778
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
          Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
          an outbreak of aseptic meningitis in Belgium during the summer of
          2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
          Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
          Virology, Department of Microbiology and Immunology, Rega Institute
          for Medical Research, University of Leuven, Minderbroedersstraat
          10, Leuven BE-3000, Belgium
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          /isolate="BE00-2"
          /isolation_source="patient 2 - zipcode Belgium 3001"
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5'UTR
ORIGIN
Query Match 100.0%; Score 25; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
          |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
          |||||
RESULT 50
AF521447/c
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LOCUS AF521447 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-30 5' UTR, partial sequence.
ACCESSION AF521447
VERSION AF521447.1 GI:31790789
KEYWORDS
SOURCE
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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/isolate="BE00-30"
/isolation_source="patient 30 - zipcode Belgium 9310"
/db_xref="taxon:41846"
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Query Match 100.0%; Score 25; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
RESULT 51
LOCUS AF521449/c
DEFINITION Human echovirus 30 isolate BE00-32 5' UTR, partial sequence.
ACCESSION AF521449
VERSION AF521449.1 GI:31790791
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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source
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/isolation_source="patient 30 - zipcode Belgium 9310"
/db_xref="taxon:41846"
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5'UTR
ORIGIN
Query Match 100.0%; Score 25; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
RESULT 52
LOCUS AF521450/c
DEFINITION Human echovirus 30 isolate BE00-33 5' UTR, partial sequence.
ACCESSION AF521450
VERSION AF521450.1 GI:31790792
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
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/organism="Human echovirus 30"
/vtron
/mol_type="genomic RNA"
/isolate="BE00-33"
/isolation_source="patient 33 - zipcode Belgium 1745"
/db_xref="taxon:41846"
<1..>185
5'UTR
ORIGIN
Query Match 100.0%; Score 25; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
RESULT 53
LOCUS AF521451/c
DEFINITION Human echovirus 30 isolate BE00-34 5' UTR, partial sequence.
ACCESSION AF521451
VERSION AF521451.1 GI:31790793
KEYWORDS
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/isolation_source="patient 32 - zipcode Belgium 1703"
/db_xref="taxon:41846"
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
RESULT 54
LOCUS AF521451/c
DEFINITION Human echovirus 30 isolate BE00-34 5' UTR, partial sequence.
ACCESSION AF521451
VERSION AF521451.1 GI:31790793
KEYWORDS

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SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
FEATURES   Location/Qualifiers
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              /viral
              /mol_type="genomic RNA"
              /isolate="BE00-34"
              /isolation_source="patient 34 - zipcode Belgium 1770"
              /db_xref="taxon:41846"
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ORIGIN
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 56
AF521474/c
LOCUS      AF521474
DEFINITION Human echovirus 30 isolate BE00-43 5' UTR, partial sequence.
ACCESSION AF521474
VERSION    AF521474.1 GI:31790800
KEYWORDS   .
SOURCE     Human echovirus 30
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
FEATURES   Location/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 55
AF521461/c
LOCUS      AF521461
DEFINITION Human echovirus 30 isolate BE00-48 5' UTR, partial sequence.
ACCESSION AF521461
VERSION    AF521461.1 GI:31790803
KEYWORDS   .
SOURCE     Human echovirus 30
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
FEATURES   Location/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 56
AF521474/c
LOCUS      AF521474
DEFINITION Human echovirus 30 isolate BE00-16 5' UTR, partial sequence.
ACCESSION AF521474
VERSION    AF521474.1 GI:31790816
KEYWORDS   .
SOURCE     Human echovirus 30
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)

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AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroederstraat 10, Leuven BE-3000, Belgium
FEATURES
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Location/Qualifiers
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/db_xref="taxon:41846"
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QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
RESULT 57
AF521475/c
LOCUS AF521475 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-17 5' UTR, partial sequence.
ACCESSION AF521475
VERSION AF521475.1 GI:31790817
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroederstraat 10, Leuven BE-3000, Belgium
FEATURES
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Location/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
RESULT 58
AF521476/c
LOCUS AF521476 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-18 5' UTR, partial sequence.
ACCESSION AF521476
VERSION AF521476.1 GI:31790818
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroederstraat 10, Leuven BE-3000, Belgium
FEATURES
source
Location/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
RESULT 59
AF521477/c
LOCUS AF521477 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-19 5' UTR, partial sequence.
ACCESSION AF521477
VERSION AF521477.1 GI:31790819
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

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J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
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RESULT 60
AF521478/c
LOCUS AF521478 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-20 5' UTR, partial sequence.
ACCESSION AF521478
VERSION AF521478.1 GI:31790820
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
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RESULT 62
AF521485/c
LOCUS AF521485 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-76 5' UTR, partial sequence.
ACCESSION AF521485
VERSION AF521485.1 GI:31790827
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
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|||||
98 TCCGCTGCAGAGTTGCCCGTTACGA 74
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RESULT 61
AF521483/c
LOCUS AF521483 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-74 5' UTR, partial sequence.
ACCESSION AF521483
VERSION AF521483.1 GI:31790825
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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|||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
|||||

RESULT 62
AF521485/c
LOCUS AF521485 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-76 5' UTR, partial sequence.
ACCESSION AF521485
VERSION AF521485.1 GI:31790827
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
SOURCE
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
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TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 63
AF521486/c
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DEFINITION Human echovirus 30 isolate BE00-77 5' UTR, partial sequence.
ACCESSION AF521486
VERSION AF521486.1 GI:31790828
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
AUTHORS 1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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RESULT 64
AF521492/c
LOCUS
DEFINITION Human echovirus 30 isolate BE00-83 5' UTR, partial sequence.
ACCESSION AF521492
VERSION AF521492.1 GI:31790834
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
AUTHORS 1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

AF521492/c
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DEFINITION Human echovirus 30 isolate BE00-83 5' UTR, partial sequence.
ACCESSION AF521492
VERSION AF521492.1 GI:31790834
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
AUTHORS 1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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/db_xref="taxon:41846"
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

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AF521495/c
LOCUS
DEFINITION Human echovirus 30 isolate BE00-58 5' UTR, partial sequence.
ACCESSION AF521495
VERSION AF521495.1 GI:31790837
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
AUTHORS 1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 66
AF521495/c
LOCUS
DEFINITION Human echovirus 30 isolate BE00-58 5' UTR, partial sequence.
ACCESSION AF521495
VERSION AF521495.1 GI:31790837
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
AUTHORS 1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74


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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 69
AF521505/c
LOCUS      AF521505      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-68 5' UTR, partial sequence.
ACCESSION  AF521505
VERSION     AF521505.1 GI:31790847
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS     Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE       Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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            /viroion
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            /isolate="BE00-68"
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 70
AF521515/c
LOCUS      AF521515      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-90 5' UTR, partial sequence.
ACCESSION  AF521515
VERSION     AF521515.1 GI:31790857
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.

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1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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    |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 71
AF521517/c
LOCUS      AF521517      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-92 5' UTR, partial sequence.
ACCESSION  AF521517
VERSION     AF521517.1 GI:31790859
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS     Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE       Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.32;
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    |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 72
AF521519/c
LOCUS          AF521519          185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION    Human echovirus 30 isolate BE00-95 5' UTR, partial sequence.
ACCESSION     AF521519
VERSION       AF521519.1 GI:31790861
KEYWORDS
SOURCE        Human echovirus 30
ORGANISM      Human echovirus 30
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE     1 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemeij,P., Van Der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Molecular typing and epidemiology of enteroviruses identified from
               an outbreak of aseptic meningitis in Belgium during the summer of
               2000
JOURNAL       J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED        12767006
AUTHORS       Thoenen,I., Lemeij,P., van der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Direct Submission
JOURNAL       Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
               Virology, Department of Microbiology and Immunology, Rega Institute
               for Medical Research, University of Leuven, Minderbroedersstraat
               10, Leuven BE-3000, Belgium
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 73
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LOCUS          AF521525          185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION    Human echovirus 30 isolate BE00-54 5' UTR, partial sequence.
ACCESSION     AF521525
VERSION       AF521525.1 GI:31790867
KEYWORDS
SOURCE        Human echovirus 30
ORGANISM      Human echovirus 30
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE     1 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemeij,P., Van Der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Molecular typing and epidemiology of enteroviruses identified from
               an outbreak of aseptic meningitis in Belgium during the summer of

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2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
REFERENCE      2 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemeij,P., van der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Direct Submission
JOURNAL       Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
               Virology, Department of Microbiology and Immunology, Rega Institute
               for Medical Research, University of Leuven, Minderbroedersstraat
               10, Leuven BE-3000, Belgium
FEATURES      source
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               /viroion
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    |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 74
AF521538/c
LOCUS          AF521538          185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION    Human echovirus 30 isolate BE00-111 5' UTR, partial sequence.
ACCESSION     AF521538
VERSION       AF521538.1 GI:31790890
KEYWORDS
SOURCE        Human echovirus 30
ORGANISM      Human echovirus 30
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE     1 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemeij,P., Van Der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Molecular typing and epidemiology of enteroviruses identified from
               an outbreak of aseptic meningitis in Belgium during the summer of
               2000
JOURNAL       J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED        12767006
REFERENCE      2 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemeij,P., van der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Direct Submission
JOURNAL       Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
               Virology, Department of Microbiology and Immunology, Rega Institute
               for Medical Research, University of Leuven, Minderbroedersstraat
               10, Leuven BE-3000, Belgium
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QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 75
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DEFINITION Human echovirus 7 isolate BE00-113 5' UTR, partial sequence.
ACCESSION AF521539
VERSION AF521539.1 GI:31790881
KEYWORDS
SOURCE
ORGANISM Human echovirus 7
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
TITLE Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
LOCATION/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 76
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LOCUS AF521542 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-116 5' UTR, partial sequence.
ACCESSION AF521542
VERSION AF521542.1 GI:31790884
KEYWORDS
SOURCE
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,

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Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
LOCATION/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 77
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LOCUS AF521543 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B4 isolate BE00-117 5' UTR, partial sequence.
ACCESSION AF521543
VERSION AF521543.1 GI:31790885
KEYWORDS
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ORGANISM Human coxsackievirus B4
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
TITLE Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
LOCATION/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

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RESULT 78
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LOCUS AF521546 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-120 5' UTR, partial sequence.
ACCESSION AF521546
VERSION AF521546.1 GI:31790888
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemeij, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
JOURNAL
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemeij, P., van der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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RESULT 79
AF521547/c
LOCUS AF521547 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-121 5' UTR, partial sequence.
ACCESSION AF521547
VERSION AF521547.1 GI:31790889
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemeij, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
JOURNAL
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Lemeij, P., van der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat

10, Leuven BE-3000, Belgium
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
RESULT 80
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LOCUS AY342855 185 bp RNA linear VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-CC2313 5' UTR, partial sequence.
ACCESSION AY342855
VERSION AY342855.1 GI:37623508
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Moes, E., Lemeij, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)
JOURNAL
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen, I., Moes, E., Lemeij, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium
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/db_xref="taxon:41846"
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Query Match 100.0%; Score 25; DB 13; Length 185;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
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LOCUS AF521454 186 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-37 5' UTR, partial sequence.
ACCESSION AF521454
VERSION AF521454.1 GI:31790796
KEYWORDS

SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 186)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006

REFERENCE 2 (bases 1 to 186)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

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/isolate="BE00-37"
/isolation_source="patient 37 - zipcode Belgium 2110"
/db_xref="taxon:41846"
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ORIGIN

Query Match 100.0%; Score 25; DB 13; Length 186;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 82
AF521479/c
LOCUS AF521479 Human echovirus 30 isolate BE00-23 186 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-23 5' UTR, partial sequence.
ACCESSION AF521479
VERSION AF521479.1 GI:31790821
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 186)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006

REFERENCE 2 (bases 1 to 186)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES
source
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/organism="Human echovirus 30"
/vifion
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/isolate="BE00-23"

/isolation_source="patient 23 - zipcode Belgium 9472"
/db_xref="taxon:41846"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 83
AY343038/c
LOCUS AY343038 Human echovirus 5 patient BE02-3792 186 bp RNA linear VRL 04-MAR-2004
DEFINITION Human echovirus 5 patient BE02-3792 5' UTR, partial sequence.
ACCESSION AY343038
VERSION AY343038.1 GI:37623691
KEYWORDS
SOURCE Human echovirus 5
ORGANISM Human echovirus 5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 186)
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

TITLE Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

JOURNAL J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE 2 (bases 1 to 186)
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

FEATURES
source
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/organism="Human echovirus 5"
/mol_type="genomic RNA"
/isolate="patient BE02-3792"
/db_xref="taxon:40280"
/country="Belgium"
/note="isolated in July 2002"
<1..>186

5'UTR
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 84
AY343032/c
LOCUS AY343032 Human echovirus 30 patient BE02-7181 187 bp RNA linear VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE02-7181 5' UTR, partial sequence.
ACCESSION AY343032
VERSION AY343032.1 GI:37623685
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 187)
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

TITLE Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

JOURNAL J. Clin. Microbiol. 42 (3), 963-971 (2004)

REFERENCE 2 (bases 1 to 187)

AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

FEATURES Location/Qualifiers

source 1..187

5'UTR /organism="Human echovirus 30"

ORIGIN /mol_type="genomic RNA"

Query Match 100.0%; Score 25; DB 13; Length 187;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 85

LOCUS AF521468/c 188 bp RNA linear VRL 17-JUN-2003

DEFINITION Human echovirus 30 isolate BE00-26 5' UTR, partial sequence.

ACCESSION AF521468

VERSION AF521468.1 GI:31790810

KEYWORDS Human echovirus 30

SOURCE Human echovirus 30

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 188)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

REFERENCE 2 (bases 1 to 188)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES Location/Qualifiers

source 1..188

5'UTR /organism="Human echovirus 30"

ORIGIN /mol_type="genomic RNA"

Query Match 100.0%; Score 25; DB 13; Length 188;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 86

LOCUS AY342837/c 188 bp RNA linear VRL 04-MAR-2004

DEFINITION Human echovirus 11 patient BE99-135 5' UTR, partial sequence.

ACCESSION AY342837

VERSION AY342837.1 GI:37623490

KEYWORDS Human echovirus 11

SOURCE Human echovirus 11

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 188)

AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

TITLE Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

JOURNAL J. Clin. Microbiol. 42 (3), 963-971 (2004)

REFERENCE 2 (bases 1 to 188)

AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

FEATURES Location/Qualifiers

source 1..188

5'UTR /organism="Human echovirus 11"

ORIGIN /mol_type="genomic RNA"

Query Match 100.0%; Score 25; DB 13; Length 188;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 87

LOCUS AY342838/c 188 bp RNA linear VRL 04-MAR-2004

DEFINITION Human echovirus 11 patient BE99-1509 5' UTR, partial sequence.

ACCESSION AY342838

VERSION AY342838.1 GI:37623491

KEYWORDS Human echovirus 11

SOURCE Human echovirus 11

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 188)

AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

TITLE Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

JOURNAL J. Clin. Microbiol. 42 (3), 963-971 (2004)

REFERENCE 2 (bases 1 to 188)

AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,

FEATURES source
 Laboratory of Clinical and Epidemiological Virology, Rega Institute
 for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
 Location/Qualifiers
 1. .188
 /organism="Human echovirus 11"
 /mol_type="genomic RNA"
 /isolate="patient BE99-1509"
 /db_xref="taxon:12078"
 /country="Belgium"
 /note="isolated in February 1999"
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ORIGIN

Query Match 100.0%; Score 25; DB 13; Length 188;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 88

AY342840/c
 LOCUS AY342840 188 bp RNA linear VRL 04-MAR-2004
 DEFINITION Human coxsackievirus B4 patient BE99-3672 5' UTR, partial sequence.
 ACCESSION AY342840
 VERSION AY342840.1 GI:37623493

KEYWORDS

SOURCE Human coxsackievirus B4
 ORGANISM Human coxsackievirus B4
 Viruses; ssRNA positive-strand viruses, no DNA stage;
 Picornaviridae; Enterovirus.

REFERENCE

1 (bases 1 to 188)
 Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

AUTHORS

Analysis of the serotype and genotype correlation of VP1 and the 5'
 noncoding region in an epidemiological survey of the human
 enterovirus B species
 J. Clin. Microbiol. 42 (3), 963-971 (2004)

JOURNAL

2 (bases 1 to 188)
 Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

REFERENCE

Submitted (16-JUL-2003) Department of Microbiology and Immunology,
 Laboratory of Clinical and Epidemiological Virology, Rega Institute
 for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium

TITLE

Location/Qualifiers
 1. .188
 /organism="Human coxsackievirus B4"
 /mol_type="genomic RNA"
 /isolate="patient BE99-3672"
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 /country="Belgium"
 /note="isolated in March 1999"
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5'UTR

Query Match 100.0%; Score 25; DB 13; Length 188;
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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 89

AY342841/c
 LOCUS AY342841 188 bp RNA linear VRL 04-MAR-2004
 DEFINITION Human echovirus 11 patient BE99-4376 5' UTR, partial sequence.
 ACCESSION AY342841
 VERSION AY342841.1 GI:37623494

KEYWORDS

SOURCE Human echovirus 11
 ORGANISM Human echovirus 11
 Viruses; ssRNA positive-strand viruses, no DNA stage;
 Picornaviridae; Enterovirus.

REFERENCE

1 (bases 1 to 188)
 Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

AUTHORS

Analysis of the serotype and genotype correlation of VP1 and the 5'
 noncoding region in an epidemiological survey of the human
 enterovirus B species
 J. Clin. Microbiol. 42 (3), 963-971 (2004)

JOURNAL

2 (bases 1 to 188)
 Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

REFERENCE

Submitted (16-JUL-2003) Department of Microbiology and Immunology,
 Laboratory of Clinical and Epidemiological Virology, Rega Institute
 for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium

TITLE

Location/Qualifiers
 1. .188
 /organism="Human echovirus 11"
 /mol_type="genomic RNA"
 /isolate="patient BE99-4376"
 /db_xref="taxon:12078"
 /country="Belgium"
 /note="isolated in April 1999"
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5'UTR

Query Match 100.0%; Score 25; DB 13; Length 188;
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ORIGIN

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 90

AY342843/c
 LOCUS AY342843 188 bp RNA linear VRL 04-MAR-2004
 DEFINITION Human coxsackievirus A9 patient BE99-5750 5' UTR, partial sequence.
 ACCESSION AY342843
 VERSION AY342843.1 GI:37623496

KEYWORDS

SOURCE Human coxsackievirus A9
 ORGANISM Human coxsackievirus A9
 Viruses; ssRNA positive-strand viruses, no DNA stage;
 Picornaviridae; Enterovirus.

REFERENCE

1 (bases 1 to 188)
 Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

AUTHORS

Analysis of the serotype and genotype correlation of VP1 and the 5'
 noncoding region in an epidemiological survey of the human
 enterovirus B species
 J. Clin. Microbiol. 42 (3), 963-971 (2004)

JOURNAL

2 (bases 1 to 188)
 Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

REFERENCE

Submitted (16-JUL-2003) Department of Microbiology and Immunology,
 Laboratory of Clinical and Epidemiological Virology, Rega Institute
 for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium

TITLE

Location/Qualifiers
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 /db_xref="taxon:12067"
 /country="Belgium"
 /note="isolated in May 1999"
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5'UTR

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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 Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

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ORIGIN
Query Match      100.0%; Score 25; DB 13; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 91
AY342844/c
LOCUS AY342844 188 bp RNA linear VRL 04-MAR-2004
DEFINITION Human coxsackievirus B4 patient BE99-6504 5' UTR, partial sequence.
ACCESSION AY342844
VERSION AY342844.1 GI:37623497
KEYWORDS
SOURCE Human coxsackievirus B4
ORGANISM Human coxsackievirus B4
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 188)
Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE 2 (bases 1 to 188)
Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Direct Submission
Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium
FEATURES
source
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/organism="Human coxsackievirus B4"
/mol_type="genomic RNA"
/isolate="patient BE99-6504"
/db_xref="taxon:12073"
/country="Belgium"
/note="isolated in June 1999"
<1..>188

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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 92
AY342846/c
LOCUS AY342846 188 bp RNA linear VRL 04-MAR-2004
DEFINITION Human echovirus 11 patient BE99-7222 5' UTR, partial sequence.
ACCESSION AY342846
VERSION AY342846.1 GI:37623499
KEYWORDS
SOURCE Human echovirus 11
ORGANISM Human echovirus 11
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 188)
Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
enterovirus B species

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J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE 2 (bases 1 to 188)
Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Direct Submission
Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium
FEATURES
source
1..188
/organism="Human echovirus 11"
/mol_type="genomic RNA"
/isolate="patient BE99-7222"
/db_xref="taxon:12078"
/country="Belgium"
/note="isolated in June 1999"
<1..>188

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Query Match      100.0%; Score 25; DB 13; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 93
AY342854/c
LOCUS AY342854 188 bp RNA linear VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-518 5' UTR, partial sequence.
ACCESSION AY342854
VERSION AY342854.1 GI:37623507
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 188)
Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE 2 (bases 1 to 188)
Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Direct Submission
Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium
FEATURES
source
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/organism="Human echovirus 30"
/mol_type="genomic RNA"
/isolate="patient BE00-518"
/db_xref="taxon:41846"
/country="Belgium"
/note="isolated in February 2000"
<1..>188

5'UTR
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

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RESULT 94
AY342856/c
LOCUS      AY342856      188 bp      RNA      linear      VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-CC3574 5' UTR, partial sequence.
ACCESSION  AY342856
VERSION     AY342856.1  GI:37623509
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1  (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Analysis of the serotype and genotype correlation of VP1 and the 5'
            noncoding region in an epidemiological survey of the human
            enterovirus B species
JOURNAL     J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE   2  (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2003) Department of Microbiology and Immunology,
            Laboratory of Clinical and Epidemiological Virology, Rega Institute
            for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
FEATURES   Location/Qualifiers
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            /db_xref="taxon:41846"
            /country="Belgium"
            /note="isolated in April 2000"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1  TCCGCTGCAGAGTTGCCCGTTACGA 25
          |||||||
Db      101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 95
AY342857/c
LOCUS      AY342857      188 bp      RNA      linear      VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-CC2641 5' UTR, partial sequence.
ACCESSION  AY342857
VERSION     AY342857.1  GI:37623510
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1  (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Analysis of the serotype and genotype correlation of VP1 and the 5'
            noncoding region in an epidemiological survey of the human
            enterovirus B species
JOURNAL     J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE   2  (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2003) Department of Microbiology and Immunology,
            Laboratory of Clinical and Epidemiological Virology, Rega Institute
            for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
FEATURES   Location/Qualifiers
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            /organism="Human echovirus 30"
            /mol_type="genomic RNA"
            /isolate="patient BE00-CC2641"
            /db_xref="taxon:41846"
            /country="Belgium"
            /note="isolated in April 2000"
            <1..>188
5'UTR
ORIGIN
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LOCUS      AY342858      188 bp      RNA      linear      VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-CC3916 5' UTR, partial sequence.
ACCESSION  AY342858
VERSION     AY342858.1  GI:37623511
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1  (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Analysis of the serotype and genotype correlation of VP1 and the 5'
            noncoding region in an epidemiological survey of the human
            enterovirus B species
JOURNAL     J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE   2  (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2003) Department of Microbiology and Immunology,
            Laboratory of Clinical and Epidemiological Virology, Rega Institute
            for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
FEATURES   Location/Qualifiers
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LOCUS      AY342859      188 bp      RNA      linear      VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-CC4049 5' UTR, partial sequence.
ACCESSION  AY342859
VERSION     AY342859.1  GI:37623512
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ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
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RESULT 96
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DEFINITION Human echovirus 30 patient BE00-CC3916 5' UTR, partial sequence.
ACCESSION  AY342858
VERSION     AY342858.1  GI:37623511
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
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AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
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TITLE       Analysis of the serotype and genotype correlation of VP1 and the 5'
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            enterovirus B species
JOURNAL     J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE   2  (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
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TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2003) Department of Microbiology and Immunology,
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Db      101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 97
AY342859/c
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DEFINITION Human echovirus 30 patient BE00-CC4049 5' UTR, partial sequence.
ACCESSION  AY342859
VERSION     AY342859.1  GI:37623512
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
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              Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
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TITLE        Analysis of the serotype and genotype correlation of VP1 and the 5'
              noncoding region in an epidemiological survey of the human
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TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2003) Department of Microbiology and Immunology,
              Laboratory of Clinical and Epidemiological Virology, Rega Institute
              for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
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DEFINITION
ACCESSION   AY342860
VERSION     AY342860.1 GI:37623513
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
REFERENCE    Viruses; ssRNA positive-strand viruses, no DNA stage;
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AUTHORS      Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
              Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE        Analysis of the serotype and genotype correlation of VP1 and the 5'
              noncoding region in an epidemiological survey of the human
              enterovirus B species
JOURNAL      J. Clin. Microbiol. 42 (3), 963-971 (2004)
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TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2003) Department of Microbiology and Immunology,
              Laboratory of Clinical and Epidemiological Virology, Rega Institute
              for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
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ORGANISM    Human echovirus 30
REFERENCE    Viruses; ssRNA positive-strand viruses, no DNA stage;
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AUTHORS      Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
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TITLE        Analysis of the serotype and genotype correlation of VP1 and the 5'
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REFERENCE    2 (bases 1 to 188)
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TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2003) Department of Microbiology and Immunology,
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              for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
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AUTHORS      Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
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TITLE        Analysis of the serotype and genotype correlation of VP1 and the 5'
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REFERENCE    Viruses; ssRNA positive-strand viruses, no DNA stage;
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JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

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GenCore version 5.1.7
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C 54	16	64.0	2940	3	US-09-703-414-1	Sequence 1, Appli
C 55	16	64.0	2940	3	US-10-171-229-1	Sequence 1, Appli
C 56	16	64.0	2940	3	US-10-429-398-1	Sequence 1, Appli
C 57	16	64.0	7868	9	5175383-1	Patent No. 5175383
C 58	16	64.0	36171	3	US-09-949-016-13876	Sequence 13876, A
C 59	16	64.0	36274	3	US-09-949-016-12389	Sequence 12389, A
C 60	16	64.0	30776	3	US-09-949-016-17230	Sequence 17230, A
C 61	16	64.0	183770	3	US-09-949-016-15494	Sequence 15494, A
C 62	16	64.0	236474	3	US-09-949-016-13418	Sequence 13418, A
C 63	16	64.0	536165	3	US-09-214-808-1	Sequence 1, Appli
C 64	15.8	63.2	290	3	US-09-513-999C-30616	Sequence 30616, A
C 65	15.8	63.2	3394	3	US-09-953-118-100	Sequence 100, App
C 66	15.8	63.2	6055	3	US-09-953-118-10	Sequence 10, Appli
C 67	15.8	63.2	7620	3	US-09-949-016-14973	Sequence 14973, A
C 68	15.6	62.4	25	3	US-09-396-196G-74495	Sequence 74495, A
C 69	15.6	62.4	452	3	US-09-976-594-305	Sequence 305, App
C 70	15.6	62.4	685	3	US-09-533-559-4705	Sequence 4705, Ap
C 71	15.6	62.4	1059	3	US-09-543-681A-1424	Sequence 1424, Ap
C 72	15.6	62.4	1136	2	US-08-106-981-5	Sequence 5, Appli
C 73	15.6	62.4	1701	3	US-09-232-468A-13	Sequence 13, Appli
C 74	15.6	62.4	1701	3	US-09-784-984B-11	Sequence 11, Appli
C 75	15.6	62.4	1994	2	US-08-537-152-11	Sequence 1, Appli
C 76	15.6	62.4	5276	3	US-09-233-857-2	Sequence 2, Appli
C 77	15.6	62.4	25165	3	US-09-453-702B-39	Sequence 39, Appli
C 78	15.6	62.4	25165	3	US-10-114-170-39	Sequence 39, Appli
C 79	15.6	62.4	26664	3	US-09-564-805-28	Sequence 28, Appli
C 80	15.6	62.4	26664	3	US-09-434-382-28	Sequence 28, Appli
C 81	15.6	62.4	29558	3	US-09-949-016-15607	Sequence 15607, A
C 82	15.6	62.4	22452	3	US-09-949-016-12968	Sequence 12968, A
C 83	15.4	61.6	267	3	US-09-513-999C-3441	Sequence 3441, Ap
C 84	15.4	61.6	268	3	US-09-313-294A-2507	Sequence 2507, Ap
C 85	15.4	61.6	282	3	US-09-313-294A-5359	Sequence 5359, Ap
C 86	15.4	61.6	325	3	US-09-702-705-1202	Sequence 1202, Ap
C 87	15.4	61.6	325	3	US-09-736-457-1202	Sequence 1202, Ap
C 88	15.4	61.6	325	3	US-09-614-124B-1202	Sequence 1202, Ap
C 89	15.4	61.6	325	3	US-09-671-325-1202	Sequence 1202, Ap
C 90	15.4	61.6	325	3	US-09-658-824-1202	Sequence 1202, Ap
C 91	15.4	61.6	325	3	US-10-017-754-1202	Sequence 1202, Ap
C 92	15.4	61.6	325	3	US-09-651-563-1202	Sequence 1202, Ap
C 93	15.4	61.6	363	3	US-09-700-820C-25	Sequence 25, Appli
C 94	15.4	61.6	535	3	US-08-754-477A-119	Sequence 119, App
C 95	15.4	61.6	582	3	US-09-023-655-1384	Sequence 1384, Ap
C 96	15.4	61.6	582	3	US-09-533-559-1903	Sequence 1903, Ap
C 97	15.4	61.6	601	3	US-09-949-016-47406	Sequence 47406, A

c 98	15.4	61.6	601	3	US-09-949-016-47418	Sequence 47418, A	171	15.2	60.8	601	3	US-09-949-016-98284	Sequence 98284, A
c 99	15.4	61.6	601	3	US-09-949-016-47430	Sequence 47430, A	172	15.2	60.8	601	3	US-09-949-016-98549	Sequence 98549, A
c 100	15.4	61.6	601	3	US-09-949-002-1736	Sequence 1736, Ap	173	15.2	60.8	601	3	US-09-949-016-98550	Sequence 98550, A
c 101	15.4	61.6	601	3	US-09-949-002-6426	Sequence 6426, Ap	174	15.2	60.8	601	3	US-09-949-016-98815	Sequence 98815, A
c 102	15.4	61.6	618	2	US-08-646-981-9	Sequence 9, Appli	175	15.2	60.8	601	3	US-09-949-016-98816	Sequence 98816, A
c 103	15.4	61.6	620	3	US-09-602-787A-427	Sequence 427, App	176	15.2	60.8	601	3	US-09-949-016-99081	Sequence 99081, A
c 104	15.4	61.6	684	3	US-09-489-039A-3021	Sequence 3021, Ap	177	15.2	60.8	601	3	US-09-949-016-99082	Sequence 99082, A
c 105	15.4	61.6	1029	2	US-08-096-182A-3	Sequence 3, Appli	178	15.2	60.8	601	3	US-09-949-016-99347	Sequence 99347, A
c 106	15.4	61.6	1029	2	US-08-877-109-3	Sequence 3, Appli	179	15.2	60.8	601	3	US-09-949-016-99348	Sequence 99348, A
c 107	15.4	61.6	1029	2	US-08-798-760-3	Sequence 3, Appli	180	15.2	60.8	601	3	US-09-949-016-99613	Sequence 99613, A
c 108	15.4	61.6	1029	6	PCT-US94-08327-3	Sequence 3, Appli	181	15.2	60.8	601	3	US-09-949-016-99614	Sequence 99614, A
c 109	15.4	61.6	1092	2	US-08-096-182A-5	Sequence 5, Appli	182	15.2	60.8	601	3	US-09-949-016-99879	Sequence 99879, A
c 110	15.4	61.6	1092	2	US-08-877-109-5	Sequence 5, Appli	183	15.2	60.8	601	3	US-09-949-016-99880	Sequence 99880, A
c 111	15.4	61.6	1092	3	US-08-798-760-5	Sequence 5, Appli	184	15.2	60.8	601	3	US-09-949-016-100145	Sequence 100145, A
c 112	15.4	61.6	1092	6	PCT-US94-08327-5	Sequence 5, Appli	185	15.2	60.8	601	3	US-09-949-016-100146	Sequence 100146, A
c 113	15.4	61.6	1143	3	US-09-700-820C-27	Sequence 27, Appli	186	15.2	60.8	601	3	US-09-949-016-100411	Sequence 100411, A
c 114	15.4	61.6	1205	3	US-09-949-002-177	Sequence 177, App	187	15.2	60.8	601	3	US-09-949-016-100412	Sequence 100412, A
c 115	15.4	61.6	1298	3	US-08-911-894-73	Sequence 73, Appl	188	15.2	60.8	601	3	US-09-949-016-100677	Sequence 100677, A
c 116	15.4	61.6	1540	2	US-07-932-915-1	Sequence 1, Appli	189	15.2	60.8	601	3	US-09-949-016-100678	Sequence 100678, A
c 117	15.4	61.6	1540	6	PCT-US91-05926-1	Sequence 1, Appli	190	15.2	60.8	601	3	US-09-949-016-100981	Sequence 100981, A
c 118	15.4	61.6	1710	3	US-09-902-540-2848	Sequence 2848, Ap	191	15.2	60.8	601	3	US-09-949-016-100982	Sequence 100982, A
c 119	15.4	61.6	1782	3	US-09-949-002-37	Sequence 37, Appl	192	15.2	60.8	601	3	US-09-949-016-101247	Sequence 101247, A
c 120	15.4	61.6	1800	3	US-10-104-047-1254	Sequence 1254, Ap	193	15.2	60.8	601	3	US-09-949-016-101248	Sequence 101248, A
c 121	15.4	61.6	1806	2	US-08-980-060-1	Sequence 1, Appli	194	15.2	60.8	601	3	US-09-949-016-101513	Sequence 101513, A
c 122	15.4	61.6	1806	3	US-09-307-185-1	Sequence 1, Appli	195	15.2	60.8	601	3	US-09-949-016-101514	Sequence 101514, A
c 123	15.4	61.6	1806	3	US-09-773-753-1	Sequence 1, Appli	196	15.2	60.8	601	3	US-09-949-016-101779	Sequence 101779, A
c 124	15.4	61.6	1920	3	US-09-700-820C-39	Sequence 39, Appl	197	15.2	60.8	601	3	US-09-949-016-101780	Sequence 101780, A
c 125	15.4	61.6	1983	3	US-09-066-281B-18	Sequence 18, Appl	c 198	15.2	60.8	789	3	US-09-023-855-1300	Sequence 1300, Ap
c 126	15.4	61.6	1983	3	US-09-468-433C-18	Sequence 18, Appl	c 199	15.2	60.8	845	3	US-09-949-016-14992	Sequence 4992, Ap
c 127	15.4	61.6	2313	3	US-08-738-168B-14	Sequence 14, Appl	c 200	15.2	60.8	849	3	US-09-270-767-11094	Sequence 11094, A
c 128	15.4	61.6	2553	3	US-09-620-312D-340	Sequence 340, App	c 201	15.2	60.8	858	3	US-09-248-796A-6414	Sequence 6414, Ap
c 129	15.4	61.6	2940	3	US-09-066-281B-20	Sequence 20, Appl	c 202	15.2	60.8	1288	3	US-09-602-787A-417	Sequence 417, App
c 130	15.4	61.6	2940	3	US-09-468-433C-20	Sequence 20, Appl	c 203	15.2	60.8	1354	3	US-09-902-540-167	Sequence 167, App
c 131	15.4	61.6	3459	2	US-08-980-060-3	Sequence 3, Appli	c 204	15.2	60.8	1380	3	US-09-513-783A-169	Sequence 169, App
c 132	15.4	61.6	3459	3	US-09-307-185-3	Sequence 3, Appli	c 205	15.2	60.8	1380	3	US-10-100-957A-169	Sequence 169, App
c 133	15.4	61.6	3459	3	US-09-773-753-3	Sequence 3, Appli	c 206	15.2	60.8	1599	3	US-09-252-991A-13921	Sequence 13921, A
c 134	15.4	61.6	3722	3	US-10-164-595-9	Sequence 9, Appli	c 207	15.2	60.8	2077	3	US-09-321-017B-821	Sequence 821, App
c 135	15.4	61.6	3862	3	US-10-164-595-5	Sequence 5, Appli	c 208	15.2	60.8	2280	3	US-09-252-991A-13535	Sequence 13535, A
c 136	15.4	61.6	3937	3	US-10-164-595-7	Sequence 7, Appli	c 209	15.2	60.8	2992	3	US-09-362-123A-3	Sequence 3, Appli
c 137	15.4	61.6	3972	3	US-09-489-039A-6774	Sequence 6774, Ap	c 210	15.2	60.8	3805	3	US-09-220-132-9	Sequence 9, Appli
c 138	15.4	61.6	3985	3	US-10-164-595-3	Sequence 3, Appli	c 211	15.2	60.8	5688	3	US-09-949-016-167934	Sequence 16734, A
c 139	15.4	61.6	4977	2	US-08-030-096-7	Sequence 7, Appli	c 212	15.2	60.8	17590	3	US-09-762-311-1	Sequence 1, Appli
c 140	15.4	61.6	15132	3	US-09-902-540-1137	Sequence 1137, Ap	c 213	15.2	60.8	17710	3	US-08-976-259-70	Sequence 70, Appl
c 141	15.4	61.6	18917	3	US-09-949-016-13129	Sequence 13129, A	c 214	15.2	60.8	17710	3	US-09-956-004-70	Sequence 70, Appl
c 142	15.4	61.6	18917	3	US-09-949-016-13130	Sequence 13130, A	c 215	15.2	60.8	19988	3	US-09-596-002-10	Sequence 10, Appl
c 143	15.4	61.6	18917	3	US-09-949-016-13131	Sequence 13131, A	c 216	15.2	60.8	26492	3	US-09-902-540-1234	Sequence 1234, Ap
c 144	15.4	61.6	36907	3	US-09-949-002-749	Sequence 749, App	c 217	15.2	60.8	44971	3	US-09-949-016-17049	Sequence 17049, A
c 145	15.4	61.6	56737	3	US-09-782-378A-17	Sequence 17, Appl	c 218	15.2	60.8	87870	3	US-09-949-016-14461	Sequence 14461, A
c 146	15.4	61.6	65902	3	US-09-949-002-509	Sequence 609, App	c 219	15.2	60.8	107085	3	US-09-949-016-13157	Sequence 13157, A
c 147	15.4	61.6	247299	3	US-09-621-976-1578	Sequence 17590, A	c 220	15.2	60.8	120727	3	US-09-949-016-15787	Sequence 15787, A
c 148	15.2	60.8	404	3	US-09-621-976-1578	Sequence 13708, A	c 221	15.2	60.8	120727	3	US-09-949-016-15788	Sequence 15788, A
c 149	15.2	60.8	468	3	US-09-252-991A-13708	Sequence 4137, Ap	c 222	15.2	60.8	818128	3	US-09-949-016-14546	Sequence 14546, A
c 150	15.2	60.8	487	3	US-09-602-787A-419	Sequence 419, App	c 223	15.2	60.8	818128	3	US-09-949-016-14547	Sequence 14547, A
c 151	15.2	60.8	531	3	US-09-489-039A-5535	Sequence 5535, App	c 224	15.2	60.8	818128	3	US-09-949-016-14548	Sequence 14548, A
c 152	15.2	60.8	601	3	US-09-949-016-27835	Sequence 27835, A	c 225	15.2	60.8	818128	3	US-09-949-016-14549	Sequence 14549, A
c 153	15.2	60.8	601	3	US-09-949-016-27836	Sequence 27836, A	c 226	15.2	60.8	818128	3	US-09-949-016-14550	Sequence 14550, A
c 154	15.2	60.8	601	3	US-09-949-016-94157	Sequence 94157, A	c 227	15.2	60.8	818128	3	US-09-949-016-14551	Sequence 14551, A
c 155	15.2	60.8	601	3	US-09-949-016-94158	Sequence 94158, A	c 228	15.2	60.8	818128	3	US-09-949-016-14552	Sequence 14552, A
c 156	15.2	60.8	601	3	US-09-949-016-96421	Sequence 96421, A	c 229	15.2	60.8	818128	3	US-09-949-016-14553	Sequence 14553, A
c 157	15.2	60.8	601	3	US-09-949-016-96422	Sequence 96422, A	c 230	15.2	60.8	818128	3	US-09-949-016-14554	Sequence 14554, A
c 158	15.2	60.8	601	3	US-09-949-016-96687	Sequence 96687, A	c 231	15.2	60.8	818128	3	US-09-949-016-14555	Sequence 14555, A
c 159	15.2	60.8	601	3	US-09-949-016-96688	Sequence 96688, A	c 232	15.2	60.8	818128	3	US-09-949-016-14556	Sequence 14556, A
c 160	15.2	60.8	601	3	US-09-949-016-96953	Sequence 96953, A	c 233	15.2	60.8	818128	3	US-09-949-016-14557	Sequence 14557, A
c 161	15.2	60.8	601	3	US-09-949-016-96954	Sequence 96954, A	c 234	15.2	60.8	818128	3	US-09-949-016-14558	Sequence 14558, A
c 162	15.2	60.8	601	3	US-09-949-016-97219	Sequence 97219, A	c 235	15.2	60.8	818128	3	US-09-949-016-14559	Sequence 14559, A
c 163	15.2	60.8	601	3	US-09-949-016-97220	Sequence 97220, A	c 236	15.2	60.8	818128	3	US-09-949-016-14560	Sequence 14560, A
c 164	15.2	60.8	601	3	US-09-949-016-97485	Sequence 97485, A	c 237	15.2	60.8	818128	3	US-09-949-016-14561	Sequence 14561, A
c 165	15.2	60.8	601	3	US-09-949-016-97486	Sequence 97486, A	c 238	15.2	60.8	818128	3	US-09-949-016-14562	Sequence 14562, A
c 166	15.2	60.8	601	3	US-09-949-016-97751	Sequence 97751, A	c 239	15.2	60.8	818128	3	US-09-949-016-14564	Sequence 14564, A
c 167	15.2	60.8	601	3	US-09-949-016-97752	Sequence 97752, A	c 240	15.2	60.8	818128	3	US-09-949-016-14565	Sequence 14565, A
c 168	15.2	60.8	601	3	US-09-949-016-98017	Sequence 98017, A	c 241	15.2	60.8	818128	3	US-09-949-016-14566	Sequence 14566, A
c 169	15.2	60.8	601	3	US-09-949-016-98018	Sequence 98018, A	c 242	15.2	60.8	818128	3	US-09-949-016-14567	Sequence 14567, A
c 170	15.2	60.8	601	3	US-09-949-016-98283	Sequence 98283, A	c 243	15	60.0	30	3	US-09-085-686-9	Sequence 9, Appli

244	15	60.0	30	3	US-09-085-686-10	Sequence 10, Appl	C 317	14.8	59.2	612	3	US-08-998-416-752	Sequence 752, App
C 245	15	60.0	135	3	US-09-533-559-3714	Sequence 3714, Ap	C 318	14.8	59.2	705	3	US-09-270-767-13560	Sequence 13560, A
C 246	15	60.0	234	3	US-09-252-991A-3316	Sequence 3316, Ap	C 319	14.8	59.2	860	3	US-09-636-499-18	Sequence 18, Appl
C 247	15	60.0	267	3	US-09-313-294A-659	Sequence 659, App	C 320	14.8	59.2	1026	3	US-09-614-221A-512	Sequence 512, App
248	15	60.0	266	3	US-09-023-655-499	Sequence 499, App	321	14.8	59.2	1296	3	US-10-037-927B-9	Sequence 9, Appl
249	15	60.0	321	3	US-09-513-999C-2705	Sequence 2705, Ap	322	14.8	59.2	1464	3	US-09-636-499-3	Sequence 3, Appl
C 250	15	60.0	399	3	US-09-903-540-6974	Sequence 6974, Ap	323	14.8	59.2	1584	3	US-09-636-499-2	Sequence 2, Appl
251	15	60.0	409	3	US-09-513-999C-15817	Sequence 15817, A	324	14.8	59.2	1695	3	US-09-227-853A-1	Sequence 1, Appl
252	15	60.0	463	3	US-09-621-976-3068	Sequence 3068, Ap	325	14.8	59.2	1695	6	PCT-US95-06385-1	Sequence 27, Appl
253	15	60.0	480	3	US-09-270-767-2307	Sequence 2307, Ap	326	14.8	59.2	1721	3	US-08-820-170A-27	Sequence 27, Appl
254	15	60.0	480	3	US-09-270-767-17589	Sequence 17589, A	327	14.8	59.2	1721	3	US-09-055-699-27	Sequence 27, Appl
255	15	60.0	601	3	US-09-949-016-47146	Sequence 47146, A	328	14.8	59.2	1721	3	US-09-273-565-27	Sequence 27, Appl
256	15	60.0	601	3	US-09-949-016-58170	Sequence 58170, A	329	14.8	59.2	1721	3	US-09-565-538-27	Sequence 27, Appl
C 257	15	60.0	601	3	US-09-949-016-70149	Sequence 70149, A	330	14.8	59.2	1721	3	US-09-661-468-27	Sequence 27, Appl
C 258	15	60.0	601	3	US-09-949-016-155131	Sequence 155131, A	331	14.8	59.2	1721	3	US-09-976-165-27	Sequence 27, Appl
259	15	60.0	601	3	US-09-252-991A-3988	Sequence 3988, Ap	332	14.8	59.2	1920	3	US-10-104-047-1847	Sequence 1847, Ap
C 260	15	60.0	765	3	US-09-252-991A-3980	Sequence 3980, Ap	333	14.8	59.2	1920	3	US-09-636-499-1	Sequence 1, Appl
C 261	15	60.0	895	3	US-09-270-767-10093	Sequence 10093, A	334	14.8	59.2	2612	3	US-10-104-047-1320	Sequence 1320, Ap
262	15	60.0	896	3	US-09-533-559-1448	Sequence 1448, Ap	335	14.8	59.2	2992	2	US-08-426-236-3	Sequence 3, Appl
263	15	60.0	1218	3	US-09-489-039A-170	Sequence 170, App	336	14.8	59.2	4898	3	US-09-636-499-17	Sequence 17, Appl
264	15	60.0	1301	2	US-08-641-314C-1	Sequence 1, Appl	337	14.8	59.2	24593	3	US-09-949-016-13433	Sequence 13433, A
265	15	60.0	1302	3	US-09-252-991A-7155	Sequence 7155, Ap	338	14.8	59.2	26763	3	US-09-949-016-11984	Sequence 11984, A
266	15	60.0	1335	3	US-09-252-991A-3925	Sequence 3925, Ap	339	14.8	59.2	26764	3	US-09-949-016-15566	Sequence 15566, A
C 267	15	60.0	1344	3	US-09-489-039A-534	Sequence 534, App	340	14.8	59.2	28770	3	US-09-817-198C-3	Sequence 3, Appl
C 268	15	60.0	1347	3	US-09-252-991A-7339	Sequence 7339, Ap	341	14.8	59.2	31867	3	US-09-949-016-16874	Sequence 16874, A
269	15	60.0	1500	3	US-09-252-991A-7277	Sequence 7277, Ap	342	14.8	59.2	31875	3	US-09-949-016-12864	Sequence 12864, A
C 270	15	60.0	1504	3	US-09-949-016-2633	Sequence 2633, Ap	343	14.8	59.2	41755	3	US-09-949-016-15728	Sequence 15728, A
C 271	15	60.0	1896	2	US-08-605-541B-11	Sequence 11, Appl	344	14.8	59.2	52661	3	US-09-949-016-17191	Sequence 17191, A
C 272	15	60.0	2223	3	US-09-252-991A-4015	Sequence 4015, Ap	345	14.8	59.2	73757	3	US-09-949-016-15369	Sequence 15369, A
C 273	15	60.0	2574	3	US-08-887-534A-46	Sequence 46, Appl	346	14.6	58.4	66	3	US-08-952-793-368	Sequence 368, App
C 274	15	60.0	2574	3	US-09-527-431-46	Sequence 46, Appl	347	14.6	58.4	66	3	US-09-849-928-368	Sequence 368, App
C 275	15	60.0	2574	3	US-09-446-861-46	Sequence 46, Appl	348	14.6	58.4	66	6	PCT-US96-09455A-368	Sequence 368, App
C 276	15	60.0	2574	3	US-09-960-428-20	Sequence 20, Appl	349	14.6	58.4	400	3	US-09-513-999C-30170	Sequence 30170, A
C 277	15	60.0	2657	3	US-10-104-047-879	Sequence 879, App	350	14.6	58.4	441	2	US-08-266-311-5	Sequence 5, Appl
278	15	60.0	2858	3	US-10-104-047-1226	Sequence 1226, Ap	351	14.6	58.4	441	2	US-08-467-527A-5	Sequence 5, Appl
C 279	15	60.0	3380	3	US-09-902-540-606	Sequence 606, App	352	14.6	58.4	441	3	US-08-467-528-5	Sequence 5, Appl
C 280	15	60.0	4417	3	US-07-741-453A-57	Sequence 57, Appl	353	14.6	58.4	447	3	US-09-222-575-61	Sequence 61, Appl
C 281	15	60.0	5749	3	US-09-262-537-48	Sequence 48, Appl	354	14.6	58.4	447	3	US-09-389-681-61	Sequence 61, Appl
282	15	60.0	8514	3	US-09-949-016-11938	Sequence 11938, A	355	14.6	58.4	447	3	US-09-620-405B-61	Sequence 61, Appl
C 283	15	60.0	9442	3	US-09-949-016-12571	Sequence 12571, A	356	14.6	58.4	447	3	US-09-339-338-61	Sequence 61, Appl
C 284	15	60.0	9443	3	US-09-949-016-15877	Sequence 15877, A	357	14.6	58.4	447	3	US-09-433-826B-61	Sequence 61, Appl
285	15	60.0	9792	3	US-09-635-872A-14	Sequence 14, Appl	358	14.6	58.4	447	3	US-09-604-287A-61	Sequence 61, Appl
286	15	60.0	9792	3	US-09-636-077A-14	Sequence 14, Appl	359	14.6	58.4	447	3	US-09-285-480-61	Sequence 61, Appl
287	15	60.0	9792	3	US-09-986-552-14	Sequence 14, Appl	360	14.6	58.4	447	3	US-09-834-759-61	Sequence 61, Appl
288	15	60.0	9792	3	US-09-636-596C-14	Sequence 14, Appl	361	14.6	58.4	447	3	US-09-590-751A-61	Sequence 61, Appl
289	15	60.0	9792	3	US-10-023-894-21	Sequence 21, Appl	362	14.6	58.4	447	3	US-09-551-621A-61	Sequence 61, Appl
290	15	60.0	9792	3	US-10-306-686-14	Sequence 14, Appl	363	14.6	58.4	447	3	US-09-551-621A-61	Sequence 61, Appl
291	15	60.0	9792	3	US-09-895-072-14	Sequence 14, Appl	364	14.6	58.4	447	3	US-10-076-622-61	Sequence 61, Appl
292	15	60.0	9792	3	US-10-023-888-21	Sequence 21, Appl	365	14.6	58.4	514	3	US-09-270-767-10269	Sequence 10269, A
C 293	15	60.0	10701	3	US-09-949-016-14375	Sequence 14375, A	366	14.6	58.4	525	3	US-09-489-039A-335	Sequence 335, App
294	15	60.0	11820	3	US-09-949-016-11887	Sequence 11887, A	367	14.6	58.4	594	3	US-09-702-705-812	Sequence 812, App
295	15	60.0	11826	3	US-09-949-016-13767	Sequence 13767, A	368	14.6	58.4	594	3	US-09-736-457-812	Sequence 812, App
296	15	60.0	15472	3	US-09-453-702B-71	Sequence 71, Appl	369	14.6	58.4	594	3	US-09-328-352-3456	Sequence 3456, Ap
C 297	15	60.0	15472	3	US-10-114-170-71	Sequence 71, Appl	370	14.6	58.4	594	3	US-09-614-124B-812	Sequence 812, App
C 298	15	60.0	16780	3	US-09-949-002-796	Sequence 796, App	371	14.6	58.4	594	3	US-09-671-325-812	Sequence 812, App
299	15	60.0	16780	3	US-09-949-016-12912	Sequence 12912, A	372	14.6	58.4	594	3	US-09-589-184-812	Sequence 812, App
300	15	60.0	18466	3	US-09-949-016-16081	Sequence 16081, A	373	14.6	58.4	594	3	US-09-658-824-812	Sequence 812, App
C 301	15	60.0	33885	3	US-08-311-731A-122	Sequence 122, App	374	14.6	58.4	594	3	US-10-017-754-812	Sequence 812, App
C 302	15	60.0	41171	3	US-09-949-016-14581	Sequence 14581, A	375	14.6	58.4	594	3	US-09-651-563-812	Sequence 812, App
303	15	60.0	64309	3	US-09-949-016-11804	Sequence 11804, A	376	14.6	58.4	601	3	US-09-949-016-22151	Sequence 22151, A
C 304	15	60.0	7479	3	US-09-949-016-12416	Sequence 12416, A	377	14.6	58.4	601	3	US-09-949-016-25898	Sequence 25898, A
305	15	60.0	76985	3	US-09-949-016-13120	Sequence 13120, A	378	14.6	58.4	601	3	US-09-949-016-30906	Sequence 30906, A
306	15	60.0	76986	3	US-09-949-016-13427	Sequence 13427, A	379	14.6	58.4	601	3	US-09-949-016-61328	Sequence 61328, A
C 307	15	60.0	110585	3	US-09-497-855A-32	Sequence 32, Appl	380	14.6	58.4	601	3	US-09-949-016-64776	Sequence 64776, A
C 308	15	60.0	118067	3	US-09-949-016-13765	Sequence 13765, A	381	14.6	58.4	601	3	US-09-949-016-66465	Sequence 66465, A
C 309	15	60.0	128470	3	US-09-949-016-13807	Sequence 13807, A	382	14.6	58.4	601	3	US-09-949-016-105276	Sequence 105276, A
C 310	15	60.0	168971	3	US-09-949-016-17175	Sequence 17175, A	383	14.6	58.4	601	3	US-09-949-016-115513	Sequence 115513, A
C 311	15	60.0	227750	3	US-09-705-400-64	Sequence 64, Appl	384	14.6	58.4	601	3	US-09-949-016-115606	Sequence 115606, A
312	15	60.0	229354	3	US-09-094-207A-2	Sequence 2, Appl	385	14.6	58.4	601	3	US-09-949-016-115699	Sequence 115699, A
C 313	14.8	59.2	308	3	US-10-109-725A-2	Sequence 2, Appl	386	14.6	58.4	601	3	US-09-949-016-115792	Sequence 115792, A
C 314	14.8	59.2	308	3	US-09-621-976-11034	Sequence 11034, A	387	14.6	58.4	601	3	US-09-949-016-115978	Sequence 115978, A
C 315	14.8	59.2	484	3	US-09-949-016-58342	Sequence 58342, A	388	14.6	58.4	601	3	US-09-949-016-116071	Sequence 116071, A
C 316	14.8	59.2	601	3			389	14.6	58.4	601	3		


```
RESULT 2
US-09-116-032-2/c
; Sequence 2, Application US/09116032
; Patent No. 6200576
; GENERAL INFORMATION:
; APPLICANT: HWONG, CHING LONG
; APPLICANT: LO, CHENG-KAI
; APPLICANT: YANG, YING-CHUAN
; APPLICANT: JENG, KING-SONG
; APPLICANT: CHANG, EDWARD L.
; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
; TITLE OF INVENTION: PREPARATION PROCESS AND USE THEREOF
; FILE REFERENCE: 9751.79US01
; CURRENT APPLICATION NUMBER: US/09/116,032
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: CHINA 86105814
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1220
; TYPE: DNA
; ORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-2
Query Match 93.6%; Score 23.4; DB 3; Length 1220;
Best Local Similarity 96.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 538 TCCGCTGCAGAGTTGCCCGTTACGA 514

RESULT 3
US-09-116-032-1/c
; Sequence 1, Application US/09116032
; Patent No. 6200576
; GENERAL INFORMATION:
; APPLICANT: HWONG, CHING LONG
; APPLICANT: LO, CHENG-KAI
; APPLICANT: YANG, YING-CHUAN
; APPLICANT: JENG, KING-SONG
; APPLICANT: CHANG, EDWARD L.
; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
; TITLE OF INVENTION: PREPARATION PROCESS AND USE THEREOF
; FILE REFERENCE: 9751.79US01
; CURRENT APPLICATION NUMBER: US/09/116,032
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: CHINA 86105814
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 7400
; TYPE: DNA
; ORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-1
Query Match 93.6%; Score 23.4; DB 3; Length 7400;
Best Local Similarity 96.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 538 TCCGCTGCAGAGTTGCCCGTTACGA 514

RESULT 4
US-09-116-032-1/c
; Sequence 1, Application US/09116032
; Patent No. 6200576
; GENERAL INFORMATION:
; APPLICANT: HWONG, CHING LONG
; APPLICANT: LO, CHENG-KAI
; APPLICANT: YANG, YING-CHUAN
; APPLICANT: JENG, KING-SONG
; APPLICANT: CHANG, EDWARD L.
; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
; TITLE OF INVENTION: PREPARATION PROCESS AND USE THEREOF
; FILE REFERENCE: 9751.79US01
; CURRENT APPLICATION NUMBER: US/09/116,032
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: CHINA 86105814
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 7400
; TYPE: DNA
; ORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-1
Query Match 93.6%; Score 23.4; DB 3; Length 7400;
Best Local Similarity 96.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 538 TCCGCTGCAGAGTTGCCCGTTACGA 514
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US-09-724-678D-10/c
; Sequence 10, Application US/09724678D
; Patent No. 6818397
; GENERAL INFORMATION:
; APPLICANT: Lee, Kang-Hung
; APPLICANT: Bair, Chi-Hong
; APPLICANT: Tseng, Yang-Yuan
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Wang, Shing-Hwan
; TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses and the p
; TITLE OF INVENTION: and Probes Therefor
; FILE REFERENCE: TAI 316
; CURRENT APPLICATION NUMBER: US/09/724,678D
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 10
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Sequence is Synthesized
; Patent No. 6818397
US-09-724-678D-10
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Query Match 92.0%; Score 23; DB 3; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 27 TCCGCTGCAGAGTTGCCCGTTACGA 3
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RESULT 5
US-09-489-039A-680/c
; Sequence 680, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 680
; LENGTH: 3366
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-680
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Query Match 75.2%; Score 18.8; DB 3; Length 3366;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTAC 23
|||||
Db 1112 CCGCTGCAGAGTTGCCCGTTAC 1091
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```
RESULT 6
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
```

```

RESULT 8
US-09-949-016-15569
; Sequence 15669, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN K
; TITLE OF INVENTION: WITH HUMAN DISEAS
; FILE REFERENCE: CLO01307

```

Query Match 69.6%; Score 17.4; DB 3; Length 919;

Best Local Similarity 94.7%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 18; Conservative 0;

QY 5 CTGCAGAGTTGCCCGTTAC 23

Db 491 CTGCAGAGTTGCCCGTTAC 509

RESULT 10

US-08-998-416-523/c
; Sequence 523, Application US/08998416
; Patent No. 6239264

GENERAL INFORMATION:

APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPPII

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 1152

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6239264artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: No. 6239264th Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416

FILING DATE: 24-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 523:

SEQUENCE CHARACTERISTICS:

LENGTH: 824 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: PAG1367RP

US-08-998-416-523

Query Match 68.8%; Score 17.2; DB 3; Length 824;

Best Local Similarity 86.4%; Pred. No. 1.3e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCOCCTGCAGAGTTGCCCGTTA 22

Db 559 TCGCGGCAGAGTTGCCCGGTA 538

RESULT 11

US-08-688-988-27

; Sequence 27, Application US/0868988B

; Patent No. 6096545

GENERAL INFORMATION:

APPLICANT: Lefebvre, Daniel D.

APPLICANT: Malboobi, Mohammad A.

TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS

FILE REFERENCE: PTL96-03

CURRENT APPLICATION NUMBER: US/08/688,988B

CURRENT FILING DATE: 1996-07-31

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 27

LENGTH: 319

TYPE: DNA

ORGANISM: Brassica Nigra

US-08-688-988-27

Query Match

Best Local Similarity

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 162 TCGCTTCAGATTGCCCGTTGAGA 186

RESULT 12

US-08-387-845-5/c

; Sequence 5, Application US/08387845

; Patent No. 5665567

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a

TITLE OF INVENTION: bicomponent vector system in mammalian cells

NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPA)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,845

FILING DATE:

CLASSIFICATION: 435

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 628 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

ORIGINAL SOURCE:

ORGANISM: Poliovirus Typ 1 (Mahoney strain)

IMMEDIATE SOURCE:

CLONE: pGEM 3-5' Polio (M) (4708 bp), (Sarnow, 1989)

FEATURE:

NAME/KEY: -

LOCATION: 1..628

OTHER INFORMATION: /note= "shown are the first

OTHER INFORMATION: 628 nt of the 5' non-translated region of

OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"

FEATURE:

NAME/KEY: -

LOCATION: 610

OTHER INFORMATION: /note= "non-authentic sequence

OTHER INFORMATION: due to a base pair substitution from C to G

OTHER INFORMATION: at position 610"

PUBLICATION INFORMATION:

AUTHORS: Sarnow, P.

JOURNAL: J. Virol.

VOLUME: 63

PAGES: 467-470

DATE: 1989

US-08-387-845-5

Query Match

68.0%; Score 17; DB 2; Length 628;

Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 535 TCCGCCACGGACTTGCGGTTACGA 511

RESULT 13

US-08-778-275-5/c
; Sequence 5, Application US/08778275
; Patent No. 5935819
; GENERAL INFORMATION:

;; APPLICANT:
;; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
;; NUMBER OF SEQUENCES: 16
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/778,275
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/387,845
;; FILING DATE:
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 628 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
;; IMMEDIATE SOURCE:
;; CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..628
;; OTHER INFORMATION: /note= "shown are the first
;; OTHER INFORMATION: 628 nt of the 5' non-translated region of
;; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
;;

;; NAME/KEY: -
;; LOCATION: 610
;; OTHER INFORMATION: /note= "non-authentic sequence
;; OTHER INFORMATION: due to a base pair substitution from C to G
;; PUBLICATION INFORMATION:
;; AUTHORS: Sarnow, P.
;; JOURNAL: J. Virol.
;; VOLUME: 63
;; PAGES: 467-470
;; DATE: 1989
US-08-778-275-5
Query Match 68.0%; Score 17; DB 2; Length 628;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 535 TCCGCCACGGACTTGCGGTTACGA 511

RESULT 14

US-08-867-352-5/c
; Sequence 5, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:

;; APPLICANT: Ross, Bruce C.
;; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;; NUMBER OF SEQUENCES: 1120
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows

;; APPLICANT:
;; TITLE OF INVENTION: Multicistronic expression units and their use
;; NUMBER OF SEQUENCES: 25
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/867,352
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/387,847
;; FILING DATE:
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 628 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
;; IMMEDIATE SOURCE:
;; CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..628
;; OTHER INFORMATION: /note= "shown are the first
;; OTHER INFORMATION: 628 nt of the 5' non-translated region of
;; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
;;

;; NAME/KEY: -
;; LOCATION: 610
;; OTHER INFORMATION: /note= "non-authentic sequence
;; OTHER INFORMATION: due to a base pair substitution from C to G
;; PUBLICATION INFORMATION:
;; AUTHORS: Sarnow, P.
;; JOURNAL: J. Virol.
;; VOLUME: 63
;; PAGES: 467-470
;; DATE: 1989
US-08-867-352-5
Query Match 68.0%; Score 17; DB 3; Length 628;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 535 TCCGCCACGGACTTGCGGTTACGA 511

RESULT 15

US-09-221-017B-435/c
; Sequence 435, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:

;; APPLICANT: Ross, Bruce C.
;; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;; NUMBER OF SEQUENCES: 1120
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows

RESULT 16
US-09-949-016-5300/c
; Sequence 5300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 5300
; LENGTH: 1865
; TYPE: DNA
; ORGANISM: Human

US-08-403-388-1/c
Sequence 1, Application US/08403388
Patent No. 5587289
GENERAL INFORMATION:
APPLICANT: Lurquin, Christophe; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,388
FILING DATE: 14-MARCH-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5587289man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5408

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1866 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-388-1

Query Match      68.0%; Score 17; DB 2; Length 1866;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
Db 973 TCGGTGGCAGAGTTGCCCTTTAAGA 949

RESULT 19
US-08-658-578-1/c
; Sequence 1, Application US/08658578
; Patent No. 5759783
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,578
; FILING DATE: 5-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,388
; FILING DATE: 14-MARCH-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5759783man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5444
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1866 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-658-578-1

Query Match      68.0%; Score 17; DB 2; Length 1866;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
Db 973 TCGGTGGCAGAGTTGCCCTTTAAGA 949

RESULT 20
```

```
US-08-846-111D-1/c
; Sequence 1, Application US/08846111D
; Patent No. 6017705
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect For DOS 6.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,111D
; FILING DATE: 25-APRIL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/658,578
; FILING DATE: 5-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,388
; FILING DATE: 14-MARCH-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6017705man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5444.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1866 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-846-111D-1

Query Match      68.0%; Score 17; DB 3; Length 1866;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
Db 973 TCGGTGGCAGAGTTGCCCTTTAAGA 949

RESULT 21
US-09-056-105-19/c
; Sequence 19, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 1866
; TYPE: DNA
```



```
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
US-07-852-260-1

Query Match 68.0%; Score 17; DB 2; Length 7432;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
||||| ||||| ||||| ||||| |||||
Db 538 TCCGCCACGAGCTTGGCGTTACGA 514

RESULT 25
US-08-461-503-1/c
; Sequence 1, Application US/08461503
; Patent No. 5834302
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatam, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
; TITLE OF INVENTION: FROM CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,503
; FILING DATE: 5-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,503
; FILING DATE: 5-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
US-08-461-503-1

Query Match 68.0%; Score 17; DB 2; Length 7432;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
||||| ||||| ||||| ||||| |||||
Db 538 TCCGCCACGAGCTTGGCGTTACGA 514

RESULT 26
US-08-465-250-1/c
; Sequence 1, Application US/08465250
; Patent No. 6136570
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatam, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,250
; FILING DATE: 6-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-E-PCT-US
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
US-08-465-250-1

Query Match 68.0%; Score 17; DB 3; Length 7432;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
||||| ||||| ||||| ||||| |||||
Db 538 TCCGCCACGAGCTTGGCGTTACGA 514

RESULT 27
US-09-284-349B-1/c
; Sequence 1, Application US/09284349B
; Patent No. 6696289
; GENERAL INFORMATION:
; APPLICANT: Yong Soo, Bae
; APPLICANT: Jung, Hye Rhan
; TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain
; FILE REFERENCE: Docket No. 6696289; 4220-109 US
; CURRENT APPLICATION NUMBER: US/09/284,349B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: PCT/KR98/00242
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: KR 97/37812
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 30
```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7441
; TYPE: DNA
; ORGANISM: Human poliovirus 1
US-09-284-349B-1

Query Match      68.0%; Score 17; DB 3; Length 7441;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 535 TCCGCCACGAGCTTGGCGGTACGA 511

RESULT 28
US-09-949-016-17042/c
; Sequence 17042, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 17042
; LENGTH: 12309
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17042

Query Match      68.0%; Score 17; DB 3; Length 12309;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 9414 TCGTGGCAGAGTTGCCCTTTAAGA 9390

RESULT 29
US-09-949-016-17043/c
; Sequence 17043, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17043
; LENGTH: 12309
; TYPE: DNA
; ORGANISM: Human

```

```

US-09-949-016-17043

Query Match      68.0%; Score 17; DB 3; Length 12309;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 9414 TCGTGGCAGAGTTGCCCTTTAAGA 9390

RESULT 30
US-08-846-111D-15/c
; Sequence 15, Application US/08846111D
; Patent No. 6017705
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect For DOS 6.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,111D
; FILING DATE: 25-APRIL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/658,578
; FILING DATE: 5-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,388
; FILING DATE: 14-MARCH-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6017705man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5444.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-846-111D-15

Query Match      68.0%; Score 17; DB 3; Length 40352;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 38797 TCGTGGCAGAGTTGCCCTTTAAGA 38773

RESULT 31
US-09-443-077-15/c
; Sequence 15, Application US/09443077
; Patent No. 6392016
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; Boon-Falleur, Thierry

```

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are Members Of The Mage-B Family and Uses Thereof

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felre & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022-7513

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect For DOS 6.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/443,077

FILING DATE: 26-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/846,111

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/403,388

FILING DATE: 14-MARCH-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6392016man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5444.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 40352 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Query Match 68.0%; Score 17; DB 3; Length 40352;

Best Local Similarity 80.0%; Pred. No. 2.6e+02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 38797 TCGTGGCAGAGTTGCCCTTTAAGA 38773

RESULT 32

US-09-902-540-1132/c

; Sequence 1132, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 1132

; LENGTH: 13226

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-1132

Query Match

Best Local Similarity 66.4%; Score 16.6; DB 3; Length 13226;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTAC 23

Db 2224 TCCGTCGCCAGTTGCCCGGTGC 2202

RESULT 33

US-09-949-016-12171

; Sequence 12171, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 12171

; LENGTH: 85369

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(85369)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12171

Query Match

Best Local Similarity 66.4%; Score 16.6; DB 3; Length 85369;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTAC 23

Db 51764 TCTGCTGCAGAGATGCCCTGTAC 51786

RESULT 34

US-09-103-840A-1

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match

Best Local Similarity 66.4%; Score 16.6; DB 3; Length 4411529;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACG 24

Db 356524 CCAATGCCAGTTGCCCGATACG 356546

RESULT 35

US-09-221-017B-301/c
; Sequence 301, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: ROSS, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 301:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 508 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...508
US-09-221-017B-301

Query Match 64.8%; Score 16.2; DB 3; Length 508;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTTGCCCGTTACG 24

Db 201 GCTGCAGAGTAGCCCATTCG 181

RESULT 36

US-09-949-016-5147
; Sequence 5147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5147
; LENGTH: 3378
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5147

Query Match 64.8%; Score 16.2; DB 3; Length 3378;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTGCAGAGTTGCCCGTTACGA 25

Db 2711 CTGCATAGATGCCCGTTACTA 2731

RESULT 37

US-09-949-016-16889
; Sequence 16889, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16889
; LENGTH: 17154
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16889

Query Match 64.8%; Score 16.2; DB 3; Length 17154;
Best Local Similarity 85.7%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTGCAGAGTTGCCCGTTACGA 25

Db 14079 CTGCATAGATGCCCGTTACTA 14099

RESULT 38

US-09-949-016-13873/c
; Sequence 13873, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13873
; LENGTH: 106450
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13873

Query Match 64.8%; Score 16.2; DB 3; Length 106450;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTT 21
Db 64365 TCTGCTGCAGAGTTGCTTTGTT 64345

RESULT 39
US-09-891-735-5
; Sequence 5, Application US/09891735
; Patent No. 6511837
; GENERAL INFORMATION:
; APPLICANT: No. 6511837ozymes A/S
; APPLICANT: Teutsumi, No. 6511837iko
; TITLE OF INVENTION: Lipolytic Enzymes
; FILE REFERENCE: 10057.200-US
; CURRENT APPLICATION NUMBER: US/09/891,735
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-891-735-5

Query Match 64.0%; Score 16; DB 3; Length 32;
Best Local Similarity 79.2%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
Db 6 CTGGTGGAGAGTTCCGCGTTACGA 29

RESULT 40
US-10-131-827-4079
; Sequence 4079, Application US/10131827
; Patent No. 6305827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131.827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4079
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-4079

Query Match 64.0%; Score 16; DB 3; Length 50;
Best Local Similarity 79.2%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
Db 18 CCGCTCCAGCTTTCACGTTTCGA 41

RESULT 41
US-09-252-991A-4772
; Sequence 4772, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4772
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4772

Query Match 64.0%; Score 16; DB 3; Length 372;
Best Local Similarity 79.2%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTTACG 24
Db 66 TGGCTGCAGAACTGCCCGCAACG 89

RESULT 42
US-09-252-991A-4736/C
; Sequence 4736, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4736
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4736

```

Query Match      64.0%; Score 16; DB 3; Length 447;
Best Local Similarity 79.2%; Pred. No. 4.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 TCCGCTGCAGAGTTGCCCGTTACG 24
      |||||
DB      376 TCGCTGCAGAACTGCCCGCAACG 353

RESULT 43
US-09-270-767-1180
; Sequence 1180, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1180
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1180

Query Match      64.0%; Score 16; DB 3; Length 465;
Best Local Similarity 79.2%; Pred. No. 4.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 CCGCTGCAGAGTTGCCCGTTACGA 25
      |||||
DB      28 CCGCTCCAGGGTTGCCCATTTGGA 51

RESULT 44
US-09-270-767-16462
; Sequence 16462, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16462
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16462

Query Match      64.0%; Score 16; DB 3; Length 465;
Best Local Similarity 79.2%; Pred. No. 4.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 CCGCTGCAGAGTTGCCCGTTACGA 25
      |||||
DB      28 CCGCTCCAGGGTTGCCCATTTGGA 51

RESULT 45
US-09-949-016-30653
; Sequence 30653, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13356
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13356

Query Match      64.0%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTCGCCGTTACGA 25
Db 453 CCTCTACAGAGTTCGCTTCTGA 476

RESULT 48
US-08-998-416-961/c
; Sequence 961, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHAYA GOSSYPHII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 961:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAGL593RP
US-08-998-416-961

Query Match      64.0%; Score 16; DB 3; Length 718;
Best Local Similarity 79.2%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTCGCCGTTACGA 25
Db 26 CCGTTCAGAGTTGCTCTATTTCGA 3

RESULT 49
US-09-799-451-300/c
; Sequence 300, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 300
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(807)
US-09-799-451-300

Query Match      64.0%; Score 16; DB 3; Length 942;
Best Local Similarity 79.2%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACG 24
Db 190 TCCGCTGCAGAGTTCGCCGTTACG 167

RESULT 50
US-09-640-211A-154/c
; Sequence 154, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000,1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 1144

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; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-154

Query Match      64.0%; Score 16; DB 3; Length 1144;
Best Local Similarity 79.2%; Pred. No. 5.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24
   ||| ||| ||| ||| ||| ||| ||| |||
Db 1129 TCCACCGCGAGTTGCCCGTACCG 1106

RESULT 51
US-09-891-735-1
; Sequence 1, Application US/09891735
; Patent No. 6511837
; GENERAL INFORMATION:
; APPLICANT: No. 6511837ozymes A/S
; APPLICANT: Tsutsumi, No. 6511837iko
; TITLE OF INVENTION: Lipolytic Enzymes
; FILE REFERENCE: 10057.200-US
; CURRENT APPLICATION NUMBER: US/09/891,735
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Fusarium sp.
US-09-891-735-1

Query Match      64.0%; Score 16; DB 3; Length 1159;
Best Local Similarity 79.2%; Pred. No. 5.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
   ||| ||| ||| ||| ||| ||| ||| |||
Db 759 CTGGTGAGAGTTCCGCGTTACGA 782

RESULT 52
US-09-489-039A-2930/c
; Sequence 2930, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2930
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2930

Query Match      64.0%; Score 16; DB 3; Length 1431;
Best Local Similarity 79.2%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
   ||| ||| ||| ||| ||| ||| ||| |||
Db 610 CCTCCGAGAGTTGCCCGCCACCA 587

RESULT 53
US-09-703-416-1
; Sequence 1, Application US/09703416

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; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-10-171-229-1

Query Match      64.0%; Score 16; DB 3; Length 2940;
Best Local Similarity 79.2%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
    ||||| ||||| ||||| ||||| |||||
Db 2132 CTGCTGGAGAGTTCCGCGTTACGA 2155

RESULT 56
US-10-429-398-1
; Sequence 1, Application US/10429398
; Patent No. 6730346
; GENERAL INFORMATION:
; APPLICANT: Rev. Michael W.
; APPLICANT: Golightly, Elizabeth J.
; APPLICANT: Spendler, Tina
; TITLE OF INVENTION: Methods For Using Lipases In Baking
; FILE REFERENCE: 10074.000-US
; CURRENT APPLICATION NUMBER: US/10/429,398
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US/09/703,414
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-10-429-398-1

Query Match      64.0%; Score 16; DB 3; Length 2940;
Best Local Similarity 79.2%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
    ||||| ||||| ||||| ||||| |||||
Db 2132 CTGCTGGAGAGTTCCGCGTTACGA 2155

RESULT 57
5175383-1
; Patent No. 5175383
; APPLICANT: LEDER, PHILIP; MULLER, WILLIAM J.
; TITLE OF INVENTION: ANIMAL MODEL FOR BENIGN PROSTATIC DISEASE
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/312,641
; FILING DATE: 17-FEB-1989
; SEQ ID NO:1
; LENGTH: 7868
5175383-1

Query Match      64.0%; Score 16; DB 9; Length 7868;
Best Local Similarity 79.2%; Pred. No. 6.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
    ||||| ||||| ||||| ||||| |||||
Db 5893 CTGCTGCAGAGTAGCCAGCCACGA 5916

RESULT 58
US-09-949-016-13876
; Sequence 13876, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 2000-04-14
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13876
; LENGTH: 36171
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13876

Query Match      64.0%; Score 16; DB 3; Length 36171;
Best Local Similarity 79.2%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24
    ||||| ||||| ||||| ||||| |||||
Db 26651 TCCGCTTCAGAGCTGCCCTGGCG 26674

RESULT 59
US-09-949-016-12389
; Sequence 12389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12389
; LENGTH: 36274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12389

Query Match      64.0%; Score 16; DB 3; Length 36274;
Best Local Similarity 79.2%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24
    ||||| ||||| ||||| ||||| |||||
Db 26762 TCCGCTTCAGAGCTGCCCTGGCG 26785

RESULT 60
US-09-949-016-17230/c
; Sequence 17230, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17230
; LENGTH: 90776
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17230

Query Match 64.0%; Score 16; DB 3; Length 90776;
Best Local Similarity 79.2%; Pred. No. 8.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CCGTGCAGAGTTGCCGTTACGA 25
DB 85436 CCAAGTGCAGAGTTGACCGTTTCCA 85413

RESULT 61
US-09-949-016-15494
; Sequence 15494, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15494
; LENGTH: 183770
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(183770)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15494

Query Match 64.0%; Score 16; DB 3; Length 183770;
Best Local Similarity 79.2%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CCGTGCAGAGTTGCCGTTACGA 25
DB 66481 CCTCTACAGAGTTGCCTGTCTGA 66504

RESULT 62
US-09-949-016-13418
; Sequence 13418, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13418
; LENGTH: 236474
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(236474)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13418

Query Match 64.0%; Score 16; DB 3; Length 236474;
Best Local Similarity 79.2%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCGTTACG 24
DB 34694 TCCGCTGCAGAGTTGCCGTTCCG 34717

RESULT 63
US-09-214-808-1
; Sequence 1, Application US/09214808A
; Patent No. 6475793
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; Patent No. 6475793
; TITLE OF INVENTION: Plasmid
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/214,808A
; CURRENT FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/IB97/00950
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-214-808-1

Query Match 64.0%; Score 16; DB 3; Length 536165;
Best Local Similarity 79.2%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCGTTACG 24
DB 510096 TCCGCTGCAGAGTTGCTGTGACG 510119

RESULT 64
US-09-513-999C-30616
; Sequence 30616, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487

```

; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 30616
; LENGTH: 290
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-30616

Query Match      63.2%; Score 15.8; DB 3; Length 290;
Best Local Similarity 89.5%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCGCTGCAGAGTTGCCGT 20
Db      106 CCCCTGCAGAGTTGCCGT 124

RESULT 65
US-09-953-318-100/c
; Sequence 100, Application US/09953318
; Patent No. 6710174
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/09/953,318
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 100
; LENGTH: 3394
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (252)...(2318)
US-09-953-318-100

Query Match      63.2%; Score 15.8; DB 3; Length 3394;
Best Local Similarity 89.5%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 GCTGCAGAGTTGCCGTGA 22
Db      524 GCTGCAGAGTTGCCGTGA 506

RESULT 66
US-09-953-318-10/c
; Sequence 10, Application US/09953318
; Patent No. 6710174
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/09/953,318
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 10
; LENGTH: 6055
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)...(4028)
US-09-953-318-10

Query Match      63.2%; Score 15.8; DB 3; Length 6055;
Best Local Similarity 89.5%; Pred. No. 7.7e+02;

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 GCTGCAGAGTTGCCGTGA 22
Db      299 GCTGCAGAGTTGCCGTGA 281

RESULT 67
US-09-949-016-14973/c
; Sequence 14973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14973
; LENGTH: 7620
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14973

Query Match      63.2%; Score 15.8; DB 3; Length 7620;
Best Local Similarity 89.5%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TCCGCTGCAGAGTTGCCCG 19
Db      7418 TCCGCTGCAGAGTTGCCCG 7400

RESULT 68
US-09-396-196G-74495
; Sequence 74495, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74495
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-74495

Query Match      62.4%; Score 15.6; DB 3; Length 25;
Best Local Similarity 81.8%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 TCCGCTGCAGAGTTGCCGTGA 22
Db      4 TCCACTGCAGAGTTGGACGTCA 25

```

RESULT 69

US-09-976-594-305/c
; Sequence 305, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 305
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1329120.10
; NAME/KEY: unsure
; LOCATION: 299
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-305

Query Match 62.4%; Score 15.6; DB 3; Length 452;

Best Local Similarity 81.8%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTGGCCGGTTACG 24

Db 212 CGCTCCACAGATGCCAGTTACG 191

RESULT 70

US-09-533-559-4705
; Sequence 4705, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: Expression
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4705
; LENGTH: 685
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-4705

Query Match 62.4%; Score 15.6; DB 3; Length 685;

Best Local Similarity 81.8%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGGCCGGTTACGA 25

Db 186 GCTGCAGAGTGGCCGGCTAAGA 207

RESULT 71

US-09-543-681A-1424

; Sequence 1424, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1424
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1424

Query Match 62.4%; Score 15.6; DB 3; Length 1059;

Best Local Similarity 81.8%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTGGCCGGTTA 22

Db 124 TCCGCTGCTGATTTACCCGGTA 145

RESULT 72

US-08-106-981-5
; Sequence 5, Application US/08106981
; Patent No. 5731419
; GENERAL INFORMATION:
; APPLICANT: SARHAN, Pathy
; APPLICANT: HOUE, Mario
; APPLICANT: LALIBERT, Jean-Fran ois
; TITLE OF INVENTION: DNA MOLECULES ENCODING FREEZING
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,981
; FILING DATE: 16-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 163-23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1136
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE: Triticum aestivum L.
US-08-106-981-5

Query Match

62.4%; Score 15.6; DB 2; Length 1136;

Best Local Similarity 81.8%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTGGCCCGTTACG 24
Db 674 CGCTGCTGCGGTGCCCGTCACG 695

RESULT 73

US-09-232-468A-13/c
; Sequence 13, Application US/09232468A
; Patent No. 6207165
; GENERAL INFORMATION:
; APPLICANT: AUDONNET et al.
; TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
; TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
; FILE REFERENCE: 454313-2230
; CURRENT APPLICATION NUMBER: US/09/232.468A
; CURRENT FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Porcine Flu Virus (SIV, H1N1 "SW" Strain)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1698)
US-09-232-468A-13

Query Match 62.4%; Score 15.6; DB 3; Length 1701;
Best Local Similarity 81.8%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGGCCCGTTACGA 25
Db 180 GCTGCAGAGTGGCCCGTTATGA 159

RESULT 74

US-09-784-984B-11/c
; Sequence 11, Application US/09784984B
; Patent No. 6576243
; GENERAL INFORMATION:
; APPLICANT: Merial Ltd.
; APPLICANT: Audonnet, Jean-Christophe
; APPLICANT: Bouchardon, Annabelle
; APPLICANT: Baudu, Philippe
; APPLICANT: Riviere, Michael
; TITLE OF INVENTION: Polynucleotide Vaccine Formula Against Porcine Reproductive and
; TITLE OF INVENTION: Respiratory Pathologies
; FILE REFERENCE: 454313-2230.1
; CURRENT APPLICATION NUMBER: US/09/784.984B
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: FR 96/09338
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCR/FR97/01313
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: US 6,207,165
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Porcine Flu Virus (SIV, H1N1 "SW" Strain)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1698)
; OTHER INFORMATION:
US-09-784-984B-11

Query Match 62.4%; Score 15.6; DB 3; Length 1701;

Best Local Similarity 81.8%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGGCCCGTTACGA 25
Db 180 GCTGCAGAGTGGCCCGTTATGA 159

RESULT 75

US-08-527-152-1/c
; Sequence 1, Application US/08527152
; Patent No. 5827655
; GENERAL INFORMATION:
; APPLICANT: Chaudy, Kanianthara G.
; APPLICANT: Cahalan, Michael D.
; APPLICANT: Grissmer, Stephan
; APPLICANT: Goldin, Alan L.
; APPLICANT: Dethlefs, Brent A.
; APPLICANT: Gutman, George A.
; APPLICANT: Wasmuth, John J.
; TITLE OF INVENTION: Assay, Methods and Products Based On n
; TITLE OF INVENTION: K+ Channel Expression
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: W.H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/527,152
; FILING DATE: UNKNOWN
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/170,418
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/558,568
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-54444-2/WHID
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELETYPE: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 150..1736
US-08-527-152-1

Query Match 62.4%; Score 15.6; DB 2; Length 1994;
Best Local Similarity 81.8%; Pred. No. 8.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGGCCCGTTACGA 25
Db 1669 GCTGTGGAGTGGCCCGTTTGA 1648

```
RESULT 76
US-09-233-857-2/c
; Sequence 2, Application US/09233857
; Patent No. 6495353
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Flanagan, Peter
; TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
; FILE REFERENCE: 239/251
; CURRENT APPLICATION NUMBER: US/09/233,857
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: USN 60/072,023
; EARLIER FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 5276
; TYPE: DNA
; ORGANISM: HUMAN
US-09-233-857-2

Query Match          62.4%; Score 15.6; DB 3; Length 5276;
Best Local Similarity 81.8%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCTGCAGAGTTGCCCGTTAC 23
DB      663 CAGCTGCAGAGTTGCCCGATT 642

RESULT 77
US-09-453-702B-39/c
; Sequence 39, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25165
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25165
; TYPE: nucleic acid
```

```
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-453-702B-39

Query Match          62.4%; Score 15.6; DB 3; Length 25165;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TCCGCTGCAGAGTTGCCCGTTA 22
DB      17400 TCGCTCCAGTTTGGCCGTTA 17379

RESULT 78
US-10-114-170-39/c
; Sequence 39, Application US/10114170
; Patent No. 685814
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 685814e1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25165
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-114-170-39

Query Match          62.4%; Score 15.6; DB 3; Length 25165;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TCCGCTGCAGAGTTGCCCGTTA 22
DB      17400 TCGCTCCAGTTTGGCCGTTA 17379
```

```

; TITLE OF INVENTION: Gene
; FILE REFERENCE: HPC2 Gene
; CURRENT APPLICATION NUMBER: US/09/434,382
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: US 60/107,468
; EARLIER FILING DATE: 1999-11-06
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (910)..(13104)
; OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
; OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
; OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
; OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
; OTHER INFORMATION: 13032-13104;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13756)..(22917)
; OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon
; OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
; OTHER INFORMATION: 18583-18701; exon 16: 20349-20445; exon 17:
; OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23045)..(26452)
; OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon
; OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23:
; OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation
; OTHER INFORMATION: signal: 26447-26452
; FEATURE:
; NAME/KEY: variation
; LOCATION: (826)..(23879)
; OTHER INFORMATION: s at positions 826 and 23180 is G or C; Y at
; OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
; OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at
; OTHER INFORMATION: positions 22211 and 23879 is A or G.
US-09-434-382-28

Query Match          62.4%; Score 15.6; DB 3; Length 26664;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4   GCTGCAGAGTTGCCCGTTACGA 25
        ||| ||| ||||| ||| |||
Db      24888 GCTACGAGGTGGCCCGTTAAGA 24909

RESULT 81
US-09-949-016-15607
; Sequence 15607, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15607
; LENGTH: 29558

```

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15607

Query Match 62.4%; Score 15.6; DB 3; Length 29558;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCTGCAGAGTGGCCCGTTACGA 25
DB 25979 GCTACGAGGTGGCCCGTTAAGA 26000

RESULT 82

US-09-949-016-12968
; Sequence 12968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12968
; LENGTH: 222452
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12968

Query Match 62.4%; Score 15.6; DB 3; Length 222452;
Best Local Similarity 81.8%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGTCGACAGTGGCCCGTTAC 23
DB 21889 CAGTCGACAGTAGACAGTTAC 21910

RESULT 83

US-09-513-999C-3441/c
; Sequence 3441, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3441
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..265
US-09-513-999C-3441

Query Match 61.6%; Score 15.4; DB 3; Length 267;
Best Local Similarity 76.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTGGCCCGTTACGA 25
DB 180 TCTCTGCAAGTGGCCTGTGACGA 156

RESULT 84

US-09-313-294A-2507/c
; Sequence 2507, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 2507
; LENGTH: 268
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700552775H1
; NAME/KEY: unsure
; LOCATION: 26, 132, 191, 211, 239, 245, 266-267
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-2507

Query Match 61.6%; Score 15.4; DB 3; Length 268;
Best Local Similarity 76.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTGGCCCGTTACGA 25
DB 164 TCGCTGCACAACTGTGCGCTACTA 140

RESULT 85

US-09-313-294A-5359/c
; Sequence 5359, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 5359
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700350024H1
; NAME/KEY: unsure
; LOCATION: 44, 150, 262, 267
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5359

Query Match 61.6%; Score 15.4; DB 3; Length 282;
Best Local Similarity 76.0%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 97 TCCGCTGCAGAACTGTTCGCTACTA 73
|||||

RESULT 86

US-09-702-705-1202/c
; Sequence 1202, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702.705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1202
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;
Best Local Similarity 76.0%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 59 TCCGGGGAGAGAGCCCGTCACCA 35
|||||

RESULT 87

US-09-736-457-1202/c
; Sequence 1202, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736.457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1202
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;
Best Local Similarity 76.0%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 59 TCCGGGGAGAGAGCCCGTCACCA 35
|||||

RESULT 88

US-09-614-124B-1202/c
; Sequence 1202, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614.124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1202
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;
Best Local Similarity 76.0%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 59 TCCGGGGAGAGAGCCCGTCACCA 35
|||||

RESULT 89

US-09-671-325-1202/c
; Sequence 1202, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671.325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1202
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;
Best Local Similarity 76.0%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 59 TCCGCGGAGAGAGCCCGTCACCA 35
|||||

RESULT 90
US-09-658-824-1202/c
; Sequence 1202, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1202
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-658-824-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;
Best Local Similarity 76.0%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 59 TCCGCGGAGAGAGCCCGTCACCA 35
|||||

RESULT 91
US-10-017-754-1202/c
; Sequence 1202, Application US/10017754
; Patent No. 6858204
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1202
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-754-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;
Best Local Similarity 76.0%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 59 TCCGCGGAGAGAGCCCGTCACCA 35
|||||

RESULT 92
US-09-651-563-1202/c
; Sequence 1202, Application US/09651563
; Patent No. 6914132
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C10
; CURRENT APPLICATION NUMBER: US/09/651,563
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 1679
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1202
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-563-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;
Best Local Similarity 76.0%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 59 TCCGCGGAGAGAGCCCGTCACCA 35
|||||

RESULT 93
US-09-700-820C-25/c
; Sequence 25, Application US/09700820C
; Patent No. 6610485
; GENERAL INFORMATION:
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Saito, Mikiyoshi
; APPLICANT: Ohtomo, Toshihiko
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
; FILE REFERENCE: 06501-070001
; CURRENT APPLICATION NUMBER: US/09/700,820C
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/JP99/02341
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: JP 10/138652
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/279876
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 25
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(363)
US-09-700-820C-25

Query Match 61.6%; Score 15.4; DB 3; Length 363;
Best Local Similarity 76.0%; Pred. No. 8.4e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 110 TCCGGGGAGAGAGCCCGTACCA 86
|||||

RESULT 94

US-08-754-477A-119/c
; Sequence 119, Application US/08754477A
; Patent No. 6518411
; GENERAL INFORMATION:
; APPLICANT: Murray, Jeffrey
; APPLICANT: Semina, Elena
; TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/754.477A
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UTA-022.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-754-477A-119

Query Match 61.6%; Score 15.4; DB 3; Length 515;
Best Local Similarity 76.0%; Pred. No. 8.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 57 TCTGGGGCAGAGTTGCCCACTCCGA 33
|||||

RESULT 95

US-09-023-655-1384/c
; Sequence 1384, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1384:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g38405_2
US-09-023-655-1384

Query Match 61.6%; Score 15.4; DB 3; Length 540;
Best Local Similarity 76.0%; Pred. No. 8.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 239 TCCGGGGAGAGAGCCCGTACCA 215
|||||

RESULT 96

US-09-533-559-1903/c
; Sequence 1903, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1903
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(582)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1903

Query Match 61.6%; Score 15.4; DB 3; Length 582;
Best Local Similarity 76.0%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 545 TCCGATTCGAATGCCCGTCATGA 521

RESULT 97
US-09-949-016-47406/c
; Sequence 47406, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47406
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-47406

Query Match 61.6%; Score 15.4; DB 3; Length 601;
Best Local Similarity 76.0%; Pred. No. 9e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 262 TCCACAGCAGAGTTGCCCGTGAGA 238

RESULT 98
US-09-949-016-47418/c
; Sequence 47418, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47418
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-47418

Query Match 61.6%; Score 15.4; DB 3; Length 601;
Best Local Similarity 76.0%; Pred. No. 9e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 262 TCCACAGCAGAGTTGCCCGTGAGA 238

RESULT 99
US-09-949-016-47430/c
; Sequence 47430, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47430
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-47430

Query Match 61.6%; Score 15.4; DB 3; Length 601;
Best Local Similarity 76.0%; Pred. No. 9e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 262 TCCACAGCAGAGTTGCCCGTGAGA 238

RESULT 100
US-09-949-002-1736/c
; Sequence 1736, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1736
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1736

Query Match 61.6%; Score 15.4; DB 3; Length 601;
Best Local Similarity 76.0%; Pred. No. 9e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 376 TCCATTGCAGGATGCCCGTGAGA 352

Search completed: March 8, 2006, 21:08:21
Job time : 131.903 secs

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c 99	18.2	72.8	1499	7	US-10-424-599-2070	Sequence 2070, Ap	c 172	17	68.0	237	9	US-10-760-048-59	Sequence 59, Appl
c 100	17.6	70.4	1182	3	US-09-738-626-2740	Sequence 2740, Ap	c 173	17	68.0	237	9	US-10-760-048-60	Sequence 60, Appl
c 101	17.6	70.4	2692	10	US-11-037-143-25478	Sequence 25478, A	c 174	17	68.0	237	9	US-10-760-048-63	Sequence 63, Appl
c 102	17.6	70.4	3663	10	US-11-037-143-23542	Sequence 23542, A	c 175	17	68.0	237	9	US-10-760-048-64	Sequence 64, Appl
c 103	17.6	70.4	6051	10	US-11-037-143-25477	Sequence 25477, A	c 176	17	68.0	237	9	US-10-760-048-66	Sequence 66, Appl
c 104	17.6	70.4	6462	8	US-10-775-169-329	Sequence 329, App	c 177	17	68.0	238	9	US-10-760-048-17	Sequence 17, Appl
c 105	17.6	70.4	3309400	3	US-09-738-626-1	Sequence 1, Appli	c 178	17	68.0	238	9	US-10-760-048-58	Sequence 58, Appl
c 106	17.4	69.6	919	5	US-10-228-794-45	Sequence 45, Appl	c 179	17	68.0	238	9	US-10-760-048-55	Sequence 55, Appl
c 107	17.2	68.8	514	4	US-09-925-065A-465485	Sequence 465485,	c 180	17	68.0	294	7	US-10-424-599-132735	Sequence 132735,
c 108	17.2	68.8	584	4	US-09-925-065A-696948	Sequence 696948,	c 181	17	68.0	537	3	US-09-864-761-20582	Sequence 20582, A
c 109	17.2	68.8	606	3	US-09-974-300-6658	Sequence 6658, Ap	c 182	17	68.0	548	3	US-09-864-761-12453	Sequence 12453, A
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c 111	17	68.0	26	9	US-10-829-474-36	Sequence 36, Appl	c 184	17	68.0	743	8	US-10-839-729-21	Sequence 21, Appl
c 112	17	68.0	26	9	US-10-829-474-37	Sequence 37, Appl	c 185	17	68.0	745	8	US-10-489-136-10	Sequence 10, Appl
c 113	17	68.0	66	6	US-10-157-305A-54	Sequence 54, Appl	c 186	17	68.0	1575	6	US-10-369-493-32283	Sequence 32283, A
c 114	17	68.0	66	6	US-10-157-305A-57	Sequence 57, Appl	c 187	17	68.0	1604	8	US-10-425-115-82479	Sequence 82479, A
c 115	17	68.0	66	6	US-10-157-391-54	Sequence 54, Appl	c 188	17	68.0	1782	8	US-10-800-023-37	Sequence 37, Appl
c 116	17	68.0	66	6	US-10-157-391-57	Sequence 57, Appl	c 189	17	68.0	1823	5	US-10-194-163-435	Sequence 435, App
c 117	17	68.0	66	6	US-10-157-096-54	Sequence 54, Appl	c 190	17	68.0	1950	3	US-09-864-761-3816	Sequence 3816, Ap
c 118	17	68.0	66	6	US-10-157-086-57	Sequence 57, Appl	c 191	17	68.0	2076	3	US-09-884-586A-3	Sequence 3, Appli
c 119	17	68.0	66	6	US-10-157-302-54	Sequence 54, Appl	c 192	17	68.0	2337	3	US-09-938-842A-1123	Sequence 1123, Ap
c 120	17	68.0	66	6	US-10-157-302-57	Sequence 57, Appl	c 193	17	68.0	2337	3	US-09-938-842A-1123	Sequence 1123, Ap
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c 125	17	68.0	66	6	US-10-154-951B-54	Sequence 54, Appl	c 198	17	68.0	2544	6	US-10-157-215A-3	Sequence 3, Appli
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c 130	17	68.0	66	6	US-10-157-147-57	Sequence 57, Appl	c 203	17	68.0	2544	6	US-10-157-166-3	Sequence 3, Appli
c 131	17	68.0	66	6	US-10-157-166-54	Sequence 54, Appl	c 204	17	68.0	2544	6	US-10-156-902-3	Sequence 3, Appli
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c 140	17	68.0	66	6	US-10-156-792A-57	Sequence 57, Appl	c 213	17	68.0	2544	6	US-10-157-418A-3	Sequence 3, Appli
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c 142	17	68.0	66	6	US-10-157-213-57	Sequence 57, Appl	c 215	17	68.0	2544	6	US-10-157-491-3	Sequence 3, Appli
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c 145	17	68.0	66	6	US-10-157-073-54	Sequence 54, Appl	c 218	17	68.0	2785	3	US-09-764-891-7798	Sequence 7798, Ap
c 146	17	68.0	66	6	US-10-157-073-57	Sequence 57, Appl	c 219	17	68.0	4203	3	US-09-764-891-7800	Sequence 7800, Ap
c 147	17	68.0	66	6	US-10-157-106A-54	Sequence 54, Appl	c 220	17	68.0	4203	3	US-09-764-891-7801	Sequence 7801, Ap
c 148	17	68.0	66	6	US-10-157-106A-57	Sequence 57, Appl	c 221	17	68.0	49646	9	US-10-915-740A-5	Sequence 5, Appli
c 149	17	68.0	66	6	US-10-157-320A-54	Sequence 54, Appl	c 222	17	68.0	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap
c 150	17	68.0	66	6	US-10-157-320A-57	Sequence 57, Appl	c 223	17	68.0	9025608	6	US-10-156-761-1	Sequence 1, Appli
c 151	17	68.0	66	6	US-10-157-418A-54	Sequence 54, Appl	c 224	16.8	67.2	285	3	US-09-294-093B-4801	Sequence 4801, Ap
c 152	17	68.0	66	6	US-10-157-418A-57	Sequence 57, Appl	c 225	16.8	67.2	294	3	US-09-728-445-347	Sequence 347, App
c 153	17	68.0	66	6	US-10-157-171-54	Sequence 54, Appl	c 226	16.8	67.2	294	9	US-10-964-549-347	Sequence 347, App
c 154	17	68.0	66	6	US-10-157-171-57	Sequence 57, Appl	c 227	16.8	67.2	398	8	US-10-357-930-649	Sequence 649, App
c 155	17	68.0	66	6	US-10-157-491-54	Sequence 54, Appl	c 228	16.8	67.2	398	8	US-10-357-930-9818	Sequence 9818, Ap
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c 157	17	68.0	66	6	US-10-157-317-54	Sequence 54, Appl	c 230	16.8	67.2	450	8	US-10-357-930-39988	Sequence 39988, A
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c 159	17	68.0	66	6	US-10-157-339-54	Sequence 54, Appl	c 232	16.8	67.2	787	7	US-10-151-803-228	Sequence 228, App
c 160	17	68.0	66	6	US-10-157-339-57	Sequence 57, Appl	c 233	16.8	67.2	787	7	US-10-152-319A-1963	Sequence 1963, Ap
c 161	17	68.0	69	9	US-10-295-787D-30	Sequence 30, Appli	c 234	16.8	67.2	1130	7	US-10-425-114-5	Sequence 5, Appli
c 162	17	68.0	70	9	US-10-295-787D-2	Sequence 2, Appli	c 235	16.8	67.2	1192	7	US-10-425-114-18401	Sequence 18401, A
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c 166	17	68.0	70	9	US-10-295-787D-113	Sequence 113, App	c 239	16.8	67.2	1891	6	US-10-316-253-108	Sequence 108, App
c 167	17	68.0	73	9	US-10-295-787D-1	Sequence 1, Appli	c 240	16.8	67.2	180227	7	US-10-322-281-308	Sequence 308, App
c 168	17	68.0	74	9	US-10-295-787D-80	Sequence 80, Appl	c 241	16.6	66.4	272	8	US-10-425-115-180307	Sequence 180307, A
c 169	17	68.0	236	9	US-10-760-048-55	Sequence 55, Appl	c 242	16.6	66.4	297	3	US-09-823-887C-2	Sequence 2, Appli

C 243	16.6	66.4	415	3	US-09-864-761-18894	Sequence 18894, A	C 316	16	64.0	25	10	US-11-036-317-630624	Sequence 630624,
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C 250	16.6	66.4	820	7	US-10-260-238-4789	Sequence 4789, Ap	C 323	16	64.0	307	5	US-10-198-846-12777	Sequence 12777, A
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C 253	16.6	66.4	1762	9	US-10-450-763-22719	Sequence 22719, A	C 326	16	64.0	339	7	US-10-437-963-12819	Sequence 12819, A
C 254	16.6	66.4	1878	7	US-10-282-132A-13742	Sequence 13742, A	C 327	16	64.0	369	7	US-10-282-122A-33432	Sequence 33432, A
C 255	16.6	66.4	1894	6	US-10-094-749-1535	Sequence 1535, Ap	C 328	16	64.0	390	9	US-10-631-467-250	Sequence 250, App
C 256	16.6	66.4	2358	9	US-10-450-763-22717	Sequence 22717, A	C 329	16	64.0	419	8	US-10-437-963-61126	Sequence 61126, A
C 257	16.6	66.4	2746	6	US-10-108-260A-22334	Sequence 22334, Ap	C 330	16	64.0	430	8	US-10-357-930-33928	Sequence 33928, A
C 258	16.6	66.4	3335	8	US-10-739-930-314	Sequence 314, App	C 331	16	64.0	430	8	US-10-357-930-42805	Sequence 42805, A
C 259	16.6	66.4	3342	5	US-10-016-634A-52	Sequence 52, Appli	C 332	16	64.0	449	7	US-10-424-599-51763	Sequence 51763, A
C 260	16.6	66.4	12104	6	US-09-764-877-2761	Sequence 2761, Ap	C 333	16	64.0	495	5	US-10-106-698-524	Sequence 524, App
C 261	16.6	66.4	12104	6	US-10-242-515-2761	Sequence 2761, Ap	C 334	16	64.0	506	5	US-10-027-632-265404	Sequence 265404, A
C 262	16.6	66.4	23229	6	US-10-017-161-2003	Sequence 2003, Ap	C 335	16	64.0	530	6	US-10-027-632-265404	Sequence 265404, A
C 263	16.6	66.4	23229	6	US-10-292-798-1649	Sequence 1649, Ap	C 336	16	64.0	530	6	US-10-357-930-15891	Sequence 15891, A
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C 266	16.6	65.6	517	4	US-09-925-065A-814933	Sequence 814933, A	C 339	16	64.0	559	5	US-10-027-632-221365	Sequence 221365, A
C 267	16.4	65.6	2061	7	US-10-282-132A-41544	Sequence 41544, A	C 340	16	64.0	559	5	US-10-027-632-221365	Sequence 221365, A
C 268	16.4	65.6	96598	7	US-10-394-948-25	Sequence 25, Appli	C 341	16	64.0	638	4	US-09-925-065A-88728	Sequence 88728, A
C 269	16.4	65.6	96598	7	US-10-052-482-115	Sequence 115, App	C 342	16	64.0	738	7	US-10-322-281-640	Sequence 640, App
C 270	16.4	65.6	2731748	7	US-10-297-465A-1	Sequence 1, Appli	C 343	16	64.0	561	3	US-09-918-995-28616	Sequence 28616, A
C 271	16.2	64.8	274	6	US-10-393-840-854	Sequence 854, App	C 344	16	64.0	593	4	US-09-925-065A-154453	Sequence 154453, A
C 272	16.2	64.8	288	7	US-10-437-963-24655	Sequence 24655, A	C 345	16	64.0	596	9	US-10-450-763-10679	Sequence 10679, A
C 273	16.2	64.8	323	6	US-10-393-840-812	Sequence 812, App	C 346	16	64.0	618	8	US-10-357-930-45719	Sequence 45719, A
C 274	16.2	64.8	359	6	US-10-393-840-851	Sequence 851, App	C 347	16	64.0	638	4	US-09-925-065A-88728	Sequence 88728, A
C 275	16.2	64.8	400	6	US-10-393-840-774	Sequence 774, App	C 348	16	64.0	738	7	US-10-322-281-640	Sequence 640, App
C 276	16.2	64.8	403	6	US-10-393-840-773	Sequence 773, App	C 349	16	64.0	778	8	US-10-425-115-63943	Sequence 63943, A
C 277	16.2	64.8	412	3	US-09-960-352-11235	Sequence 11235, A	C 350	16	64.0	820	7	US-10-260-238-4789	Sequence 4789, Ap
C 278	16.2	64.8	417	6	US-10-393-840-848	Sequence 848, App	C 351	16	64.0	828	7	US-10-282-122A-6927	Sequence 6927, Ap
C 279	16.2	64.8	430	6	US-10-393-840-813	Sequence 813, App	C 352	16	64.0	918	5	US-10-198-846-5399	Sequence 5399, Ap
C 280	16.2	64.8	442	3	US-09-918-995-5137	Sequence 5137, App	C 353	16	64.0	941	9	US-10-450-763-15002	Sequence 15002, A
C 281	16.2	64.8	460	6	US-10-393-840-822	Sequence 822, App	C 354	16	64.0	942	9	US-10-302-172-300	Sequence 300, App
C 282	16.2	64.8	463	3	US-09-732-627A-1531	Sequence 1531, Ap	C 355	16	64.0	950	3	US-09-974-300-1143	Sequence 1143, Ap
C 283	16.2	64.8	477	4	US-09-925-065A-500218	Sequence 500218, A	C 356	16	64.0	960	3	US-09-974-300-1086	Sequence 1086, Ap
C 284	16.2	64.8	508	5	US-10-194-163-301	Sequence 301, App	C 357	16	64.0	975	7	US-10-282-122A-39509	Sequence 39509, A
C 285	16.2	64.8	524	4	US-09-925-065A-418795	Sequence 418795, A	C 358	16	64.0	1004	7	US-10-282-122A-36877	Sequence 36877, A
C 286	16.2	64.8	524	4	US-09-925-065A-418796	Sequence 418796, A	C 359	16	64.0	1098	3	US-09-954-456-740	Sequence 740, App
C 287	16.2	64.8	524	4	US-09-925-065A-418797	Sequence 418797, A	C 360	16	64.0	1098	5	US-10-198-846-5485	Sequence 5485, Ap
C 288	16.2	64.8	527	4	US-09-925-065A-606466	Sequence 606466, A	C 361	16	64.0	1098	9	US-10-843-641A-3767	Sequence 3767, Ap
C 289	16.2	64.8	593	4	US-09-925-065A-404208	Sequence 404208, A	C 362	16	64.0	1144	8	US-10-856-499-154	Sequence 154, App
C 290	16.2	64.8	593	4	US-09-925-065A-404209	Sequence 404209, A	C 363	16	64.0	1149	10	US-11-097-143-18662	Sequence 18662, A
C 291	16.2	64.8	599	9	US-10-972-079-9670	Sequence 9670, Ap	C 364	16	64.0	1157	9	US-10-450-763-17882	Sequence 17882, A
C 292	16.2	64.8	599	9	US-10-972-079-9671	Sequence 9671, Ap	C 365	16	64.0	1159	3	US-09-891-735-1	Sequence 1, Appli
C 293	16.2	64.8	600	9	US-10-972-079-9672	Sequence 9672, Ap	C 366	16	64.0	1233	6	US-10-369-493-46565	Sequence 46565, A
C 294	16.2	64.8	754	3	US-10-424-599-131436	Sequence 131436, A	C 367	16	64.0	1242	7	US-10-434-599-27799	Sequence 27799, A
C 295	16.2	64.8	1233	3	US-09-925-298-256	Sequence 256, App	C 368	16	64.0	1346	9	US-10-450-763-17919	Sequence 17919, A
C 296	16.2	64.8	1233	5	US-10-102-806-256	Sequence 256, App	C 369	16	64.0	1376	10	US-11-097-143-2627	Sequence 2627, Ap
C 297	16.2	64.8	1254	8	US-10-484-788-13	Sequence 13, Appli	C 370	16	64.0	1417	7	US-10-282-122A-24031	Sequence 24031, A
C 298	16.2	64.8	1317	9	US-10-492-782-1	Sequence 1, Appli	C 371	16	64.0	1629	10	US-11-097-143-23900	Sequence 23900, A
C 299	16.2	64.8	1473	3	US-09-815-242-5960	Sequence 5960, Ap	C 372	16	64.0	1649	7	US-10-425-114-16108	Sequence 16108, A
C 300	16.2	64.8	1473	6	US-10-369-493-24407	Sequence 24407, A	C 373	16	64.0	1734	5	US-10-198-846-10103	Sequence 10103, A
C 301	16.2	64.8	1473	7	US-10-282-122A-20254	Sequence 20254, A	C 374	16	64.0	1734	8	US-10-357-930-30216	Sequence 30216, A
C 302	16.2	64.8	1697	9	US-10-492-782-43	Sequence 43, Appli	C 375	16	64.0	1822	8	US-10-425-115-118423	Sequence 118423, A
C 303	16.2	64.8	1733	6	US-10-397-635-13	Sequence 13, Appli	C 376	16	64.0	2015	6	US-10-369-493-35038	Sequence 35038, A
C 304	16.2	64.8	2442	7	US-10-437-963-40322	Sequence 40322, A	C 377	16	64.0	2101	9	US-10-450-763-24645	Sequence 24645, A
C 305	16.2	64.8	3313	5	US-10-027-632-115534	Sequence 115534, A	C 378	16	64.0	2322	9	US-10-450-763-28905	Sequence 28905, A
C 306	16.2	64.8	3313	6	US-10-027-632-115534	Sequence 115534, A	C 379	16	64.0	2322	9	US-10-450-763-24813	Sequence 24813, A
C 307	16.2	64.8	3391	3	US-09-968-007A-990	Sequence 990, App	C 380	16	64.0	2326	9	US-10-369-493-24645	Sequence 24645, A
C 308	16.2	64.8	3391	9	US-10-843-641A-7460	Sequence 7460, App	C 381	16	64.0	2346	6	US-10-369-493-24645	Sequence 24645, A
C 309	16.2	64.8	3994	7	US-10-764-425-20	Sequence 20, Appli	C 382	16	64.0	2415	7	US-10-282-122A-18994	Sequence 18994, A
C 310	16.2	64.8	4253	8	US-10-723-860-5312	Sequence 5312, Ap	C 383	16	64.0	2577	10	US-11-097-143-36076	Sequence 36076, A
C 311	16.2	64.8	5824	10	US-11-097-143-8608	Sequence 8608, Ap	C 384	16	64.0	2766	10	US-11-097-143-37163	Sequence 37163, A
C 312	16.2	64.8	7513	3	US-09-880-107-3869	Sequence 3869, Ap	C 385	16	64.0	2940	5	US-10-171-229-1	Sequence 1, Appli
C 313	16	64.0	24	9	US-10-829-474-32	Sequence 32, Appli	C 386	16	64.0	2940	6	US-10-429-398-1	Sequence 1, Appli
C 314	16	64.0	24	9	US-10-829-474-33	Sequence 33, Appli	C 387	16	64.0	2949	5	US-10-114-893-59	Sequence 59, Appli
C 315	16	64.0	25	10	US-11-036-317-99351	Sequence 99351, A	C 388	16	64.0	3149	10	US-11-097-143-18661	Sequence 18661, A


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RESULT 2
US-10-829-474-46
; Sequence 46, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-46
Query Match          100.0%; Score 25; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 3
US-10-829-474-47
; Sequence 47, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-47
Query Match          100.0%; Score 25; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||
Db 2 TCCGCTGCAGAGTTGCCCGTTACGA 26

RESULT 4
US-10-295-787D-27
; Sequence 27, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 70
; TYPE: DNA
; ORGANISM: echovirus 8
; CURRENT APPLICATION NUMBER: US/10/295,787D
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; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Echovirus 7
US-10-295-787D-27
Query Match          100.0%; Score 25; DB 9; Length 69;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 5
US-10-295-787D-6
; Sequence 6, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 70
; TYPE: DNA
; ORGANISM: echovirus 30
US-10-295-787D-6
Query Match          100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 6
US-10-295-787D-7
; Sequence 7, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 70
; TYPE: DNA
; ORGANISM: echovirus 8
; CURRENT APPLICATION NUMBER: US/10/295,787D
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RESULT 9
US-10-295-787D-14
; Sequence 14, Application US/102955787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie virus B2
US-10-295-787D-14

Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      TCCGCTGCGAGGTTGCCCGTTACGA      25
Db      1      TCCGCTGCGAGGTTGCCCGTTACGA      25

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RESULT 10
US-10-295-787D-16
; Sequence 16, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie Virus B5
US-10-295-787D-16

Query Match          100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
US-10-295-787D-18
; Sequence 18, Application US/10295787D
; Publication NO. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu

```
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie Virus A9
US-10-295-787D-18

Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 12
US-10-295-787D-19
; Sequence 19, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie Virus B4
US-10-295-787D-19

Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 13
US-10-295-787D-20
; Sequence 20, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; NUMBER OF SEQ ID NOS: 113
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Ev Stuttgart Virus
US-10-295-787D-20

Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 14
US-10-295-787D-22
; Sequence 22, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie
US-10-295-787D-22

Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 15
US-10-295-787D-35
; Sequence 35, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie b1
US-10-295-787D-35

Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 16

US-10-760-048-53/c

; Sequence 53, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 53
; LENGTH: 107
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-53

Query Match 100.0%; Score 25; DB 9; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
| | | | | | | | | | | | | | | | | | | | | |
Db 72 TCCGCTGCAGAGTTGCCCGTTACGA 48

RESULT 17

US-10-760-048-18/c

; Sequence 18, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 126
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-18

Query Match 100.0%; Score 25; DB 9; Length 126;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
| | | | | | | | | | | | | | | | | | | | | |
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 18

US-10-760-048-32/c

; Sequence 32, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-32

Query Match 100.0%; Score 25; DB 9; Length 237;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
| | | | | | | | | | | | | | | | | | | | | |
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 19

US-10-760-048-13/c

; Sequence 13, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-13

Query Match 100.0%; Score 25; DB 9; Length 238;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
| | | | | | | | | | | | | | | | | | | | | |
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 20

US-10-760-048-14/c

; Sequence 14, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048

; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-14

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 21

US-10-760-048-15/c
; Sequence 15, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-15

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 22

US-10-760-048-19/c
; Sequence 19, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-19

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 23

US-10-760-048-22/c
; Sequence 22, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-22

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 24

US-10-760-048-24/c
; Sequence 24, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-24

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 25

US-10-760-048-25/c
; Sequence 25, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 25
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-25

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 26

US-10-760-048-26/c
; Sequence 26, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-26

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 27

US-10-760-048-27/c
; Sequence 27, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY

; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 27
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-27

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 28

US-10-760-048-28/c
; Sequence 28, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 28
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-28

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 29

US-10-760-048-29/c
; Sequence 29, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 29

```

Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGATTGCCCGTTACGA 25
Db 75 TCCGCTGCAGATTGCCCGTTACGA 51

RESULT 32
US-10-760-048-42/c
; Sequence 42, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 42
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-42

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGATTGCCCGTTACGA 25
Db 75 TCCGCTGCAGATTGCCCGTTACGA 51

RESULT 33
US-10-760-048-43/c
; Sequence 43, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 43
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-43

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGATTGCCCGTTACGA 25
Db 75 TCCGCTGCAGATTGCCCGTTACGA 51

RESULT 34
```

US-10-760-048-46/c
; Sequence 46, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 46
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-46

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 35

US-10-760-048-47/c
; Sequence 47, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 47
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-47

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 36

US-10-760-048-48/c
; Sequence 48, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS

; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 48
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-48

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 37

US-10-760-048-54/c
; Sequence 54, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 54
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-54

Query Match 100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 38

US-10-760-048-67/c
; Sequence 67, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 67
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-760-048-67

```
Query Match      100.0%; Score 25; DB 9; Length 660;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 457 TCCGCTGCAGAGTTGCCCGTTACGA 433

RESULT 39
US-10-614-283-1/c
; Sequence 1, Application US/10614283
; Publication No. US20050112095A1
; GENERAL INFORMATION:
; APPLICANT: HSU, TSU-AN
; APPLICANT: WU, TZONG-YUAN
; APPLICANT: LEE, JIN-CHING
; TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 08842.0002-00000
; CURRENT APPLICATION NUMBER: US/10/614,283
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/394,269
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 1
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-10-614-283-1

Query Match      100.0%; Score 25; DB 9; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 504 TCCGCTGCAGAGTTGCCCGTTACGA 480

RESULT 40
US-10-136-819-7/c
; Sequence 7, Application US/10136819
; Publication No. US20030166593A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific gen
; FILE REFERENCE: 6627-PA1198
; CURRENT APPLICATION NUMBER: US/10/136,819
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/287,423
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 7
; LENGTH: 7399
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-136-819-7

Query Match      100.0%; Score 25; DB 6; Length 7399;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 538 TCCGCTGCAGAGTTGCCCGTTACGA 514

RESULT 41
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US-10-829-474-42
; Sequence 42, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 42
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-42

Query Match      96.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24

RESULT 42
US-10-829-474-43
; Sequence 43, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 43
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-43

Query Match      96.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24
    |||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACG 24

RESULT 43
US-10-295-787D-28
; Sequence 28, Application US/10295787D
; Publication No. US200502414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
```

US-10-295-78/D-15

; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: r = a or g
US-10-829-474-56

Query Match 95.2%; Score 23.8; DB 9; Length 26;
Best Local Similarity 88.0%; Pred. No. 0.16;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||:|||||:|||||
Db 1 TCCGCTGCGAGTTTCCCRTTACGA 25

RESULT 48

US-10-829-474-57
; Sequence 57, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA

; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: r = a or g
US-10-829-474-57

Query Match 95.2%; Score 23.8; DB 9; Length 26;
Best Local Similarity 88.0%; Pred. No. 0.16;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||:|||||:|||||
Db 2 TCCGCTGCGAGTTTCCCRTTACGA 26

RESULT 49

US-10-295-787D-21
; Sequence 21, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A

; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Echovirus 12
US-10-295-787D-21

Query Match 93.6%; Score 23.4; DB 9; Length 70;
Best Local Similarity 96.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||:|||||:|||||
Db 1 TCCGCTGCAGAGTTGCCCAATTACGA 25

RESULT 50

US-10-295-787D-23
; Sequence 23, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie A16
US-10-295-787D-23

Query Match 93.6%; Score 23.4; DB 9; Length 70;
Best Local Similarity 96.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||:|||||:|||||
Db 1 TCCGCTGCAGAGTTACCCGTTACGA 25

RESULT 51

US-10-295-787D-31
; Sequence 31, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 70
; TYPE: DNA

; ORGANISM: Ev sp virus
US-10-295-787D-31

Query Match 93.6%; Score 23.4; DB 9; Length 70;
Best Local Similarity 96.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 52

US-10-295-787D-112
; Sequence 112, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie virus B6
US-10-295-787D-112

Query Match 93.6%; Score 23.4; DB 9; Length 70;
Best Local Similarity 96.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 53

US-10-295-787D-17
; Sequence 17, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Echovirus 9
US-10-295-787D-17

Query Match 93.6%; Score 23.4; DB 9; Length 71;
Best Local Similarity 96.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||

Db 1 TCCGCTGCAGAGTTACCCGTTACGA 25

RESULT 54

US-10-295-787D-8
; Sequence 8, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Echovirus 3
US-10-295-787D-8

Query Match 93.6%; Score 23.4; DB 9; Length 75;
Best Local Similarity 96.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 6 TCCGCTGCAGAGTTACCCGTTACGA 30

RESULT 55

US-10-760-048-39/c
; Sequence 39, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 39
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-39

Query Match 93.6%; Score 23.4; DB 9; Length 117;
Best Local Similarity 96.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 56

US-10-760-048-40/c
; Sequence 40, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY

; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 40
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-40

Query Match 93.6%; Score 23.4; DB 9; Length 117;
Best Local Similarity 96.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 57
US-10-760-048-37/c
; Sequence 37, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-37

Query Match 93.6%; Score 23.4; DB 9; Length 236;
Best Local Similarity 96.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 58
US-10-760-048-49/c
; Sequence 49, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 49

; LENGTH: 236
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-49

Query Match 93.6%; Score 23.4; DB 9; Length 236;
Best Local Similarity 96.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 59
US-10-760-048-50/c
; Sequence 50, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 50
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-50

Query Match 93.6%; Score 23.4; DB 9; Length 236;
Best Local Similarity 96.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 60
US-10-760-048-51/c
; Sequence 51, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 51
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-51

Query Match 93.6%; Score 23.4; DB 9; Length 236;

Best Local Similarity 96.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 61

US-10-760-048-44/c
; Sequence 44, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-44

Query Match 93.6%; Score 23.4; DB 9; Length 237;
Best Local Similarity 96.0%; Pred. No. 0.24; Mismatches 1; Indels 0; Gaps 0;
Matches 24; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 62

US-10-760-048-45/c
; Sequence 45, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 45
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-45

Query Match 93.6%; Score 23.4; DB 9; Length 237;
Best Local Similarity 96.0%; Pred. No. 0.24; Mismatches 1; Indels 0; Gaps 0;
Matches 24; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 63

US-10-829-474-38

; Sequence 38, Application US/10829474

US-10-760-048-33/c
; Sequence 33, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 33
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-33

Query Match 93.6%; Score 23.4; DB 9; Length 238;
Best Local Similarity 96.0%; Pred. No. 0.24; Mismatches 1; Indels 0; Gaps 0;
Matches 24; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 64

US-10-332-123-55/c
; Sequence 55, Application US/10332123
; Publication No. US20040072239A1
; GENERAL INFORMATION:
; APPLICANT: RENAUD, Patricia
; APPLICANT: GUILLOT, Emmanuelle
; APPLICANT: MABILAT, Claude
; APPLICANT: VACHON, Carole
; APPLICANT: LACROIX, Bruno
; APPLICANT: VERNET, Guy
; APPLICANT: ARMAND, Marie-Astrid
; APPLICANT: LAFFAIRE, Philippe
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
; FILE REFERENCE: 114502
; CURRENT APPLICATION NUMBER: US/10/332,123
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: PCT/FR01/02191
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: FR00-08839
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Echovirus (X77708)
US-10-332-123-55

Query Match 93.6%; Score 23.4; DB 7; Length 525;
Best Local Similarity 96.0%; Pred. No. 0.24; Mismatches 1; Indels 0; Gaps 0;
Matches 24; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 475 TCCGCTGCAGAGTTGCCCGTTACGA 451

RESULT 65

US-10-829-474-38
; Sequence 38, Application US/10829474

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-41

Query Match          92.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCTGCAGAGTTGCCCGTTACG 24
    |||||
Db 1 CCGCTGCAGAGTTGCCCGTTACG 23
    |||||

RESULT 68
US-10-408-519-2/c
; Sequence 2, Application US/10408519
; Publication No. US20030228683A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Kan-Hung
; APPLICANT: Shih, Yu-Hau
; APPLICANT: Tsai, Chuan-Mei
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Hsiao, Hsiung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Wang, Shin-Hwan
; TITLE OF INVENTION: BIOMOLECULE-BOUND SUBSTRATES
; FILE REFERENCE: 12674-002002
; CURRENT APPLICATION NUMBER: US/10/408,519
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 09/522,417
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe from 5' ends of enterovirus genes
US-10-408-519-2

Query Match          92.0%; Score 23; DB 6; Length 58;
Best Local Similarity 80.0%; Pred. No. 0.39;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 52 TCCGCTGCAGAGTTGCCCGTTACGA 28
    |||||

RESULT 69
US-10-829-474-52
; Sequence 52, Application US/10829474
; Publication No. US2005023905A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVP
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)

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; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: r = a or g
US-10-829-474-52

Query Match 91.2%; Score 22.8; DB 9; Length 24;
Best Local Similarity 87.5%; Pred. No. 0.5;
Matches 21; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
|||||:|||||:|||||
Db 1 CCGCTGCRGAGTTGCCCTTACGA 24

RESULT 70

US-10-829-474-53
; Sequence 53, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA

; NAME/KEY: misc feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: r = a or g
US-10-829-474-53

Query Match 91.2%; Score 22.8; DB 9; Length 24;
Best Local Similarity 87.5%; Pred. No. 0.5;
Matches 21; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24
|||||:|||||:|||||
Db 1 TCCGCTGCRGAGTTGCCCTTACG 24

RESULT 71

US-10-366-823-5/c
; Sequence 5, Application US/10366823
; Publication No. US20030211526A1
; GENERAL INFORMATION:
; APPLICANT: Juang, Jyh-Iyh
; APPLICANT: Hsiung, Chao Agnes
; APPLICANT: Lin, Chung-Yen
; TITLE OF INVENTION: CROSS-SPECIES NUCLEIC ACID PROBES
; FILE REFERENCE: 12563-006001
; CURRENT APPLICATION NUMBER: US/10/366,823

; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,541
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-10-366-823-5

Query Match 90.4%; Score 22.6; DB 6; Length 62;
Best Local Similarity 76.0%; Pred. No. 0.61;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||:|||||:|||||
Db 27 TCCGTCRCGASITGCCSRTTACGA 3

RESULT 72

US-10-295-787D-13
; Sequence 13, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN-015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 70
; TYPE: DNA
; ORGANISM: echovirus 2
US-10-295-787D-13

Query Match 89.6%; Score 22.4; DB 9; Length 70;
Best Local Similarity 95.8%; Pred. No. 0.76;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
|||||:|||||:|||||
Db 1 CCGCTGCAGAGTTGCCCTTACGA 24

RESULT 73

US-10-829-474-44
; Sequence 44, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA

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; LOCATION: (8)..(8)
; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: r = a or g
US-10-829-474-51

Query Match      87.2%; Score 21.8; DB 9; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.5;
Matches 20; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACG 24
    |||||:||||:||||:||||
Db 1 CCGCTGCGAGTTRCCCRTTACG 23

RESULT 78
US-10-295-787D-26
; Sequence 26, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie virus b6
US-10-295-787D-26

Query Match      87.2%; Score 21.8; DB 9; Length 70;
Best Local Similarity 92.0%; Pred. No. 1.5;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||:||||:||||:||||
Db 1 TCCGCTGCGAGTTGCCCATACGA 25

RESULT 79
US-10-295-787D-29
; Sequence 29, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 70
; TYPE: DNA
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; ORGANISM: Echovirus 1
US-10-295-787D-29

Query Match      87.2%; Score 21.8; DB 9; Length 70;
Best Local Similarity 92.0%; Pred. No. 1.5;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||:||||:||||:||||
Db 1 TCCGCTGCAGAGTTACCCATTACGA 25

RESULT 80
US-10-760-048-52/c
; Sequence 52, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 52
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-52

Query Match      87.2%; Score 21.8; DB 9; Length 110;
Best Local Similarity 92.0%; Pred. No. 1.5;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||:||||:||||:||||
Db 75 TCCGCTGCAGAGTTACCCATTACGA 51

RESULT 81
US-10-760-048-41/c
; Sequence 41, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 41
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-41

Query Match      87.2%; Score 21.8; DB 9; Length 235;
Best Local Similarity 92.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||:||||:||||:||||
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Db 75 TCCGCTGCAGAGTTACCCATTACGA 51

RESULT 82

US-10-760-048-21/c
; Sequence 21, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-21

Query Match 87.2%; Score 21.8; DB 9; Length 237;
Best Local Similarity 92.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTACCCATTACGA 51

RESULT 83

US-10-760-048-23/c
; Sequence 23, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-23

Query Match 87.2%; Score 21.8; DB 9; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTCCCGTTACGA 51

RESULT 84

US-10-760-048-34/c
; Sequence 34, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY

; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 34
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-34

Query Match 87.2%; Score 21.8; DB 9; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTCCCGTTACGA 51

RESULT 85

US-10-760-048-35/c
; Sequence 35, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 35
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-35

Query Match 87.2%; Score 21.8; DB 9; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTCCCGTTACGA 51

RESULT 86

US-10-760-048-36/c
; Sequence 36, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36

; LENGTH: 238
; TYPE: DNA

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-36

Query Match 87.2%; Score 21.8; DB 9; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCGGAGTTGCCCATACGA 51

RESULT 87

US-10-829-474-40

; Sequence 40, Application US/10829474

; Publication No. US20050239055A1

; GENERAL INFORMATION:

; APPLICANT: Genetics & IVF

; APPLICANT: MARIANI, Brian D.

; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES

; FILE REFERENCE: 043956-0121

; CURRENT APPLICATION NUMBER: US/10/829,474

; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 40

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA

US-10-829-474-40

Query Match 84.0%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CGCTGCAGAGTTGCCCGTTAC 23

Db 1 CGCTGCAGAGTTGCCCGTTAC 21

RESULT 88

US-10-829-474-54

; Sequence 54, Application US/10829474

; Publication No. US20050239055A1

; GENERAL INFORMATION:

; APPLICANT: Genetics & IVF

; APPLICANT: MARIANI, Brian D.

; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES

; FILE REFERENCE: 043956-0121

; CURRENT APPLICATION NUMBER: US/10/829,474

; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 54

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (7)..(7)

; OTHER INFORMATION: r = a or g

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (13)..(13)

; OTHER INFORMATION: r = a or g

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (17)..(17)

; OTHER INFORMATION: r = a or g

US-10-829-474-54

Query Match 83.2%; Score 20.8; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 4.7;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CGCTGCAGAGTTGCCCGTTACG 24

Db 1 CGCTGCRGAGTTCCTTACG 22

RESULT 89

US-10-829-474-55

; Sequence 55, Application US/10829474

; Publication No. US20050239055A1

; GENERAL INFORMATION:

; APPLICANT: Genetics & IVF

; APPLICANT: MARIANI, Brian D.

; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES

; FILE REFERENCE: 043956-0121

; CURRENT APPLICATION NUMBER: US/10/829,474

; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 55

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (8)..(8)

; OTHER INFORMATION: r = a or g

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (14)..(14)

; OTHER INFORMATION: r = a or g

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (18)..(18)

; OTHER INFORMATION: r = a or g

US-10-829-474-55

Query Match 83.2%; Score 20.8; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 4.7;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CCGCTGCAGAGTTGCCCGTTAC 23

Db 1 CCGCTGCRGAGTTCCTTAC 22

RESULT 90

US-10-295-787D-24

; Sequence 24, Application US/10295787D

; Publication No. US2005020414A1

; GENERAL INFORMATION:

; APPLICANT: The Regents of The University of California

; APPLICANT: Jia, Xi Yu

; APPLICANT: Berger, Martina M

; APPLICANT: Tilles, Jeremiah G

; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE

; FILE REFERENCE: UCIVN--015A

; CURRENT APPLICATION NUMBER: US/10/295,787D

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/335,539

; PRIOR FILING DATE: 2001-11-15

; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Echovirus 5
US-10-295-787D-24

Query Match 83.2%; Score 20.8; DB 9; Length 69;
Best Local Similarity 91.7%; Pred. No. 4.6;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGCTGCAGAGTTCGCCGTTACGA 25
|||||
DB 1 CCGCTGCAGAGTTACCCATTACGA 24

RESULT 91

US-10-295-787D-25
; Sequence 25, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Porcine ev virus 9
US-10-295-787D-25

Query Match 83.2%; Score 20.8; DB 9; Length 70;
Best Local Similarity 91.7%; Pred. No. 4.6;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGCTGCAGAGTTCGCCGTTACGA 25
|||||
DB 1 CGGCCACAGAGTTCGCCGTTACGA 24

RESULT 92

US-10-295-787D-11
; Sequence 11, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 70
; TYPE: DNA
; ORGANISM: echovirus 25
US-10-295-787D-11

Query Match 80.8%; Score 20.2; DB 9; Length 70;

Best Local Similarity 88.0%; Pred. No. 8.9;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
|||||
DB 1 TCCGCCGACAGAGTTACCCATTACGA 25

RESULT 93

US-10-295-787D-111
; Sequence 111, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 111
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Echo virus 4
US-10-295-787D-111

Query Match 80.8%; Score 20.2; DB 9; Length 70;
Best Local Similarity 88.0%; Pred. No. 8.9;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
|||||
DB 1 TCCGCTGCAGAGTTACCCATTACGA 25

RESULT 94

US-10-760-048-38/c
; Sequence 38, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELDIER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 38
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-38

Query Match 80.8%; Score 20.2; DB 9; Length 238;
Best Local Similarity 88.0%; Pred. No. 8.7;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
|||||
DB 75 TCCGCTGCAGAGTTACCCATTACGA 51

RESULT 95

```

Query Match      72.8%; Score 18.2; DB 7; Length 1499;
Best Local Similarity 87.0%; Pred. No. 78;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTTCGCCGTTACGA 25
    |||||
Db 761 CGCTGCAGTGTTCGCGTTACCA 739

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RESULT 99

US-10-424-599-2070/c
; Sequence 2070, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 2070
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101874C.1
US-10-424-599-2070

Query Match 72.8%; Score 18.2; DB 7; Length 1645;
Best Local Similarity 87.0%; Pred. No. 78;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 905 CGCTGCAGTTGCCAGTTACCA 883

RESULT 100

US-09-738-626-2740
; Sequence 2740, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2740
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2740

Query Match 70.4%; Score 17.6; DB 3; Length 1182;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 116 CGCGCAAGTTGCTCGCTACGA 139

Search completed: March 9, 2006, 08:34:16
Job time : 741.243 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:06:59 ; Search time 250.485 Seconds
(without alignments)
665.178 Million cell updates/sec

Title: US-10-829-474-4

Perfect score: 25

Sequence: 1 tccgctgcagagttgccggttacga 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing 'first 500 summaries

Database :

1: N_Geneseq_21.*

2: geneseqn1980s.*

3: geneseqn1990s.*

4: geneseqn2000s.*

5: geneseqn2001as.*

6: geneseqn2001bs.*

7: geneseqn2002as.*

8: geneseqn2002bs.*

9: geneseqn2003as.*

10: geneseqn2003bs.*

11: geneseqn2003cs.*

12: geneseqn2004as.*

13: geneseqn2004bs.*

14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	69	12 ADP05526	Adp05526 Novel mic
2	25	100.0	70	12 ADP05510	Adp05510 Novel mic
3	25	100.0	70	12 ADP05515	Adp05515 Novel mic
4	25	100.0	70	12 ADP05513	Adp05513 Novel mic
5	25	100.0	70	12 ADP05521	Adp05521 Novel mic
6	25	100.0	70	12 ADP05504	Adp05504 Novel mic
7	25	100.0	70	12 ADP05507	Adp05507 Novel mic
8	25	100.0	70	12 ADP05517	Adp05517 Novel mic
9	25	100.0	70	12 ADP05534	Adp05534 Novel mic
10	25	100.0	70	12 ADP05503	Adp05503 Novel mic
11	25	100.0	70	12 ADP05519	Adp05519 Novel mic
12	25	100.0	70	12 ADP05518	Adp05518 Novel mic
13	25	100.0	105	14 AEB56814	Aeb56814 Human ech
14	25	100.0	107	14 AEB56869	Aeb56869 Human ech
15	25	100.0	126	14 AEB56779	Aeb56779 Viral 5'
16	25	100.0	180	14 AEB56834	Aeb56834 Human cox
17	25	100.0	198	14 AEB56858	Aeb56858 Human ech
18	25	100.0	198	14 AEB56863	Aeb56863 Human ech
19	25	100.0	237	14 AEB56848	Aeb56848 Human:cox

c 20	25	100.0	237	14	AEB56862	Aeb56862 Human ech
c 21	25	100.0	237	14	AEB56793	Aeb56793 Viral 5'
c 22	25	100.0	238	14	AEB56840	Aeb56840 Human cox
c 23	25	100.0	238	14	AEB56791	Aeb56791 Viral 5'
c 24	25	100.0	238	14	AEB56846	Aeb56846 Human cox
c 25	25	100.0	238	14	AEB56847	Aeb56847 Human cox
c 26	25	100.0	238	14	AEB56789	Aeb56789 Viral 5'
c 27	25	100.0	238	14	AEB56775	Aeb56775 Viral 5'
c 28	25	100.0	238	14	AEB56807	Aeb56807 Viral 5'
c 29	25	100.0	238	14	AEB56807	Aeb56807 Viral 5'
c 30	25	100.0	238	14	AEB56815	Aeb56815 Viral 5'
c 31	25	100.0	238	14	AEB56838	Aeb56838 Human cox
c 32	25	100.0	238	14	AEB56842	Aeb56842 Human cox
c 33	25	100.0	238	14	AEB56785	Aeb56785 Viral 5'
c 34	25	100.0	238	14	AEB56835	Aeb56835 Human cox
c 35	25	100.0	238	14	AEB56780	Aeb56780 Viral 5'
c 36	25	100.0	238	14	AEB56803	Aeb56803 Viral 5'
c 37	25	100.0	238	14	AEB56829	Aeb56829 Consensus
c 38	25	100.0	238	14	AEB56843	Aeb56843 Human cox
c 39	25	100.0	238	14	AEB56845	Aeb56845 Human cox
c 40	25	100.0	238	14	AEB56774	Aeb56774 Viral 5'
c 41	25	100.0	238	14	AEB56788	Aeb56788 Viral 5'
c 42	25	100.0	238	14	AEB56792	Aeb56792 Viral 5'
c 43	25	100.0	238	14	AEB56783	Aeb56783 Viral 5'
c 44	25	100.0	238	14	AEB56786	Aeb56786 Viral 5'
c 45	25	100.0	238	14	AEB56787	Aeb56787 Viral 5'
c 46	25	100.0	238	14	AEB56870	Aeb56870 Human cox
c 47	25	100.0	238	14	AEB56830	Aeb56830 Human cox
c 48	25	100.0	238	14	AEB56864	Aeb56864 Human ech
c 49	25	100.0	238	14	AEB56859	Aeb56859 Human ech
c 50	25	100.0	238	14	AEB56790	Aeb56790 Viral 5'
c 51	25	100.0	238	14	AEB56841	Aeb56841 Human cox
c 52	25	100.0	238	14	AEB56809	Aeb56809 Viral 5'
c 53	25	100.0	238	14	AEB56831	Aeb56831 Human cox
c 54	25	100.0	238	14	AEB56808	Aeb56808 Viral 5'
c 55	25	100.0	238	14	AEB56844	Aeb56844 Human cox
c 56	25	100.0	238	14	AEB56840	Aeb56840 Viral 5'
c 57	25	100.0	502	8	ABX12451	Abx12451 Coxackie
c 58	25	100.0	548	8	ABX12448	Abx12448 Coxackie
c 59	25	100.0	551	8	ABX12453	Abx12453 Coxackie
c 60	25	100.0	552	8	ABX12452	Abx12452 Coxackie
c 61	25	100.0	660	4	AAC85174	Aac85174 Coxackie
c 62	25	100.0	660	14	AEB56828	Aeb56828 Coxackie
c 63	25	100.0	709	14	AEA00424	Aea00424 Enterovir
c 64	25	100.0	745	4	AAC85152	Aac85152 Coxackie
c 65	25	100.0	810	12	ADP82873	Adp82873 Human cox
c 66	25	100.0	1560	13	ADU47469	Adu47469 Enterovir
c 67	25	100.0	7392	8	ABX12440	Abx12440 Diabetoge
c 68	25	100.0	7399	2	RAQ11816	Raq11816 RNA encod
c 69	25	100.0	7399	10	ABV76134	Abv76134 Coxackie
c 70	24	96.0	66	12	ADP05527	Adp05527 Novel mic
c 71	24	96.0	70	12	ADP05501	Adp05501 Novel mic
c 72	24	96.0	70	12	ADP05514	Adp05514 Novel mic
c 73	23.4	93.6	70	12	ADP05512	Adp05512 Novel mic
c 74	23.4	93.6	70	12	ADP05530	Adp05530 Novel mic
c 75	23.4	93.6	70	12	ADP05506	Adp05506 Novel mic
c 76	23.4	93.6	70	12	ADP05523	Adp05523 Novel mic
c 77	23.4	93.6	70	12	ADP05520	Adp05520 Novel mic
c 78	23.4	93.6	71	12	ADP05516	Adp05516 Novel mic
c 79	23.4	93.6	117	14	AEB56800	Aeb56800 Viral 5'
c 80	23.4	93.6	117	14	AEB56801	Aeb56801 Viral 5'
c 81	23.4	93.6	173	14	AEB56856	Aeb56856 Human ech
c 82	23.4	93.6	173	14	AEB56855	Aeb56855 Human ech
c 83	23.4	93.6	198	14	AEB56865	Aeb56865 Human ech
c 84	23.4	93.6	198	14	AEB56853	Aeb56853 Human ech
c 85	23.4	93.6	198	14	AEB56860	Aeb56860 Human ech
c 86	23.4	93.6	236	14	AEB56811	Aeb56811 Viral 5'
c 87	23.4	93.6	236	14	AEB56810	Aeb56810 Viral 5'
c 88	23.4	93.6	236	14	AEB56812	Aeb56812 Viral 5'
c 89	23.4	93.6	236	14	AEB56798	Aeb56798 Viral 5'
c 90	23.4	93.6	237	14	AEB56805	Aeb56805 Viral 5'
c 91	23.4	93.6	237	14	AEB56806	Aeb56806 Viral 5'
c 92	23.4	93.6	237	14	AEB56861	Aeb56861 Human ech

C 93	23.4	93.6	238	14	AEBS6849	Aeb56849 Human cox	166	17	68.0	66	10	ADG25387	Adg25387 Chromosom
C 94	23.4	93.6	238	14	AEBS6794	Aeb56794 Viral 5'	167	17	68.0	66	10	ADG25390	Adg25390 Chromosom
C 95	23.4	93.6	238	14	AEBS6867	Aeb56867 Human ech	168	17	68.0	66	10	ADJ47786	Adj47786 E. coli f
C 96	23.4	93.6	238	14	AEBS6866	Aeb56866 Human ech	169	17	68.0	66	10	ADJ47789	Adj47789 E. coli f
C 97	23.4	93.6	525	6	ABL53113	Ab153113 Micro-org	170	17	68.0	66	10	ADJ61978	Adj61978 Novel min
C 98	23.4	93.6	646	4	AAC85113	Aac85113 Echo viru	171	17	68.0	66	10	ADJ61981	Adj61981 Novel min
C 99	23.4	93.6	7400	3	AZ98719	Aaz98719 Swine ves	172	17	68.0	66	11	ADP70556	Adp70556 Minicell
C 100	23.4	93.6	7400	3	AZ98717	Aaz98717 Swine ves	173	17	68.0	66	11	ADP70553	Adp70553 Minicell
C 101	23.4	93.6	7400	3	AZ98718	Aaz98718 Swine ves	174	17	68.0	66	12	ADP56223	Adp56223 E. coli f
C 102	23.4	93.6	7400	3	AAZ29863	Aaz29863 Swine ves	175	17	68.0	66	12	ADP56220	Adp56220 E. coli f
C 103	23.4	93.6	7421	3	AAZ98720	Aaz98720 Swine ves	176	17	68.0	66	12	ADG43251	Adg43251 E. coli f
C 104	23	92.0	33	8	ACD26710	Acd26710 Enterovir	177	17	68.0	66	12	ADG43248	Adg43248 E. coli f
C 105	23	92.0	33	13	ADU47463	Adu47463 p2 probe	178	17	68.0	66	12	ADG43508	Adg43508 E. coli f
C 106	22.6	90.4	62	12	AECK6744	Aek6744 Picornavi	179	17	68.0	66	12	ADG43505	Adg43505 E. coli f
C 107	22.6	90.4	62	14	AEC07516	Aec07516 Picornavi	180	17	68.0	66	12	ADG68569	Adg68569 E. coli f
C 108	22.4	89.6	70	12	ADP05511	Adp05511 Novel mic	181	17	68.0	66	12	ADG68572	Adg68572 E. coli f
C 109	21.8	87.2	70	12	ADP05525	Adp05525 Novel mic	182	17	68.0	66	12	ADH56709	Adh56709 Primer to
C 110	21.8	87.2	70	12	ADP05528	Adp05528 Novel mic	183	17	68.0	66	12	ADH56712	Adh56712 Primer to
C 111	21.8	87.2	106	14	AEBS6868	Aeb56868 Human ech	184	17	68.0	66	12	ADI12801	Adi12801 Primer to
C 112	21.8	87.2	110	14	AEBS6813	Aeb56813 Viral 5'	185	17	68.0	66	12	ADI12804	Adi12804 Primer to
C 113	21.8	87.2	235	14	AEBS6802	Aeb56802 Viral 5'	186	17	68.0	66	12	ADI27706	Adi27706 Primer to
C 114	21.8	87.2	237	14	AEBS6837	Aeb56837 Human cox	187	17	68.0	66	12	ADI27703	Adi27703 Primer to
C 115	21.8	87.2	237	14	AEBS6857	Aeb56857 Human ech	188	17	68.0	66	12	ADI33772	Adi33772 E. coli f
C 116	21.8	87.2	237	14	AEBS6782	Aeb56782 Viral 5'	189	17	68.0	66	12	ADI33775	Adi33775 E. coli f
C 117	21.8	87.2	238	14	AEBS6850	Aeb56850 Human cox	190	17	68.0	66	12	ADK51506	Adk51506 Primer to
C 118	21.8	87.2	238	14	AEBS6839	Aeb56839 Human cox	191	17	68.0	66	12	ADK51509	Adk51509 Primer to
C 119	21.8	87.2	238	14	AEBS6797	Aeb56797 Viral 5'	192	17	68.0	66	12	ADM17991	Adm17991 E. coli f
C 120	21.8	87.2	238	14	AEBS6851	Aeb56851 Human cox	193	17	68.0	66	12	ADM17988	Adm17988 E. coli f
C 121	21.8	87.2	238	14	AEBS6852	Aeb56852 Human cox	194	17	68.0	66	12	ADL82586	Adl82586 Primer to
C 122	21.8	87.2	238	14	AEBS6784	Aeb56784 Viral 5'	195	17	68.0	66	12	ADL82589	Adl82589 Primer to
C 123	21.8	87.2	238	14	AEBS6795	Aeb56795 Viral 5'	196	17	68.0	66	12	ADM46224	Adm46224 Primer to
C 124	21.8	87.2	238	14	AEBS6796	Aeb56796 Viral 5'	197	17	68.0	66	12	ADM46227	Adm46227 Primer to
C 125	21.8	87.2	654	4	AAC85173	Aac85173 Coxsackie	198	17	68.0	69	12	ADP05529	Adp05529 Novel mic
C 126	20.8	83.2	69	12	ADP05523	Adp05523 Novel mic	C 199	17	68.0	70	2	AAV58283	Av58283 Type 3 Sa
C 127	20.8	83.2	70	12	ADP05524	Adp05524 Novel mic	200	17	68.0	70	12	ADP05500	Adp05500 Novel mic
C 128	20.2	80.8	70	12	ADP05505	Adp05505 Novel mic	201	17	68.0	70	12	ADP05499	Adp05499 Novel mic
C 129	20.2	80.8	70	12	ADP05509	Adp05509 Novel mic	202	17	68.0	70	12	ADP05502	Adp05502 Novel mic
C 130	20.2	80.8	198	14	AEBS6854	Aeb56854 Human ech	203	17	68.0	70	12	ADP05497	Adp05497 Novel mic
C 131	20.2	80.8	238	14	AEBS6799	Aeb56799 Viral 5'	204	17	68.0	70	12	ADP05498	Adp05498 Novel mic
C 132	18.8	75.2	366	11	ACH94885	Ach94885 Klebsiell	205	17	68.0	70	12	ADP05496	Adp05496 Novel mic
C 133	18.6	74.4	238	14	AEBS6878	Aeb56878 Human pol	C 206	17	68.0	74	12	ADP05579	Adp05579 Novel mic
C 134	18.6	74.4	238	14	AEBS6823	Aeb56823 Viral 5'	C 207	17	68.0	176	3	AAZ58488	Aaz58488 Recombina
C 135	18.6	74.4	521	6	ABL53111	Ab153111 Micro-org	C 208	17	68.0	195	10	ABZ69931	Abz69931 Polioviru
C 136	18.4	73.6	497	8	ABX12446	Abx12446 Coxsackie	C 209	17	68.0	236	14	AEBS6816	Aeb56816 Viral 5'
C 137	18.2	72.8	1499	13	ADX15059	Adx15059 Plant ful	C 210	17	68.0	237	14	AEBS6879	Aeb56879 Human pol
C 138	18.2	72.8	110000	4	AA196883_03	Continuation (4 of	C 211	17	68.0	237	14	AEBS6881	Aeb56881 Human pol
C 139	17.6	70.4	1137	8	ACA01486	Aca01486 C. glutami	C 212	17	68.0	237	14	AEBS6827	Aeb56827 Viral 5'
C 140	17.6	70.4	1182	5	AAH67705	Aah67705 C. glutami	C 213	17	68.0	237	14	AEBS6875	Aeb56875 Human pol
C 141	17.6	70.4	2381	12	ADP71896	Adp71896 Renal tox	C 214	17	68.0	237	14	AEBS6876	Aeb56876 Human pol
C 142	17.6	70.4	2692	4	ABL18825	Ab118825 Drosophil	C 215	17	68.0	237	14	AEBS6880	Aeb56880 Human pol
C 143	17.6	70.4	3663	4	ABL17534	Ab117534 Drosophil	C 216	17	68.0	237	14	AEBS6825	Aeb56825 Viral 5'
C 144	17.6	70.4	6051	4	ABL18824	Ab118824 Drosophil	C 217	17	68.0	237	14	AEBS6818	Aeb56818 Viral 5'
C 145	17.6	70.4	6462	6	ABK83473	Abk83473 Human cdn	C 218	17	68.0	237	14	AEBS6873	Aeb56873 Human pol
C 146	17.6	70.4	6462	13	ADR52978	Adr52978 Drug ther	C 219	17	68.0	237	14	AEBS6817	Aeb56817 Viral 5'
C 147	17.6	70.4	34980	5	AAH68532	Aah68532 C. glutami	C 220	17	68.0	237	14	AEBS6820	Aeb56820 Viral 5'
C 148	17.4	69.6	919	2	AAV06125	Av06125 Viral inf	C 221	17	68.0	237	14	AEBS6871	Aeb56871 Human ent
C 149	17.4	69.6	919	12	ADJ74131	Adj74131 Rat cdna	C 222	17	68.0	237	14	AEBS6821	Aeb56821 Viral 5'
C 150	17.2	68.8	606	6	ABK79367	Abk79367 Bacillus	C 223	17	68.0	237	14	AEBS6872	Aeb56872 Human pol
C 151	17.2	68.8	824	2	ADR01831	Adr01831 A. gosseyp	C 224	17	68.0	237	14	AEBS6824	Aeb56824 Viral 5'
C 152	17	68.0	66	10	ADB89060	Adb89060 E. coli ft	C 225	17	68.0	238	14	AEBS6826	Aeb56826 Viral 5'
C 153	17	68.0	66	10	ADB89063	Adb89063 E. coli ft	C 226	17	68.0	238	14	AEBS6819	Aeb56819 Viral 5'
C 154	17	68.0	66	10	ADC24410	Adc24410 E. coli ft	C 227	17	68.0	238	14	AEBS6874	Aeb56874 Human pol
C 155	17	68.0	66	10	ADC24407	Adc24407 E. coli ft	C 228	17	68.0	238	14	AEBS6833	Aeb56833 Human cox
C 156	17	68.0	66	10	ADD67680	Add67680 E. coli f	C 229	17	68.0	238	14	AEBS6778	Aeb56778 Viral 5'
C 157	17	68.0	66	10	ADD67677	Add67677 E. coli f	C 230	17	68.0	238	14	AEBS6882	Aeb56882 Human pol
C 158	17	68.0	66	10	ADE10390	Ade10390 E. coli f	C 231	17	68.0	319	2	AAV28515	Aav28515 Phosphate
C 159	17	68.0	66	10	ADE10393	Ade10393 E. coli f	C 232	17	68.0	514	3	AAZ58487	Aaz58487 Polioviru
C 160	17	68.0	66	10	ADE11315	Ade11315 E. coli f	C 233	17	68.0	537	4	AAI23152	Aai23152 Probe #13
C 161	17	68.0	66	10	ADE11312	Ade11312 E. coli f	C 234	17	68.0	537	4	ABA68253	Aba68253 Human foe
C 162	17	68.0	66	10	ADE12490	Ade12490 E. coli f	C 235	17	68.0	537	4	AAI48468	Aai48468 Probe #17
C 163	17	68.0	66	10	ADE12493	Ade12493 E. coli f	C 236	17	68.0	537	4	ABA50309	Aba50309 Human bre
C 164	17	68.0	66	10	ADE12253	Ade12253 E. coli f	C 237	17	68.0	537	4	ABA35262	Aba35262 Probe #13
C 165	17	68.0	66	10	ADE12256	Ade12256 E. coli f	C 238	17	68.0	537	4	AAK42389	Aak42389 Human bon

C 239	17	68.0	537	4	AAK16630	Aak16630 Human bra	C 312	17	68.0	7431	2	AAQ30148	Aaq30148 Attenuate
C 240	17	68.0	537	4	ABSA1999	ABSA1999 Human liv	C 313	17	68.0	7432	2	AAQ22965	AAQ22965 True type
C 241	17	68.0	537	5	Aai10808	Aai10808 Probe #87	C 314	17	68.0	7440	1	AAQ20042	AAQ20042 Sequence
C 242	17	68.0	537	6	ABSA16444	ABSA16444 Human gen	C 315	17	68.0	7441	2	AAQ26152	AAQ26152 DNA sequ
C 243	17	68.0	548	4	ABA60784	ABA60784 Human foe	C 316	17	68.0	7873	8	ACC43138	ACC43138 Nucleotid
C 244	17	68.0	548	4	AAI40677	AAI40677 Probe #93	C 317	17	68.0	7925	12	ADP74702	ADP74702 Novel bic
C 245	17	68.0	548	4	AAK34960	AAK34960 Human bon	C 318	17	68.0	7943	8	ACC43139	ACC43139 Nucleotid
C 246	17	68.0	548	4	AAK09069	AAK09069 Human bra	C 319	17	68.0	8298	2	AAV18096	AAV18096 pMCDHAP
C 247	17	68.0	548	4	ABSA34715	ABSA34715 Human liv	C 320	17	68.0	10633	12	ADQ07660	ADQ07660 Viral vec
C 248	17	68.0	628	2	AAQ58715	AAQ58715 Polioviru	C 321	17	68.0	11326	2	AAV12373	AAV12373 Chimeric
C 249	17	68.0	628	2	AAQ58726	AAQ58726 Polioviru	C 322	17	68.0	11746	12	ADQ07659	ADQ07659 Viral vec
C 250	17	68.0	639	12	ADP74707	ADP74707 Novel bic	C 323	17	68.0	38246	12	ADQ07662	ADQ07662 Viral vec
C 251	17	68.0	743	14	ADM37919	ADM37919 Polioviru	C 324	17	68.0	40352	2	AAV02032	AAV02032 MAGS-B cl
C 252	17	68.0	745	8	ACC48197	ACC48197 Polioviru	C 325	17	68.0	49646	3	AAA81457	AAA81457 N. mening
C 253	17	68.0	1575	13	ADS56609	ADS56609 Bacterial	C 326	17	68.0	110000	3	AAA81490	AAA81490 .06
C 254	17	68.0	1782	14	ADV85656	ADV85656 Human Mel	C 327	17	68.0	349980	3	AAF21608	AAF21608 Neisseria
C 255	17	68.0	1866	2	AAQ76213	AAQ76213 Human tum	C 328	16.8	67.2	285	6	ABL75427	ABL75427 Corn taag
C 256	17	68.0	1866	2	ABQ76213	ABQ76213 Arabidops	C 329	16.8	67.2	294	6	ABSA6284	ABSA6284 Novel mur
C 257	17	68.0	1927	3	AAQ45906	AAQ45906 Arabidops	C 330	16.8	67.2	398	5	ABV00658	ABV00658 Human pro
C 258	17	68.0	1930	3	AAI13936	AAI13936 Probe #38	C 331	16.8	67.2	399	5	ABV09827	ABV09827 Human pro
C 259	17	68.0	1950	4	ABSA5655	ABSA5655 Human foe	C 332	16.8	67.2	450	5	ABV31001	ABV31001 Human pro
C 260	17	68.0	1950	4	AAI35311	AAI35311 Probe #39	C 333	16.8	67.2	450	5	ABV39969	ABV39969 Human pro
C 261	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 334	16.8	67.2	787	6	ABK63521	ABK63521 Rat sequ
C 262	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 335	16.8	67.2	787	6	ABK63521	ABK63521 Rat sequ
C 263	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 336	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 264	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 337	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 265	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 338	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 266	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 339	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 267	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 340	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 268	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 341	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 269	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 342	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 270	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 343	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 271	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 344	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 272	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 345	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 273	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 346	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 274	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 347	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 275	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 348	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 276	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 349	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 277	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 350	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 278	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 351	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 279	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 352	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 280	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 353	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 281	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 354	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 282	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 355	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 283	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 356	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 284	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 357	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 285	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 358	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 286	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 359	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 287	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 360	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 288	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 361	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 289	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 362	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 290	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 363	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 291	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 364	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 292	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 365	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 293	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 366	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 294	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 367	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 295	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 368	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 296	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 369	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 297	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 370	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 298	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 371	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 299	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 372	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 300	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 373	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 301	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 374	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 302	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 375	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 303	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 376	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 304	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 377	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 305	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 378	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 306	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 379	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 307	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 380	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 308	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 381	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 309	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 382	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 310	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 383	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-
C 311	17	68.0	1950	4	ABSA5173	ABSA5173 Human bre	C 384	16.8	67.2	787	10	ADBS8686	ADBS8686 Toxicity-

C 385	16.6	66.4	12104	4	AAL36396	Aal36396 Human mus	16	64.0	738	13	ABD33481	Abd33481 Murine ca
C 386	16.6	66.4	12104	8	ABX59384	Abx59384 cDNA enco	16	64.0	738	14	ADZ13480	Adz13480 Murine ca
C 387	16.6	66.4	12104	12	ADJ30134	Adj30134 Human mus	16	64.0	757	4	AAL14285	Aal14285 Human bre
C 388	16.6	66.4	13226	14	ACL46669	Ac164669 M. xanthu	C 461	64.0	820	12	ADJ43789	Adj43789 Plant CDN
C 389	16.6	66.4	23229	10	ADC87196	Adc87196 Human GPC	C 462	64.0	828	8	ACA19057	AcA19057 Prokaryot
C 390	16.6	66.4	32376	4	AAK66113	Aak66113 Human imm	C 463	64.0	918	11	ACN84249	Acn84249 Breast ca
C 391	16.6	66.4	91141	11	ACN44280	Actn44280 Mouse gen	C 464	64.0	931	10	ADG32951	Adg32951 Human DNA
C 392	16.6	66.4	110000	4	AAI99682_03	Continuation (4 of	C 465	64.0	941	5	AAS79198	Aas79198 DNA enco
C 393	16.4	65.6	2061	8	ACA53674	AcA53674 Prokaryot	C 466	64.0	942	6	ABZ11418	Abz11418 Human pol
C 394	16.4	65.6	96598	9	ADA02609	Ada02609 Mouse Nfk	C 467	64.0	942	12	ADM443936	Adm443936 Novel hum
C 395	16.4	65.6	96598	10	ADB72347	Adb72347 Mouse Nfk	C 468	64.0	950	6	ABK73852	Abk73852 Bacillus
C 396	16.4	65.6	96598	10	ADE82941	Ade82941 Mouse Nfk	C 469	64.0	960	6	ABK73795	Abk73795 Bacillus
C 397	16.4	65.6	96598	10	ADE35857	Ade35857 Mouse Nfk	C 470	64.0	975	8	ACA51639	AcA51639 Prokaryot
C 398	16.2	64.8	274	3	AAA67853	Aaa67853 Pinus rad	C 471	64.0	1004	8	ACA49007	AcA49007 Prokaryot
C 399	16.2	64.8	323	3	AAA67811	Aaa67811 Pinus rad	C 472	64.0	1098	6	ABL5430	Ab15430 Lung canc
C 400	16.2	64.8	359	3	AAA67850	Aaa67850 Pinus rad	C 473	64.0	1098	11	ACN84335	Acn84335 Breast ca
C 401	16.2	64.8	400	3	AAA67773	Aaa67773 Pinus rad	C 474	64.0	1144	3	AAC56023	Aac56023 Eucalyptu
C 402	16.2	64.8	403	3	AAA67772	Aaa67772 Pinus rad	C 475	64.0	1149	4	ABL14281	Ab114281 Drosophil
C 403	16.2	64.8	412	8	ABX46070	Abx46070 Bovine ES	C 476	64.0	1157	5	AAS82078	Aas82078 DNA enco
C 404	16.2	64.8	417	3	AAA67847	Aaa67847 Pinus rad	C 477	64.0	1159	6	ABK27922	Abk27922 DNA enco
C 405	16.2	64.8	430	3	AAA67812	Aaa67812 Pinus rad	C 478	64.0	1233	13	ADT48127	Adt48127 Bacterial
C 406	16.2	64.8	442	9	ACH17925	Ach17925 Human adu	C 479	64.0	1346	5	AAS82115	Aas82115 DNA enco
C 407	16.2	64.8	460	3	AAA67821	Aaa67821 Pinus rad	C 480	64.0	1376	4	ABL03591	Ab103591 Drosophil
C 408	16.2	64.8	463	12	ADP92520	Adp92520 Cotton ex	C 481	64.0	1417	8	ACA36161	AcA36161 Prokaryot
C 409	16.2	64.8	1002	10	ACF72193	Acf72193 Photorhab	C 482	64.0	1431	11	ACH97135	Ach97135 Klebsiell
C 410	16.2	64.8	1233	3	AAF21869	Aaf21869 Human bre	C 483	64.0	1629	4	ABL17773	Ab117773 Drosophil
C 411	16.2	64.8	1254	10	ABS57853	Abs57853 Rabbit cd	C 484	64.0	1649	13	ADX33288	Adx33288 Plant ful
C 412	16.2	64.8	1317	8	ACC78408	Acc78408 P. chryso	C 485	64.0	1734	5	ABV30198	Abv30198 Human pro
C 413	16.2	64.8	1473	4	AAS52323	Aas52323 E. coli D	C 486	64.0	1734	11	ACN88953	Acn88953 Breast ca
C 414	16.2	64.8	1473	8	ACA523384	AcA523384 Prokaryot	C 487	64.0	1794	14	ADM16458	Adm16458 Eucalyptu
C 415	16.2	64.8	1473	13	ADS45977	Ads45977 Bacterial	C 488	64.0	1938	11	ADN97356	Adn97356 B. lichen
C 416	16.2	64.8	1697	8	ACC78415	Acc78415 P. chryso	C 489	64.0	1974	8	ACC46725	Acc46725 Human dit
C 417	16.2	64.8	1733	10	ADF28972	Adf28972 Influenza	C 490	64.0	2015	13	ADS59364	Ads59364 Bacterial
C 418	16.2	64.8	3391	6	ABL69123	Ab169123 Kidney ca	C 491	64.0	2101	5	AAS88998	Aas88998 DNA enco
C 419	16.2	64.8	3552	4	AAK51875	Aak51875 Human pol	C 492	64.0	2285	14	ADY19023	Ady19023 DNA enco
C 420	16.2	64.8	3679	4	AAK52859	Aak52859 Human pol	C 493	64.0	2322	5	AAS93101	Aas93101 DNA enco
C 421	16.2	64.8	3968	12	ADQ84976	Adq84976 Human tum	C 494	64.0	2323	5	AAS899009	Aas89009 DNA enco
C 422	16.2	64.8	3968	12	ADQ87257	Adq87257 Human tum	C 495	64.0	2326	5	AAS90384	Aas90384 DNA enco
C 423	16.2	64.8	3968	13	ADQ83799	Adq83799 Human tum	C 496	64.0	2346	13	ADS46215	AdS46215 Bacterial
C 424	16.2	64.8	4253	12	ADQ22492	Adq22492 Human sof	C 497	64.0	2415	8	ACA31124	AcA31124 Prokaryot
C 425	16.2	64.8	5824	4	ABL07578	Ab107578 Drosophil	C 498	64.0	2577	4	ABL25890	Ab125890 Drosophil
C 426	16.2	64.8	7513	6	ABK84767	Abk84767 Human cdn	C 499	64.0	2766	4	ABL26615	Ab126615 Drosophil
C 427	16.2	64.8	7513	6	ABN97374	Abn97374 Gene #387	C 500	64.0	2940	6	ABK27919	Abk27919 DNA enco
C 428	16.2	64.8	70665	6	ABT10716	Abt10716 Human bre						
C 429	16.2	64.8	70665	11	ADN95672	Adn95672 Human BEC						
C 430	16.2	64.8	96798	10	ACF65387_6	Continuation (7 of						
C 431	16.2	64.8	110000	10	ACF67367_54	Continuation (55 o						
C 432	16.2	64.8	110000	10	ACF65387_5	Continuation (6 of						
C 433	16.2	64.0	32	6	ABK27956	Abk27956 Lipolytic						
C 434	16.2	64.0	50	6	ABZ04088	Abz04088 Human leu						
C 435	16.2	64.0	50	10	ADG33453	Adg33453 Human DNA						
C 436	16.2	64.0	281	4	AAL14197	Aal14197 Human bre						
C 437	16.2	64.0	281	4	AAL23059	Aal23059 Human bre						
C 438	16.2	64.0	283	5	ABV12781	Abv12781 Human pro						
C 439	16.2	64.0	283	5	ABV22366	Abv22366 Human pro						
C 440	16.2	64.0	290	5	ABV28188	Abv28188 Human pro						
C 441	16.2	64.0	307	11	ACN91627	Acn91627 Breast ca						
C 442	16.2	64.0	321	5	ABV03612	Abv03612 Human pro						
C 443	16.2	64.0	369	8	ACA45562	AcA45562 Prokaryot						
C 444	16.2	64.0	372	11	ABD06168	Abd06168 Pseudomon						
C 445	16.2	64.0	390	12	ADJ74998	Adj74998 Marker ge						
C 446	16.2	64.0	430	5	ABV42786	Abv42786 Human pro						
C 447	16.2	64.0	430	5	ABV33910	Abv33910 Human pro						
C 448	16.2	64.0	447	11	ABD06132	Abd06132 Pseudomon						
C 449	16.2	64.0	495	4	AAB33458	Aab33458 Human col						
C 450	16.2	64.0	509	10	ADB57386	Adb57386 Toxicity-						
C 451	16.2	64.0	509	10	ADB51933	Adb51933 Primaty r						
C 452	16.2	64.0	530	5	ABV15900	Abv15900 Human pro						
C 453	16.2	64.0	540	11	ACN88053	Acn88053 Breast ca						
C 454	16.2	64.0	561	9	ACH41404	Ach41404 Human foe						
C 455	16.2	64.0	596	5	AAS74875	Aas74875 DNA enco						
C 456	16.2	64.0	618	5	ABV45700	Abv45700 Human pro						
C 457	16.2	64.0	718	2	ADR02269	Adr02269 A. gossyp						

ALIGNMENTS

RESULT 1

ID ADP05526 standard; DNA; 69 BP.

XX ADP05526;

XX AC ADP05526;

XX DT 26-AUG-2004 (first entry)

XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID31.

XX KW microbe detection; microbe identification; virus; viral particle;

XX KW pathogenic bacterium; cellular microbe; acellular microbe;

XX KW clinical diagnosis; research; epidemiological surveillance;

XX KW bioterrorism countermeasure; environmental pathogen survey;

XX KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX OS Viruses.

XX PN WO2004045365-A2.

XX PD 03-JUN-2004.

XX XX 23-MAY-2003; 2003WO-US016461.

XX XX 15-NOV-2002; 2002US-00295787.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Jia XY, Berger MA, Tilles JG;

XX DR WPI; 2004-449626/42.

XX DR

XX PT New (microarray) apparatus comprising a substrate with attached nucleic

XX PT acid probes, useful for detecting one or more microbes in a sample.

XX PS Claim 16; SEQ ID NO 31; 89pp; English.

XX CC This invention relates to a novel apparatus for detecting a microbe in a

XX CC sample which comprises a substrate having multiple microbe identification

XX CC sites, each having a unique address indicative of the position of that

XX CC microbe identification site on the substrate and groups of nucleic acid

XX CC probes disposed at the microbe identification sites, each group being

XX CC complementary to a target nucleic acid to provide a detectable signal at

XX CC one or more microbe identification sites. The apparatus is useful for

XX CC detecting the presence of one or more microbes in a sample, such as virus

XX CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular

XX CC microbe. The apparatus is particularly useful for clinical diagnosis,

XX CC research, epidemiological surveillance, bioterrorism countermeasures,

XX CC environmental pathogen surveys, and monitoring food contaminants. Current

XX CC testing procedures or devices, such as radioimmunoassays and ELISA, are

XX CC difficult to implement, time consuming, expensive, outdated, and

XX CC typically rely on the use of agents that recognise and bind to membrane

XX CC bound proteins or carbohydrates of the pathogen. These further cannot

XX CC assay multiple pathogens. The new apparatus or device for detecting

XX CC microbes overcomes these disadvantages. The apparatus is compact,

XX CC sensitive, and quick to detect the presence of any of a number of

XX CC pathogens present in a sample. The present sequence is that of an

XX CC oligonucleotide probe which is related to the microbe detection apparatus

XX CC of the invention.

XX SQ Sequence 69 BP; 11 A; 20 C; 20 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 69;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGCTGCAGAGTTCGCCGTACGA 25

DB 1 TCCGCTGCAGAGTTCGCCGTACGA 25

RESULT 2

ADP05510

ID ADP05510 standard; DNA; 70 BP.

XX AC ADP05510;

XX DT 26-AUG-2004 (first entry)

XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID15.

XX KW microbe detection; microbe identification; virus; viral particle;

XX KW pathogenic bacterium; cellular microbe; acellular microbe;

XX KW clinical diagnosis; research; epidemiological surveillance;

XX KW bioterrorism countermeasure; environmental pathogen survey;

XX KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX OS Viruses.

XX PN WO2004045365-A2.

XX PD 03-JUN-2004.

XX PF 23-MAY-2003; 2003WO-US016461.

XX PR 15-NOV-2002; 2002US-00295787.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Jia XY, Berger MA, Tilles JG;

XX DR WPI; 2004-449626/42.

XX DR

XX PT New (microarray) apparatus comprising a substrate with attached nucleic

XX PT acid probes, useful for detecting one or more microbes in a sample.

XX PS Claim 16; SEQ ID NO 15; 89pp; English.

XX CC This invention relates to a novel apparatus for detecting a microbe in a

XX CC sample which comprises a substrate having multiple microbe identification

XX CC sites, each having a unique address indicative of the position of that

XX CC microbe identification site on the substrate and groups of nucleic acid

XX CC probes disposed at the microbe identification sites, each group being

XX CC complementary to a target nucleic acid to provide a detectable signal at

XX CC one or more microbe identification sites. The apparatus is useful for

XX CC detecting the presence of one or more microbes in a sample, such as virus

XX CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular

XX CC microbe. The apparatus is particularly useful for clinical diagnosis,

XX CC research, epidemiological surveillance, bioterrorism countermeasures,

XX CC environmental pathogen surveys, and monitoring food contaminants. Current

XX CC testing procedures or devices, such as radioimmunoassays and ELISA, are

XX CC difficult to implement, time consuming, expensive, outdated, and

XX CC typically rely on the use of agents that recognise and bind to membrane

XX CC bound proteins or carbohydrates of the pathogen. These further cannot

XX CC assay multiple pathogens. The new apparatus or device for detecting

XX CC microbes overcomes these disadvantages. The apparatus is compact,

XX CC sensitive, and quick to detect the presence of any of a number of

XX CC pathogens present in a sample. The present sequence is that of an

XX CC oligonucleotide probe which is related to the microbe detection apparatus

XX CC of the invention.

XX SQ Sequence 70 BP; 12 A; 22 C; 20 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;

Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGCTGCAGAGTTCGCCGTACGA 25

DB 1 TCCGCTGCAGAGTTCGCCGTACGA 25

RESULT 3

ADP05515

ID ADP05515 standard; DNA; 70 BP.

XX AC ADP05515;

XX DT 26-AUG-2004 (first entry)

XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID20.

XX KW microbe detection; microbe identification; virus; viral particle;

XX KW pathogenic bacterium; cellular microbe; acellular microbe;

XX KW clinical diagnosis; research; epidemiological surveillance;

XX KW bioterrorism countermeasure; environmental pathogen survey;

XX KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX OS Viruses.

XX PN WO2004045365-A2.

XX PD 03-JUN-2004.

XX PF 23-MAY-2003; 2003WO-US016461.

XX PR 15-NOV-2002; 2002US-00295787.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Jia XY, Berger MA, Tilles JG;

XX WPI; 2004-449626/42.

XX New (microarray) apparatus comprising a substrate with attached nucleic

PT acid probes, useful for detecting one or more microbes in a sample.

XX Claim 16; SEQ ID NO 20; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a

CC sample which comprises a substrate having multiple microbe identification

CC sites, each having a unique address indicative of the position of that

CC microbe identification site on the substrate and groups of nucleic acid

CC probes disposed at the microbe identification sites, each group being

CC complementary to a target nucleic acid to provide a detectable signal at

CC one or more microbe identification sites. The apparatus is useful for

CC detecting the presence of one or more microbes in a sample, such as virus

CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular

CC microbe. The apparatus is particularly useful for clinical diagnosis,

CC research, epidemiological surveillance, bioterrorism countermeasures,

CC environmental pathogen surveys, and monitoring food contaminants. Current

CC testing procedures or devices, such as radioimmunoassays and ELISA, are

CC difficult to implement, time consuming, expensive, outdated, and

CC typically rely on the use of agents that recognise and bind to membrane

CC bound proteins or carbohydrates of the pathogen. These further cannot

CC assay multiple pathogens. The new apparatus or device for detecting

CC microbes overcomes these disadvantages. The apparatus is compact,

CC sensitive, and quick to detect the presence of any of a number of

CC pathogens present in a sample. The present sequence is that of an

CC oligonucleotide probe which is related to the microbe detection apparatus

CC of the invention.

XX SQ Sequence 70 BP; 13 A; 23 C; 20 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;

Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 4

ADP05513

ID ADP05513 standard; DNA; 70 BP.

XX AC ADP05513;

XX 26-AUG-2004 (first entry)

XX Novel microbe detection apparatus-related oligonucleotide probe SeqID18.

XX microbe detection; microbe identification; virus; viral particle;

XX pathogenic bacterium; cellular microbe; acellular microbe;

XX clinical diagnosis; research; epidemiological surveillance;

XX bioterrorism countermeasure; environmental pathogen survey;

XX food contaminant; radioimmunoassay; ELISA; probe; ss.

XX Viruses.

XX WO2004045365-A2.

XX 03-JUN-2004.

XX 23-MAY-2003; 2003WO-US016461.

XX 15-NOV-2002; 2002US-00295787.

XX (REGC) UNIV CALIFORNIA.

XX Jia XY, Berger MA, Tilles JG;

XX WPI; 2004-449626/42.

XX New (microarray) apparatus comprising a substrate with attached nucleic

PT acid probes, useful for detecting one or more microbes in a sample.

XX Claim 16; SEQ ID NO 18; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a

CC sample which comprises a substrate having multiple microbe identification

CC sites, each having a unique address indicative of the position of that

CC microbe identification site on the substrate and groups of nucleic acid

CC probes disposed at the microbe identification sites, each group being

CC complementary to a target nucleic acid to provide a detectable signal at

CC one or more microbe identification sites. The apparatus is useful for

CC detecting the presence of one or more microbes in a sample, such as virus

CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular

CC microbe. The apparatus is particularly useful for clinical diagnosis,

CC research, epidemiological surveillance, bioterrorism countermeasures,

CC environmental pathogen surveys, and monitoring food contaminants. Current

CC testing procedures or devices, such as radioimmunoassays and ELISA, are

CC difficult to implement, time consuming, expensive, outdated, and

CC typically rely on the use of agents that recognise and bind to membrane

CC bound proteins or carbohydrates of the pathogen. These further cannot

CC assay multiple pathogens. The new apparatus or device for detecting

CC microbes overcomes these disadvantages. The apparatus is compact,

CC sensitive, and quick to detect the presence of any of a number of

CC pathogens present in a sample. The present sequence is that of an

CC oligonucleotide probe which is related to the microbe detection apparatus

CC of the invention.

XX SQ Sequence 70 BP; 10 A; 21 C; 21 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;

Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 5

ADP05521

ID ADP05521 standard; DNA; 70 BP.

XX AC ADP05521;

XX 26-AUG-2004 (first entry)

XX Novel microbe detection apparatus-related oligonucleotide probe SeqID26.

XX microbe detection; microbe identification; virus; viral particle;

XX pathogenic bacterium; cellular microbe; acellular microbe;

XX clinical diagnosis; research; epidemiological surveillance;

XX bioterrorism countermeasure; environmental pathogen survey;

XX food contaminant; radioimmunoassay; ELISA; probe; ss.

XX Viruses.

XX WO2004045365-A2.

XX 03-JUN-2004.

XX 23-MAY-2003; 2003WO-US016461.

XX 15-NOV-2002; 2002US-00295787.

XX (REGC) UNIV CALIFORNIA.

XX Jia XY, Berger MA, Tilles JG;

XX WPI; 2004-449626/42.

XX New (microarray) apparatus comprising a substrate with attached nucleic

acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 26; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the microbe detection apparatus of the invention.

Sequence 70 BP; 11 A; 21 C; 21 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 6
 ADP05504
 ID ADP05504 standard; DNA; 70 BP.
 AC ADP05504;
 XX
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Novel microbe detection apparatus-related oligonucleotide probe SeqID9.
 XX
 KW microbe detection; microbe identification; virus; viral particle;
 KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;
 KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.
 XX
 OS Viruses.
 XX
 WO2004045365-A2.
 XX
 PD 03-JUN-2004.
 XX
 PF 23-MAY-2003; 2003WO-US016461.
 XX
 PR 15-NOV-2002; 2002US-00295787.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 FI Jia XY, Berger MA, Tilles JG;
 XX
 DR WPI; 2004-449626/42.
 XX
 PT New (microarray) apparatus comprising a substrate with attached nucleic
 XX acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 9; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the microbe detection apparatus of the invention.

Sequence 70 BP; 14 A; 22 C; 18 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 7
 ADP05507
 ID ADP05507 standard; DNA; 70 BP.
 AC ADP05507;
 XX
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Novel microbe detection apparatus-related oligonucleotide probe SeqID12.
 XX
 KW microbe detection; microbe identification; virus; viral particle;
 KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;
 KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.
 XX
 OS Viruses.
 XX
 WO2004045365-A2.
 XX
 PD 03-JUN-2004.
 XX
 PF 23-MAY-2003; 2003WO-US016461.
 XX
 PR 15-NOV-2002; 2002US-00295787.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 FI Jia XY, Berger MA, Tilles JG;
 XX
 DR WPI; 2004-449626/42.
 XX
 PT New (microarray) apparatus comprising a substrate with attached nucleic
 XX acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 12; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the microbe detection apparatus of the invention.

SQ Sequence 70 BP; 13 A; 21 C; 19 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 8	
ADP05517	
ID	ADP05517 standard; DNA; 70 BP.
XX	
AC	ADP05517;
XX	
XX	
DT	26-AUG-2004 (first entry)
XX	
DE	Novel microbe detection apparatus-related oligonucleotide probe SeqID22.
XX	
KW	microbe detection; microbe identification; virus; viral particle;
KW	pathogenic bacterium; cellular microbe; acellular microbe;
KW	clinical diagnosis; research; epidemiological surveillance;
KW	bioterrorism countermeasure; environmental pathogen survey;
KW	food contaminant; radioimmunoassay; ELISA; probe; ss.
XX	
OS	Viruses.
XX	
PN	WO2004045365-A2.
XX	
PD	03-JUN-2004.
XX	
XX	
PF	23-MAY-2003; 2003WO-US016461.
XX	
PR	15-NOV-2002; 2002US-00295787.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Jia XY, Berger MA, Tilles JG;
XX	
DR	WPI; 2004-449626/42.
XX	
PT	New (microarray) apparatus comprising a substrate with attached nucleic
PT	acid probes, useful for detecting one or more microbes in a sample.
XX	
PS	Claim 16; SEQ ID NO 22; 89pp; English.
XX	
CC	This invention relates to a novel apparatus for detecting a microbe in a
CC	sample which comprises a substrate having multiple microbe identification
CC	regions.

sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the micorbe detection apparatus of the invention.

SQ Sequence 70 BP; 8 A; 21 C; 23 G; 18 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. NO. 0.043;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 9	
ADP05534	
ID	ADP05534 standard; DNA; 70 BP.
XX	
XX	ADP05534;
XX	
XX	26-AUG-2004 (first entry)
XX	
XX	Novel microbe detection apparatus-related oligonucleotide probe SeqID39.
DE	
XX	microbe detection; microbe identification; virus; viral particle;
KW	pathogenic bacterium; cellular microbe; acellular microbe;
KW	clinical diagnosis; research; epidemiological surveillance;
KW	bioterrorism countermeasure; environmental pathogen survey;
KW	food contaminant; radioimmunoassay; ELISA; probe; ss.
XX	
XX	Viruses.
OS	
XX	WO2004045365-A2.
PN	
XX	
PD	03-JUN-2004.
XX	
XX	23-MAY-2003; 2003WO-US016461.
XX	
XX	15-NOV-2002; 2002US-00295787.
PR	
XX	
XX	(REGC) UNIV CALIFORNIA.
PA	
XX	
XX	Jia XY, Berger MA, Tilles JG;
PI	
XX	WPI; 2004-449626/42.
DR	
XX	
XX	New (microarray) apparatus comprising a substrate with attached nucleic
PT	acid probes, useful for detecting one or more microbes in a sample.
PT	
XX	
XX	Claim 16; SEQ ID NO 39; 89pp; English.
PS	
XX	
XX	This invention relates to a novel apparatus for detecting a microbe in a
CC	sample which comprises a substrate having multiple microbe identification
CC	sites, each having a unique address indicative of the position of that
CC	microbe identification site on the substrate and groups of nucleic acid
CC	microbe identification sites on the substrate and groups of nucleic acid

CC probes disposed at the microbe identification sites, each group being
 CC complementary to a target nucleic acid to provide a detectable signal at
 CC one or more microbe identification sites. The apparatus is useful for
 CC detecting the presence of one or more microbes in a sample, such as virus
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
 CC microbe. The apparatus is particularly useful for clinical diagnosis,
 CC research, epidemiological surveillance, bioterrorism countermeasures,
 CC environmental pathogen surveys, and monitoring food contaminants. Current
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are
 CC difficult to implement, time consuming, expensive, outdated, and
 CC typically rely on the use of agents that recognise and bind to membrane
 CC bound proteins or carbohydrates of the pathogen. These further cannot
 CC assay multiple pathogens. The new apparatus or device for detecting
 CC microbes overcomes these disadvantages. The apparatus is compact,
 CC sensitive, and quick to detect the presence of any of a number of
 CC pathogens present in a sample. The present sequence is that of an
 CC oligonucleotide probe which is related to the micorbe detection apparatus
 CC of the invention.

SQ Sequence 70 BP; 11 A; 20 C; 20 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
 Db 1 TCCGCTGCAGAGTTCGCCGTTACGA 25

RESULT 10

ADP05503
 ID ADP05503 standard; DNA; 70 BP.

XX AC ADP05503;

DT 26-AUG-2004 (first entry)

DE Novel microbe detection apparatus-related oligonucleotide probe SeqID8.

XX microbe detection; microbe identification; virus; viral particle;
 KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;
 KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX Viruses.

PN WO2004045365-A2.

XX PD 03-JUN-2004.

XX PF 23-MAY-2003; 2003WO-US016461.

XX PR 15-NOV-2002; 2002US-00295787.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Jia XY, Berger MA, Tilles JG;

XX DR WPI; 2004-449626/42.

XX FT New (microarray) apparatus comprising a substrate with attached nucleic
 XX acid probes, useful for detecting one or more microbes in a sample.

PS Claim 16; SEQ ID NO 8; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a
 CC sample which comprises a substrate having multiple microbe identification
 CC sites, each having a unique address indicative of the position of that
 CC microbe identification site on the substrate and groups of nucleic acid
 CC probes disposed at the microbe identification sites, each group being
 CC complementary to a target nucleic acid to provide a detectable signal at

CC one or more microbe identification sites. The apparatus is useful for
 CC detecting the presence of one or more microbes in a sample, such as virus
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
 CC microbe. The apparatus is particularly useful for clinical diagnosis,
 CC research, epidemiological surveillance, bioterrorism countermeasures,
 CC environmental pathogen surveys, and monitoring food contaminants. Current
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are
 CC difficult to implement, time consuming, expensive, outdated, and
 CC typically rely on the use of agents that recognise and bind to membrane
 CC bound proteins or carbohydrates of the pathogen. These further cannot
 CC assay multiple pathogens. The new apparatus or device for detecting
 CC microbes overcomes these disadvantages. The apparatus is compact,
 CC sensitive, and quick to detect the presence of any of a number of
 CC pathogens present in a sample. The present sequence is that of an
 CC oligonucleotide probe which is related to the micorbe detection apparatus
 CC of the invention.

SQ Sequence 70 BP; 12 A; 21 C; 19 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
 Db 1 TCCGCTGCAGAGTTCGCCGTTACGA 25

RESULT 11

ADP05519
 ID ADP05519 standard; DNA; 70 BP.

XX AC ADP05519;

DT 26-AUG-2004 (first entry)

DE Novel microbe detection apparatus-related oligonucleotide probe SeqID24.

XX microbe detection; microbe identification; virus; viral particle;
 KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;
 KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX Viruses.

PN WO2004045365-A2.

XX PD 03-JUN-2004.

XX PF 23-MAY-2003; 2003WO-US016461.

XX PR 15-NOV-2002; 2002US-00295787.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Jia XY, Berger MA, Tilles JG;

XX DR WPI; 2004-449626/42.

XX FT New (microarray) apparatus comprising a substrate with attached nucleic
 XX acid probes, useful for detecting one or more microbes in a sample.

PS Claim 16; SEQ ID NO 24; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a
 CC sample which comprises a substrate having multiple microbe identification
 CC sites, each having a unique address indicative of the position of that
 CC microbe identification site on the substrate and groups of nucleic acid
 CC probes disposed at the microbe identification sites, each group being
 CC complementary to a target nucleic acid to provide a detectable signal at
 CC one or more microbe identification sites. The apparatus is useful for
 CC detecting the presence of one or more microbes in a sample, such as virus

CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 105 BP; 22 A; 27 C; 27 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 105;
 Best Local Similarity 100.0%; Pred. No. 0.045; Mismatches 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 70 TCCGCTGCAGAGTTGCCCGTTACGA 46

RESULT 14
 AEB56814/c
 ID AEB56814 standard; DNA; 107 BP.

XX AC AEB56814;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:53.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX TS (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PI (HELL/) HELLYER T J.

XX TSang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 53; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 107 BP; 22 A; 28 C; 28 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.045; Mismatches 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 72 TCCGCTGCAGAGTTGCCCGTTACGA 48

RESULT 15

AEB56779/c

ID AEB56779 standard; DNA; 126 BP.

XX AC AEB56779;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:18.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX TS (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PI (HELL/) HELLYER T J.

XX TSang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 18; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 126 BP; 26 A; 36 C; 31 G; 33 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 126;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 16

AEB56834/c

ID AEB56834 standard; DNA; 180 BP.

XX AC AEB56834;

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XX 22-SEP-2005 (first entry)
DT Human coxsackievirus B1 5' untranslated polynucleotide sequence.
DE DNA detection; enteroviral detection; ds.
XX Human coxsackievirus B1.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; S76767.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (MI) and
XX (KI) are useful for detecting enterovirus target sequences. (I), (MI) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 25; DB 14; Length 180;
XX Best Local Similarity 100.0%; Pred. No. 0.047;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
XX 129 TCCGCTGCAGAGTTGCCCGTTACGA 105
XX
XX RESULT 17
XX AEB56858/C
XX ID AEB56858 standard; DNA; 198 BP.
XX AC AEB56858;
XX 22-SEP-2005 (first entry)
XX Human echovirus 6 5' untranslated polynucleotide sequence.
XX DNA detection; enteroviral detection; ds.
XX Human echovirus 6.
XX
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PN US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11709.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (MI) and
XX (KI) are useful for detecting enterovirus target sequences. (I), (MI) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 198 BP; 37 A; 47 C; 55 G; 59 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 25; DB 14; Length 198;
XX Best Local Similarity 100.0%; Pred. No. 0.048;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
XX 91 TCCGCTGCAGAGTTGCCCGTTACGA 67
XX
XX RESULT 18
XX AEB56863/C
XX ID AEB56863 standard; DNA; 198 BP.
XX AC AEB56863;
XX 22-SEP-2005 (first entry)
XX Human echovirus 11 5' untranslated polynucleotide sequence.
XX DNA detection; enteroviral detection; ds.
XX Human echovirus 11.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
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PA (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 PI Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; U11705.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 0.048;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 91 TCCGCTGCAGAGTTGCCCGTTACGA 67
 RESULT 19
 AEB56848/c
 ID AEB56848 standard; DNA; 237 BP.
 AC AEB56848;
 XX 22-SEP-2005 (first entry)
 DT Human coxsackievirus B5 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 DE Human coxsackievirus B5.
 KW US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; AF114383.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 0.048;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 91 TCCGCTGCAGAGTTGCCCGTTACGA 67
 RESULT 19
 AEB56862/c
 ID AEB56862 standard; DNA; 237 BP.
 AC AEB56862;
 XX 22-SEP-2005 (first entry)
 DT Human echovirus 9 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 DE Human echovirus 9.
 KW US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; X92886.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)

PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 237 BP; 48 A; 52 C; 66 G; 71 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 237;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107
 RESULT 20
 AEB56862/c
 ID AEB56862 standard; DNA; 237 BP.
 AC AEB56862;
 XX 22-SEP-2005 (first entry)
 DT Human echovirus 9 5' untranslated polynucleotide sequence.
 XX DNA detection; enteroviral detection; ds.
 DE Human echovirus 9.
 KW US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 DR GENBANK; X92886.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 237 BP; 51 A; 55 C; 62 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 130 TCCGCTGCAGAGTTGCCCGTTACGA 106

RESULT 21
AEB56793/c
ID AEB56793 standard; DNA; 237 BP.

AC AEB56793;

XX
DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:32.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PA US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 32; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 237 BP; 52 A; 52 C; 59 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 22

AEB56840/c

ID AEB56840 standard; DNA; 238 BP.

XX AC AEB56840;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B3.

XX PA US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX DR GENBANK; AH008164.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

```
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107
|||||
RESULT 23
AEB56791/c
ID AEB56791 standard; DNA; 238 BP.
XX
XX
AC AEB56791;
XX
XX
DT 22-SEP-2005 (first entry)
XX
XX
DE Vital 5' untranslated polynucleotide sequence SEQ ID NO:30.
XX
XX
KW DNA detection; enteroviral detection; ds.
XX
XX
OS Unidentified.
XX
XX
PN US2005158710-A1.
XX
XX
PD 21-JUL-2005.
XX
XX
PF 16-JAN-2004; 2004US-00760048.
XX
XX
PR 16-JAN-2004; 2004US-00760048.
XX
XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
XX
DR WPI; 2005-512251/52.
XX
XX
PT Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
XX
PS Disclosure; SEQ ID NO 30; 34pp; English.
XX
XX
CC The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
XX
SQ Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
|||||

RESULT 24
AEB56846/c
ID AEB56846 standard; DNA; 238 BP.
XX
XX
AC AEB56846;
XX
XX
DT 22-SEP-2005 (first entry)
XX
XX
DE Human coxsackievirus B4 5' untranslated polynucleotide sequence.
XX
XX
KW DNA detection; enteroviral detection; ds.
XX
XX
OS Human coxsackievirus B4.
XX
XX
PN US2005158710-A1.

22-SEP-2005 (first entry)
Human coxsackievirus B4 5' untranslated polynucleotide sequence.
DNA detection; enteroviral detection; ds.
Human coxsackievirus B4.
US2005158710-A1.
21-JUL-2005.
16-JAN-2004; 2004US-00760048.
16-JAN-2004; 2004US-00760048.
(TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
Tsang S, Price JA, Hellyer TJ;
WPI; 2005-512251/52.
GENBANK; D00149.
Novel oligonucleotide comprising sequences for binding and amplifying or
detecting target, useful for detecting enterovirus nucleic acids.
Disclosure; Fig 1A-D; 34pp; English.
The invention relates to an oligonucleotide (I) consisting of: (a) the
target binding sequence of an oligonucleotide chosen from any one of the
10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
selected amplification or detection reaction. Also described: (1) a kit
(KI) comprising (I), and one or more container that contains (I); and (2)
detecting (MI) an enterovirus target sequence, involving: (a) amplifying
the target sequence using first amplification primer having a sequence
consisting essentially of target binding sequence of any one of AEB56764
to AEB56771 and optionally a sequence required for selected amplification
reaction; and (b) detecting the amplified target sequences. (I) and
(KI) are useful for detecting enterovirus target sequences. (I)
specifically and selectively recognizes the enterovirus genome. (I)
sensitively and rapidly detects fewer than 500 copies of enteroviral
genome and allows detection of broad range of enterovirus serotypes. The
present sequence represents a viral 5' untranslated polynucleotide
sequence given in the exemplification of the present invention.
Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107
|||||

RESULT 25
AEB56847/c
ID AEB56847 standard; DNA; 238 BP.
XX
XX
AC AEB56847;
XX
XX
DT 22-SEP-2005 (first entry)
XX
XX
DE Human coxsackievirus B4 5' untranslated polynucleotide sequence.
XX
XX
KW DNA detection; enteroviral detection; ds.
XX
XX
OS Human coxsackievirus B4.
XX
XX
PN US2005158710-A1.
```

XX PD 21-JUL-2005.
 XX PF 16-JAN-2004; 2004US-00760048.
 XX PR 16-JAN-2004; 2004US-00760048.
 XX PA (TSAN/) TSANG S.
 XX PA (PRIC/) PRICE J A.
 XX PA (HELL/) HELLYER T J.
 XX PI Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX DR GENBANK; X05690.
 XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
 XX PT detecting target, useful for detecting enterovirus nucleic acids.
 XX PS Disclosure; Fig 1A-D; 34pp; English.
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107
 RESULT 26
 AEB56789/c
 ID AEB56789 standard; DNA; 238 BP.
 AC AEB56789;
 XX 22-SEP-2005 (first entry)
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:28.
 XX DNA detection; enteroviral detection; ds.
 XX Unidentified.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.

PA (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX DR Novel oligonucleotide comprising sequences for binding and amplifying or
 XX PT detecting target, useful for detecting enterovirus nucleic acids.
 XX PS Disclosure; SEQ ID NO 28; 34pp; English.
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX SQ Sequence 238 BP; 57 A; 52 C; 58 G; 71 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
 RESULT 27
 AEB56775/c
 ID AEB56775 standard; DNA; 238 BP.
 AC AEB56775;
 XX 22-SEP-2005 (first entry)
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:14.
 XX DNA detection; enteroviral detection; ds.
 XX Unidentified.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 XX (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX DR Novel oligonucleotide comprising sequences for binding and amplifying or
 XX PT detecting target, useful for detecting enterovirus nucleic acids.
 XX PS Disclosure; SEQ ID NO 14; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (KI) comprising (I), and one or more container that contains (I); and (2)
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 238 BP; 56 A; 55 C; 58 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 28
AEB56807/C
ID AEB56807 standard; DNA; 238 BP.
XX
AC AEB56807;
XX
DT 22-SEP-2005 (first entry)
XX
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:46.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Unidentified.
XX
FN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PP 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX

XX (TSAN//) TSANG S.
XX (PRIC//) PRICE J A.
XX (HELL//) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; SEQ ID NO 46; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and
CC (KI) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enterovirus
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 238 BP; 53 A; 53 C; 58 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 29
AEB56815/C
ID AEB56815 standard; DNA; 238 BP.
XX
AC AEB56815;
XX
DT 22-SEP-2005 (first entry)
XX
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:54.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Unidentified.
XX
FN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PP 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX

XX (TSAN//) TSANG S.
XX (PRIC//) PRICE J A.
XX (HELL//) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; SEQ ID NO 54; 34pp; English.
XX

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (MI) and
XX (KI) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
SQ Sequence 238 BP; 53 A; 53 C; 55 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 30
 AEB56838/c
 ID AEB56838 standard; DNA; 238 BP.
 XX
 AC AEB56838;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human coxsackievirus B3.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.
 XX
 PF 16-JAN-2004; 2004US-00760048.
 XX
 PR 16-JAN-2004; 2004US-00760048.
 XX
 PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 PI Teang S, Price JA, Hellyer TJ;
 XX
 DR WPI; 2005-512251/52.
 DR GENBANK; AF169665.
 XX
 PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 32
 AEB56785/c
 ID AEB56785 standard; DNA; 238 BP.
 XX
 AC AEB56785;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:24.

RESULT 31
 AEB56842/c
 ID AEB56842 standard; DNA; 238 BP.
 XX
 AC AEB56842;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
 XX
 KW DNA detection; enteroviral detection; ds.
 XX
 OS Human coxsackievirus B3.
 XX
 PN US2005158710-A1.
 XX
 PD 21-JUL-2005.
 XX
 PF 16-JAN-2004; 2004US-00760048.
 XX
 PR 16-JAN-2004; 2004US-00760048.
 XX
 PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 PI Teang S, Price JA, Hellyer TJ;
 XX
 DR WPI; 2005-512251/52.
 DR GENBANK; M16572.
 XX
 PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 32
 AEB56785/c
 ID AEB56785 standard; DNA; 238 BP.
 XX
 AC AEB56785;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:24.

DR WPI; 2005-512251/52.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; SEQ ID NO 19; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 57 A; 51 C; 58 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 35
 AEB56803/c
 ID AEB56803 standard; DNA; 238 BP.
 XX
 AC AEB56803;
 XX
 XX 22-SEP-2005 (first entry)
 XX
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:42.
 DE
 XX DNA detection; enteroviral detection; ds.
 XX
 XX Unidentified.
 OS
 XX US2005158710-A1.
 XX
 XX 21-JUL-2005.
 XX
 XX 16-JAN-2004; 2004US-00760048.
 XX
 XX 16-JAN-2004; 2004US-00760048.
 PR
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 XX Teang S, Price JA, Hellyer TJ;
 PI WPI; 2005-512251/52.
 XX
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; SEQ ID NO 42; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 49 A; 52 C; 60 G; 77 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 36
 AEB56829/c
 ID AEB56829 standard; DNA; 238 BP.
 XX
 AC AEB56829;
 XX
 XX 22-SEP-2005 (first entry)
 XX
 XX Consensus viral 5' untranslated polynucleotide sequence.
 DE
 XX DNA detection; enteroviral detection; ds.
 XX
 XX Synthetic.
 OS
 XX US2005158710-A1.
 XX
 XX 21-JUL-2005.
 XX
 XX 16-JAN-2004; 2004US-00760048.
 XX
 XX 16-JAN-2004; 2004US-00760048.
 PR
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 XX Teang S, Price JA, Hellyer TJ;
 PI WPI; 2005-512251/52.
 XX
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; Fig 1A-D; 34pp; English.
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a consensus viral 5' untranslated
 CC polynucleotide sequence given in the exemplification of the present
 CC invention.

XX SQ Sequence 238 BP; 51 A; 55 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 37
 AEB56843/c
 ID AEB56843 standard; DNA; 238 BP.

XX AC AEB56843;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B3.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.
 (PRIC/) PRICE J A.
 (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.
 DR GENBANK; M33854.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
 detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 target binding sequence of an oligonucleotide chosen from any one of the
 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 selected amplification or detection reaction. Also described: (1) a kit
 (KI) comprising (I), and one or more container that contains (I); and (2)
 detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 the target sequence using first amplification primer having a sequence
 consisting essentially of target binding sequence of any one of AEB56764
 to AEB56771 and optionally a sequence required for selected amplification
 reaction; and (b) detecting the amplified target sequences. (I), (MI) and
 (KI) are useful for detecting enterovirus target sequences. (I)
 specifically and selectively recognizes the enterovirus genome. (I)
 sensitively and rapidly detects fewer than 500 copies of enteroviral
 genome and allows detection of broad range of enterovirus serotypes. The
 present sequence represents a viral 5' untranslated polynucleotide
 sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 53 A; 58 C; 64 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 38

AEB56845/c
 ID AEB56845 standard; DNA; 238 BP.

XX AC AEB56845;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B3.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.
 (PRIC/) PRICE J A.
 (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.
 DR GENBANK; U57056.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
 detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 target binding sequence of an oligonucleotide chosen from any one of the
 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 selected amplification or detection reaction. Also described: (1) a kit
 (KI) comprising (I), and one or more container that contains (I); and (2)
 detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 the target sequence using first amplification primer having a sequence
 consisting essentially of target binding sequence of any one of AEB56764
 to AEB56771 and optionally a sequence required for selected amplification
 reaction; and (b) detecting the amplified target sequences. (I), (MI) and
 (KI) are useful for detecting enterovirus target sequences. (I)
 specifically and selectively recognizes the enterovirus genome. (I)
 sensitively and rapidly detects fewer than 500 copies of enteroviral
 genome and allows detection of broad range of enterovirus serotypes. The
 present sequence represents a viral 5' untranslated polynucleotide
 sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 54 A; 57 C; 62 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 39

AEB56774/c

ABE56774 standard; DNA; 238 BP.
AC ABE56774;
XX
XX 22-SEP-2005 (first entry)
XX
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:13.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Unidentified.
XX
XX OS
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.
XX
XX PF 16-JAN-2004; 2004US-00760048.
XX
XX PR 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX PF 16-JAN-2004; 2004US-00760048.
XX
XX PR 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX DR Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX
XX PS Disclosure; SEQ ID NO 13; 34pp; English.
XX
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of ABE56762 to ABE56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of ABE56764
XX CC to ABE56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequence. (I) and
XX CC (K1) are useful for detecting enterovirus target sequences. (I)
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX
XX SQ Sequence 238 BP; 59 A; 51 C; 54 G; 74 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
RESULT 40
ABE56788/c
ID ABE56788 standard; DNA; 238 BP.
XX
XX AC ABE56788;
XX
XX XX 22-SEP-2005 (first entry)
XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:27.
XX
XX KW DNA detection; enteroviral detection; ds.
XX
XX XX

Unidentified.
OS
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.
XX
XX PF 16-JAN-2004; 2004US-00760048.
XX
XX PR 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX
XX PS Disclosure; SEQ ID NO 27; 34pp; English.
XX
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of ABE56762 to ABE56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of ABE56764
XX CC to ABE56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequence. (I) and
XX CC (K1) are useful for detecting enterovirus target sequences. (I)
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX
XX SQ Sequence 238 BP; 57 A; 53 C; 58 G; 70 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
RESULT 41
ABE56792/c
ID ABE56792 standard; DNA; 238 BP.
XX
XX AC ABE56792;
XX
XX XX 22-SEP-2005 (first entry)
XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:31.
XX
XX KW DNA detection; enteroviral detection; ds.
XX
XX OS Unidentified.
XX
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.
XX
XX PF 16-JAN-2004; 2004US-00760048.
XX
XX PR 16-JAN-2004; 2004US-00760048.
XX
XX XX

CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 55 A; 53 C; 59 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 44
 AEB56787/c
 ID AEB56787 standard; DNA; 238 BP.

AC AEB56787;

DT 22-SEP-2005 (first entry)

DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:26.

KW DNA detection; enteroviral detection; ds.

OS Unidentified.

XX US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

PA (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

DR WPI; 2005-512251/52.

PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; SEQ ID NO 26; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC sensitively and selectively recognizes the enterovirus genome. (I)
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX

SQ Sequence 238 BP; 57 A; 52 C; 58 G; 71 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 45
 AEB56870/c

ID AEB56870 standard; DNA; 238 BP.

XX AEB56870;

DT 22-SEP-2005 (first entry)

DE Human echovirus 30 5' untranslated polynucleotide sequence.

KW DNA detection; enteroviral detection; ds.

XX Human echovirus 30.

OS US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

PA (PRIC/) PRICE J A.

PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

DR WPI; 2005-512251/52.

DR GENBANK; AF162711.

PT Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC sensitively and selectively recognizes the enterovirus genome. (I)
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX

SQ Sequence 238 BP; 51 A; 56 C; 61 G; 70 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 46
AEB56830/c
ID AEB56830 standard; DNA; 238 BP.
XX AC AEB56830;
XX DT 22-SEP-2005 (first entry)
XX DE Human coxsackievirus A9 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human coxsackievirus A9.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; D00627.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.

XX Query Match 100.0%; Score 25; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 0.049;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107
RESULT 47
AEB56864/c
ID AEB56864 standard; DNA; 238 BP.
XX AC AEB56864;
XX DT 22-SEP-2005 (first entry)

XX Query Match 100.0%; Score 25; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 0.049;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.

XX Human echovirus 11 5' untranslated polynucleotide sequence.
XX DNA detection; enteroviral detection; ds.
XX Human echovirus 11.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; X80059.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Query Match 100.0%; Score 25; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 0.049;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107
RESULT 48
AEB56859/c
ID AEB56859 standard; DNA; 238 BP.
XX AC AEB56859;
XX DT 22-SEP-2005 (first entry)
XX DE Human echovirus 6 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human echovirus 6.
XX PN US2005158710-A1.

```

PD 21-JUL-2005.
XX
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN//) TSANG S.
XX (PRIC//) PRICE J A.
XX (HELL//) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U16283.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX Sequence 238 BP; 47 A; 53 C; 66 G; 72 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107
RESULT 49
AEB56776/c
ID AEB56776 standard; DNA; 238 BP.
XX
XX AEB56776;
AC
XX
XX 22-SEP-2005 (first entry)
DT
XX
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:15.
DE
XX
XX DNA detection; enteroviral detection; ds.
KW
XX
XX Unidentified.
OS
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
PD
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN//) TSANG S.
XX (PRIC//) PRICE J A.
XX (HELL//) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX Sequence 238 BP; 47 A; 53 C; 66 G; 72 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
RESULT 50
AEB56790/c
ID AEB56790 standard; DNA; 238 BP.
XX
XX AEB56790;
AC
XX
XX 22-SEP-2005 (first entry)
DT
XX
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:29.
DE
XX
XX DNA detection; enteroviral detection; ds.
KW
XX
XX Unidentified.
OS
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
PD
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN//) TSANG S.
XX (PRIC//) PRICE J A.
XX (HELL//) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; SEQ ID NO 29; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX Sequence 238 BP; 58 A; 55 C; 55 G; 70 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

```

CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 57 A; 51 C; 57 G; 73 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 51
 AEB56841/c
 ID AEB56841 standard; DNA; 238 BP.
 XX AC AEB56841;
 XX DT 22-SEP-2005 (first entry)
 XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human coxsackievirus B3.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN//) TSANG S.
 XX (PRIC//) PRICE J A.
 XX (HELL//) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; M74567.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-B; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 52 A; 58 C; 65 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 52
 AEB56809/c
 ID AEB56809 standard; DNA; 238 BP.

XX AC AEB56809;

XX DT 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN//) TSANG S.

XX (PRIC//) PRICE J A.

XX (HELL//) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 48; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 53

AEBS6831/c
ID AEB56831 standard; DNA; 238 BP.

XX AC AEB56831;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus A16 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus A16.

XX FN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX DR GENBANK; U05876.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 54

AEBS6808/c
ID AEB56808 standard; DNA; 238 BP.

XX AC AEB56808;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:47.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX FN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX CC Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 47; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 55

AEBS6844/c
ID AEB56844 standard; DNA; 238 BP.

XX AC AEB56844;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX XX

DNA detection; enteroviral detection; ds.
 OS Human coxsackievirus B3.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 PD
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 PR
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 XX Tsang S, Price JA, Hellyer TJ;
 PI WPI; 2005-512251/52.
 XX GENBANK; M88483.
 DR
 DR Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 PT
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107
 RESULT 56
 AEB56804/C
 ID AEB56804 standard; DNA; 238 BP.
 AC AEB56804;
 XX
 XX 22-SEP-2005 (first entry)
 DT
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:43.
 XX
 XX DNA detection; enteroviral detection; ds.
 KW Unidentified.
 XX
 XX US2005158710-A1.
 XX 21-JUL-2005.
 PD
 XX 16-JAN-2004; 2004US-00760048.
 PF

DNA detection; enteroviral detection; ds.
 OS Human coxsackievirus B3.
 XX US2005158710-A1.
 XX 21-JUL-2005.
 PD
 XX 16-JAN-2004; 2004US-00760048.
 XX 16-JAN-2004; 2004US-00760048.
 PR
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 PA (HELL/) HELLYER T J.
 XX
 XX Tsang S, Price JA, Hellyer TJ;
 PI WPI; 2005-512251/52.
 XX GENBANK; M88483.
 DR
 DR Novel oligonucleotide comprising sequences for binding and amplifying or
 PT detecting target, useful for detecting enterovirus nucleic acids.
 PT
 PS Disclosure; Fig 1A-D; 34pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC (K1) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
 CC (K1) are useful for detecting enterovirus target sequences. (I) and
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 238 BP; 48 A; 52 C; 60 G; 78 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 14; Length 238;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
 RESULT 57
 ABX12451/C
 ID ABX12451 standard; DNA; 502 BP.
 XX
 AC ABX12451;
 XX
 XX 10-MAY-2003 (first entry)
 DT
 DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #6.
 XX
 XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
 KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
 KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
 KW renal failure; leg amputation; ds.
 XX
 XX Coxsackievirus.
 OS
 XX WO2002103060-A2.
 PN
 XX 27-DEC-2002.
 PD
 XX 19-JUN-2002; 2002WO-IB003278.
 PF
 XX 20-JUN-2001; 2001SE-00002198.
 PR
 XX (INNO-) INNOVENTUS PROJECT AB.
 PA
 XX Tuvemo HT, Frisk GE, Yin H;
 XX

DR WPI; 2003-278229/27.
XX Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetogenic coxsackie B virus-4 strain VD2921.
XX Disclosure; Page 73; 79pp; English.
XX The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX Sequence 502 BP; 120 A; 132 C; 128 G; 122 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 25; DB 8; Length 502;
Best Local Similarity 100.0%; Pred. NO. 0.053;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
DB 452 TCCGCTGCAGAGTTGCCCGTTACGA 428
RESULT 58
ABX12448/C
ID ABX12448 standard; DNA; 548 BP.
XX AC ABX12448;
XX 10-MAY-2003 (first entry)
XX Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #3.
DE Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX Coxsackievirus.
OS WO2002103060-A2.
PN 27-DEC-2002.
XX 19-JUN-2002; 2002WO-IB003278.
XX 20-JUN-2001; 2001SE-00002198.
XX (INNO-) INNOVENTUS PROJECT AB.
PA Tuvemo HT, Frisk GE, Yin H;
XX WPI; 2003-278229/27.
XX Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetogenic coxsackie B virus-4 strain VD2921.
XX Disclosure; Page 72; 79pp; English.
XX The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.

CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX Sequence 548 BP; 124 A; 145 C; 144 G; 135 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 25; DB 8; Length 548;
Best Local Similarity 100.0%; Pred. NO. 0.054;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
DB 442 TCCGCTGCAGAGTTGCCCGTTACGA 418
RESULT 59
ABX12453/C
ID ABX12453 standard; DNA; 551 BP.
XX AC ABX12453;
XX 10-MAY-2003 (first entry)
XX Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #8.
DE Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX Coxsackievirus.
OS WO2002103060-A2.
PN 27-DEC-2002.
XX 19-JUN-2002; 2002WO-IB003278.
XX 20-JUN-2001; 2001SE-00002198.
XX (INNO-) INNOVENTUS PROJECT AB.
PA Tuvemo HT, Frisk GE, Yin H;
XX WPI; 2003-278229/27.
XX Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetogenic coxsackie B virus-4 strain VD2921.
XX Disclosure; Page 74; 79pp; English.
XX The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX Sequence 551 BP; 130 A; 147 C; 140 G; 134 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 25; DB 8; Length 551;
Best Local Similarity 100.0%; Pred. NO. 0.054;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE	Coxsackievirus B3 (CVB3)/CO 5' non-translated region (NTR) sequence.
XX	
KW	Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
KW	Coxsackievirus B3; CVB3; NTR; non-translated region; ds.
XX	
OS	Coxsackievirus.
XX	
XX	WO200104136-A1.
XX	
PD	18-JAN-2001.
XX	
XX	08-JUL-2000; 2000WO-US018681.
PF	
XX	09-JUL-1999; 99US-0143104P.
PR	
XX	(UYNE-) UNIV NEBRASKA.
PA	
XX	
PI	Romero JR, Bradrick SS, Dunn JJ;
XX	
XX	WPI; 2001-138310/14.
DR	
XX	
PT	Recombinant enterovirus genome for use as vector or vaccine, modified by
PT	replacing a part or all of its 5'non-translated region by 5'NTR of
PT	enterovirus genome that encodes virus modified in tropism or virulence.
XX	
XX	Example 2; Page 25; 49pp; English.
PS	
XX	
CC	The invention provides an enterovirus genome (I) for use as a vector or
CC	vaccine, modified to produce a virus (VI) having a restricted or altered
CC	species or tissue tropism, compared to an equivalent unmodified virus, or
CC	modified to produce an attenuated virus (V2), by replacing a part or all
CC	of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an
CC	enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
CC	vector in targeting genes of interest to specific cells or tissues. (I)
CC	is also useful for diagnostic purposes, e.g. to identify virulent, versus
CC	nonvirulent strains of an enterovirus. The present sequence represents
CC	the 5' NTR (non-translated region) of a non-cardiovirulent enterovirus
CC	Coxsackievirus B3 (CVB3)/CO strain
XX	
SQ	Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;
	Query Match 100.0%; Score 25; DB 4; Length 660;
	Best Local Similarity 100.0%; Pred. No. 0.055;
	Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 TCCGCTGCAGAGTTGCCCGTTACGA 25
DB	457 TCCGCTGCAGAGTTGCCCGTTACGA 433
RESULT 62	
AE356828/c	
ID	AE356828 standard; DNA; 660 BP.
XX	
XX	AE356828;
XX	
DT	22-SEP-2005 (first entry)
XX	
DE	Coxsackie virus B5 polynucleotide sequence SEQ ID NO:67.
XX	
KW	DNA detection; enteroviral detection; ds.
OS	Human coxsackievirus B5.
XX	
XX	US2005158710-A1.
PN	
XX	
PD	21-JUL-2005.
XX	
PF	16-JAN-2004; 2004US-00760048.
XX	
PR	16-JAN-2004; 2004US-00760048.
XX	
PA	(TSAN/) TSANG S.

PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
DR WPI; 2005-512251/52.
DR GENBANK; AF169665.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
PS Disclosure; SEQ ID NO 67; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a coxsackie virus B5 polynucleotide sequence,
CC which is given in the exemplification of the present invention. Note: the
CC present sequence is designated as SEQ ID NO:67 in the Sequence Listing.
CC but corresponds with the sequence given in figure 2 designated SEQ ID
CC NO:14 in the description of the drawings.
XX
SQ Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 14; Length 660;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 457 TCCGCTGCAGAGTTGCCCGTTACGA 433
RESULT 63
AEA00424/C
ID AEA00424 standard; DNA; 709 BP.
XX
AC AEA00424;
XX
XX 28-JUL-2005 (first entry)
XX
DE Enterovirus 71 5' untranslated region internal ribosome entry site DNA.
XX
XX vector; neurological disease; ds; Gene therapy;
KW internal ribosome entry site; cystic fibrosis; cna-gen.;
KW respiratory-gen.; factor VIII deficiency; hemostatic; genetic disorder;
KW factor IX deficiency; Duchenne dystrophy; muscular-gen.;
KW Becker's disease; cancer; cytostatic; neoplasm;
KW acquired immune deficiency syndrome; anti-hiv; infectious disease;
KW antimicrobial.
XX
OS Human enterovirus 71; strain TW/2086/98.
XX
XX US2005112095-A1.
PN
XX 26-MAY-2005.
PD
XX 08-JUL-2003; 2003US-00614283.
PF
XX 09-JUL-2002; 2002US-0394269P.
PR
XX (HSUT/) HSU T.
PA

PA (WUTT/) WU T.
PA (LEEJ/) LEE J.
XX
PI Hsu T, Wu T, Lee J;
XX
DR WPI; 2005-371616/38.
XX
XX New nucleic acid vector for the expression of at least two cistrons
PT comprising a nucleotide sequence comprising an internal ribosome entry
PT site (IRES) e.g. enterovirus 71 (EV71), useful for treating a patient
PT having e.g. AIDS.
XX
PS Example 2; SEQ ID NO 1; 23pp; English.
XX
XX The present invention relates to a nucleic acid vector for the expression
CC of at least two cistrons. The vector comprises a promoter operably linked
CC to a nucleotide sequence comprising at least two cistrons and at least
CC one nucleotide sequence comprising an internal ribosome entry site (IRES)
CC selected from Human enterovirus 71 (EV71), Hepatitis C virus (HCV), or
CC Encephalomyocarditis virus (EMCV). The invention also provides a method
CC for screening of anti-viral compounds using the IRES. The invention is
CC useful for the genetic treatment of patients with cystic fibrosis,
CC hemophilia A or B, Duchenne or Becker type myopathy, cancer, AIDS and
CC other bacterial or infectious diseases due to a pathogenic organism and
CC in gene therapy. The present sequence is the enterovirus 71 5'
CC untranslated region (UTR) IRES DNA.
XX
SQ Sequence 709 BP; 165 A; 185 C; 172 G; 187 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 14; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 504 TCCGCTGCAGAGTTGCCCGTTACGA 480
RESULT 64
AAC85152/c
ID AAC85152 standard; RNA; 745 BP.
XX
AC AAC85152;
XX
XX 08-MAY-2001 (first entry)
XX
DE Cxsackievirus B3 (CVB3) 5' non-translated region (NTR) sequence.
XX
KW Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
KW Cxsackievirus B3; CVB3; NTR; non-translated region; ds.
XX
OS Cxsackievirus.
XX
XX Key Location/Qualifiers
FH
XX stem_loop 2..87
FT /*tag= d
FT /note= "Domain I"
FT 10..34
FT /*tag= a
FT /note= "stemloop B"
FT 35..45
FT /*tag= b
FT /note= "stemloop C"
FT 57..70
FT /*tag= c
FT /note= "stemloop D"
FT 105..181
FT /*tag= e
FT /note= "Domain II"
FT 184..233
FT /*tag= f
FT /note= "Domain III"
FT 241..444
FT stem_loop

```
FT      /*tag= g
FT      /note= "Domain IV"
FT      452..560
FT      /*tag= h
FT      /note= "Domain V"
FT      587..623
FT      /*tag= i
FT      /note= "Domain VI"
FT      624..644
FT      /*tag= j
FT      /note= "Domain VII"
XX
XX      WO200104136-A1.
XX      18-JAN-2001.
PD
XX      08-JUL-2000; 2000WO-US018681.
XX      09-JUL-1999; 99US-0143104P.
XX      (UYNE-) UNIV NEBRASKA.
XX      Romero JR, Bradrick SS, Dunn JJ;
XX      WPI; 2001-138310/14.
XX
XX      Recombinant enterovirus genome for use as vector or vaccine, modified by
XX      replacing a part or all of its 5'non-translated region by 5'NTR of
XX      enterovirus genome that encodes virus modified in tropism or virulence.
XX
XX      Disclosure; Fig 1; 49pp; English.
XX
XX      The invention provides an enterovirus genome (I) for use as a vector or
XX      vaccine, modified to produce a virus (Vi) having a restricted or altered
XX      species or tissue tropism, compared to an equivalent unmodified virus, or
XX      modified to produce an attenuated virus (V2), by replacing a part or all
XX      of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an
XX      enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
XX      vector in targeting genes of interest to specific cells or tissues. (I)
XX      is also useful for diagnostic purposes, e.g. to identify virulent, versus
XX      nonvirulent strains of an enterovirus. The present sequence represents
XX      the enterovirus Coxsackievirus B3 (CVB3) 5' NTR (non-translated region)
XX      sequence
XX
XX      Sequence 745 BP; 184 A; 192 C; 181 G; 1 T; 187 U; 0 Other;
XX
XX      Query Match      100.0%; Score 25; DB 4; Length 745;
XX      Best Local Similarity 100.0%; Pred. No. 0.056;
XX      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 TCCGCTGCAGAGTTGCCCGTTACGA 25
XX      539 TCCGCTGCAGAGTTGCCCGTTACGA 515
XX
XX      RESULT 65
XX      ADP82873/c
XX      ID ADP82873 standard; DNA; 810 BP.
XX
XX      AC ADP82873;
XX
XX      23-SEP-2004 (first entry)
XX
XX      Human coxsackievirus B1 complete genomic DNA.
XX
XX      hMPV detection; ds.
XX
XX      Human coxsackievirus B1.
XX
XX      WO2004057021-A2.
XX
XX      08-JUL-2004.
XX
XX      PF 19-DEC-2003; 2003WO-CA001994.
XX
XX      19-DEC-2002; 2002CA-02411264.
XX      24-JAN-2003; 2003CA-02418004.
XX
XX      (UYLA-) UNIV LAVAL.
XX
XX      Boivin G;
XX
XX      WPI; 2004-500307/47.
XX
XX      Detecting and/or quantifying human, metapneumovirus (hMPV) in a sample
XX      comprises contacting the at least one probe and/or primer with the sample
XX      to allow annealing of the probe and/or primer with the nucleic acid
XX      sequence.
XX
XX      Claim 32; SEQ ID NO 137; 158pp; English.
XX
XX      The invention relates to a novel method for detecting and/or quantifying
XX      Human metapneumovirus (hMPV) in a sample comprising providing at least
XX      one probe or primer specific for a nucleic acid sequence of hMPV,
XX      contacting the one probe and/or primer with the sample to allow annealing
XX      of the probe and/or primer with the nucleic acid sequence and detecting
XX      and/or quantifying the nucleic acid sequence using the annealed probe
XX      and/or primer. The method of the invention may be useful for detecting
XX      and/or quantifying Human metapneumovirus (hMPV) in a sample. The current
XX      sequence is that of the Human coxsackievirus B1 complete genomic DNA of
XX      the invention.
XX
XX      Sequence 810 BP; 243 A; 180 C; 190 G; 197 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 25; DB 12; Length 810;
XX      Best Local Similarity 100.0%; Pred. No. 0.056;
XX      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 TCCGCTGCAGAGTTGCCCGTTACGA 25
XX      88 TCCGCTGCAGAGTTGCCCGTTACGA 64
XX
XX      RESULT 66
XX      ADU47469/c
XX      ID ADU47469 standard; cDNA; 1560 BP.
XX
XX      AC ADU47469;
XX
XX      27-JAN-2005 (first entry)
XX
XX      DE Enterovirus type 71 (EV71) cDNA.
XX
XX      KW Detection; enterovirus type 71; EV71; ss.
XX
XX      OS Enterovirus.
XX
XX      Key Location/Qualifiers
XX      primer_bind 72..87
XX      /tag= a
XX      /note= "f1 primer"
XX      primer_bind 167..187
XX      /tag= b
XX      /note= "f2 primer"
XX      primer_bind 248..266
XX      /tag= c
XX      /note= "f3 primer"
XX      primer_bind 423..439
XX      /tag= d
XX      /note= "f5 primer"
XX      misc_binding 448..474
XX      /tag= e
XX      /bound_moiety= "p1 probe"
XX      misc_binding 514..546
XX      /tag= f
XX      /bound_moiety= "p2 probe"
```

```

FT misc_binding 547. .574
FT /*tag= g
FT /bound_moiety= "p3 probe"
FT primer_bind 583. .602
FT /*tag= h
FT /note= "r2 primer"
FT primer_bind 627. .645
FT /*tag= i
FT /note= "r1 primer"
FT primer_bind 1179. .1198
FT /*tag= j
FT /note= "f7 primer"
FT misc_binding 1344. .1373
FT /*tag= k
FT /bound_moiety= "16-1 probe"
FT misc_binding 1390. .1419
FT /*tag= l
FT /bound_moiety= "71-2/16-2 probe"
FT misc_binding 1454. .1481
FT /*tag= m
FT /bound_moiety= "71-3 probe"
FT primer_bind 1485. .1504
FT /*tag= n
FT /note= "r3 primer"
FT
FT
XX US6818397-B1.
XX
XX 16-NOV-2004.
XX
XX 28-NOV-2000; 2000US-00724678.
XX
XX 28-NOV-2000; 2000US-00724678.
XX
XX (CHIP-) CHIP BIO TECHNOLOGY INC.
XX
XX Lee K, Bair C, Tseng Y, Wang Y, Wang S;
XX WPI; 2004-793563/78.
XX GENBANK; U22521.
XX
XX New kit comprising a pair of oligonucleotide primers for nucleic acid
XX amplification, useful in detecting and differentiating an enterovirus in
XX a sample.
XX
XX Disclosure; SEQ ID NO 16; 14pp; English.
XX
XX The invention provides a method and a kit for detecting and
XX differentiating an enterovirus type 71 (EV71) in a sample. The method
XX involves contacting nucleic acids in the sample with a pair of primers to
XX form an amplification product; contacting the amplification product with
XX at least one synthetic nucleotide sequence fixed on a solid substrate and
XX detecting hybridisation. The present sequence is the enterovirus type 71
XX (EV71) cDNA.
XX
XX Sequence 1560 BP; 421 A; 401 C; 346 G; 392 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 13; Length 1560;
XX Best Local Similarity 100.0%; Pred. No. 0.061;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
XX |||||
XX
XX Db 540 TCCGCTGCAGAGTTGCCCGTTACGA 516
XX
XX RESULT 67
XX ABX12440/c
XX ID ABX12440 standard; DNA; 7392 BP.
XX
XX AC ABX12440;
XX
XX 10-MAY-2003 (first entry)
XX
DE Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.
XX
XX Coxsackievirus.
XX
XX Key Location/Qualifiers
XX misc_feature 1. .87
XX /tag= a
XX /note= "Specifically claimed in claim 16"
XX misc_feature 88. .512
XX /tag= b
XX /note= "Specifically claimed in claim 19"
XX misc_feature 513. .742
XX /tag= c
XX /note= "Specifically claimed in claim 22"
XX misc_feature 742
XX /tag= d
XX /note= "Specifically claimed in claim 25"
XX CDS 743. .7303
XX /tag= f
XX /product= "Polypeptide"
XX misc_feature 743. .952
XX /tag= e
XX /note= "Specifically claimed in claim 26"
XX misc_feature 953. .1726
XX /tag= g
XX /note= "Specifically claimed in claim 29"
XX misc_feature 1727. .2441
XX /tag= h
XX /note= "Specifically claimed in claim 32"
XX misc_feature 2442. .3296
XX /tag= i
XX /note= "Specifically claimed in claim 35"
XX misc_feature 3297. .3737
XX /tag= j
XX /note= "Specifically claimed in claim 38"
XX misc_feature 3738. .4033
XX /tag= k
XX /note= "Specifically claimed in claim 41"
XX misc_feature 4034. .5029
XX /tag= l
XX /note= "Specifically claimed in claim 44"
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX WPI; 2003-278229/27.
XX P-PSDB; ABG75961.
XX
XX Polymase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Example 5; Page 64-66; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.

```

CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
 CC cells, can improve prognosis by allowing treatment e.g. with antiviral
 CC drugs, to prevent further loss of beta cells and severe long term
 CC consequences of diabetes including blindness, renal failure and leg
 CC amputations. This sequence represents the genome of diabetogenic
 CC coxsackie B virus 4 (CBV-4) strain VD2921
 XX
 SQ Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 7392;
 Best Local Similarity 100.0%; Pred. No. 0.073;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514

RESULT 68
 AAQ11816/c
 ID AAQ11816 standard; RNA; 7399 BP.
 AC
 XX
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 05-AUG-1991 (first entry)
 XX
 DE RNA encoding enteroviral polypeptide.
 XX
 XX Enteroviruses; monoclonal antibodies; myocarditis; myositis; meningitis;
 KW encephalitis; pancreatitis; post viral fatigue syndrome; ss.
 XX
 OS Enterovirus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 742..7299
 FT /*tag= a
 FT /product= "enteroviral polypeptide"
 XX
 XX DE3939200-A.
 XX
 XX 29-MAY-1991.
 XX
 XX 27-NOV-1989; 89DE-03939200.
 XX
 XX 27-NOV-1989; 89DE-03939200.
 XX
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 XX Kandolf R;
 XX
 XX WPI; 1991-165150/23.
 DR P-PSDB; AAR12141.
 XX
 XX New enteroviral polypeptide for raising group specific antibodies - for
 PT detecting any type of enterovirus in blood or serum, also new DNA
 PT encoding it.
 XX
 XX Claim 7; Page 17-21; 26pp; German.
 PS
 XX This RNA encodes an enteroviral polypeptide which is used to raise poly-
 CC or monoclonal antibodies (Abs). These are useful in assays for detecting
 CC enterovirus specific antigens, as an indication of enteroviral disease.
 CC All 70 serotypes of the enteroviral family can be detected. Diseases such
 CC as myocarditis, myositis, menin- gitis, encephalitis and pancreatitis can
 CC be diagnosed using the Abs. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 0 T; 1740 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 7399;
 Best Local Similarity 100.0%; Pred. No. 0.073;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514

RESULT 70
 ADP05527
 ID ADP05527 standard; DNA; 66 BP.
 XX
 AC ADP05527;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514

RESULT 69
 ABV76134/c
 ID ABV76134 standard; DNA; 7399 BP.
 XX
 AC ABV76134;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE Coxsackievirus capsid protein VP1 nucleic acid.
 XX
 KW Gene therapy; vector; hepatitis B virus; cardiovascular disease; heart;
 KW cardiant; vasotropic; antiarrhythmic; antiarteriosclerotic;
 KW capsid protein; gene; ss.
 XX
 OS Coxsackievirus.
 XX
 XX WO200287594-A1.
 XX
 XX 07-NOV-2002.
 XX
 XX 30-APR-2002; 2002WO-US013644.
 XX
 XX 30-APR-2001; 2001US-0287423P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Chien KR, Hoshijima M;
 XX
 XX WPI; 2003-111844/10.
 XX
 XX Novel non-viral vector comprises vesicular membrane with hepatitis B
 PT envelope protein with cardiac targeting sequence, and nucleotide sequence
 PT for gene therapy useful for treating, e.g., heart failure, arrhythmia and
 PT atherosclerosis.
 XX
 XX Disclosure; Page 27-31; 53pp; English.
 PS
 XX The present sequence is that of a coxsackie virus B3 capsid protein VP1
 CC nucleic acid. The invention provides a non-viral vesicle vector for the
 CC delivery of nucleic acid to various cardiac cell types. The vesicle
 CC vector contains the hepatitis B virus envelope protein in which at least
 CC part of the liver targeting sequence is deleted and replaced with a
 CC specific cardiac cell targeting sequence. For example, the coxsackie
 CC virus B3, VP1 sequence can be used to target the vector to
 CC cardiomyocytes. The vesicle vector can be delivered intravenously or
 CC intra-arterially rather than by more invasive methods such as direct
 CC cardiac injection. It can be used to deliver gene products to replace or
 CC enhance expression of proteins for treatment of heart failure,
 CC arrhythmia, reperfusion injury, atherosclerosis, to promote angiogenesis,
 CC etc. The vesicles are highly stable and can be produced in large
 CC quantities, making them ideal for gene therapy
 XX
 SQ Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 1740 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 7399;
 Best Local Similarity 100.0%; Pred. No. 0.073;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 |||||
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514

RESULT 70
 ADP05527
 ID ADP05527 standard; DNA; 66 BP.
 XX
 AC ADP05527;

```
XX 26-AUG-2004 (first entry)
XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID32.
XX KW microbe detection; microbe identification; virus; viral particle;
XX KW pathogenic bacterium; cellular microbe; acellular microbe;
XX KW clinical diagnosis; research; epidemiological surveillance;
XX KW bioterrorism countermeasure; environmental pathogen survey;
XX KW food contaminant; radioimmunoassay; ELISA; probe; ss.
XX OS Viruses.
XX PN WO2004045365-A2.
XX PD 03-JUN-2004.
XX PF 23-MAY-2003; 2003WO-US016461.
XX PP 15-NOV-2002; 2002US-00295787.
XX PR (REGC ) UNIV CALIFORNIA.
XX PA Jia XY, Berger MA, Tilles JG;
XX PI WPI; 2004-449626/42.
XX DR New (microarray) apparatus comprising a substrate with attached nucleic
XX PT acid probes, useful for detecting one or more microbes in a sample.
XX PS Claim 16; SEQ ID NO 32; 89pp; English.
XX CC This invention relates to a novel apparatus for detecting a microbe in a
XX CC sample which comprises a substrate having multiple microbe identification
XX CC sites, each having a unique address indicative of the position of that
XX CC microbe identification site on the substrate and groups of nucleic acid
XX CC probes disposed at the microbe identification sites, each group being
XX CC complementary to a target nucleic acid to provide a detectable signal at
XX CC one or more microbe identification sites. The apparatus is useful for
XX CC detecting the presence of one or more microbes in a sample, such as virus
XX CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
XX CC microbe. The apparatus is particularly useful for clinical diagnosis,
XX CC research, epidemiological surveillance, bioterrorism countermeasures,
XX CC environmental pathogen surveys, and monitoring food contaminants. Current
XX CC testing procedures or devices, such as radioimmunoassays and ELISA, are
XX CC difficult to implement, time consuming, expensive, outdated, and
XX CC typically rely on the use of agents that recognise and bind to membrane
XX CC bound proteins or carbohydrates of the pathogen. These further cannot
XX CC assay multiple pathogens. The new apparatus or device for detecting
XX CC microbes overcomes these disadvantages. The apparatus is compact,
XX CC sensitive, and quick to detect the presence of any of a number of
XX CC pathogens present in a sample. The present sequence is that of an
XX CC oligonucleotide probe which is related to the microbe detection apparatus
XX CC of the invention.
XX SQ Sequence 66 BP; 13 A; 19 C; 19 G; 15 T; 0 U; 0 Other;
XX Query Match 96.0%; Score 24; DB 12; Length 66;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
XX Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24
XX RESULT 71
XX ADP05501
XX ID ADP05501 standard; DNA; 70 BP.
XX AC ADP05501;
XX DT 26-AUG-2004 (first entry)
```

```
XX Novel microbe detection apparatus-related oligonucleotide probe SeqID6.
XX DE microbe detection; microbe identification; virus; viral particle;
XX KW pathogenic bacterium; cellular microbe; acellular microbe;
XX KW clinical diagnosis; research; epidemiological surveillance;
XX KW bioterrorism countermeasure; environmental pathogen survey;
XX KW food contaminant; radioimmunoassay; ELISA; probe; ss.
XX OS Viruses.
XX PN WO2004045365-A2.
XX PD 03-JUN-2004.
XX PF 23-MAY-2003; 2003WO-US016461.
XX PP 15-NOV-2002; 2002US-00295787.
XX PR (REGC ) UNIV CALIFORNIA.
XX PA Jia XY, Berger MA, Tilles JG;
XX PI WPI; 2004-449626/42.
XX DR New (microarray) apparatus comprising a substrate with attached nucleic
XX PT acid probes, useful for detecting one or more microbes in a sample.
XX PS Claim 16; SEQ ID NO 6; 89pp; English.
XX CC This invention relates to a novel apparatus for detecting a microbe in a
XX CC sample which comprises a substrate having multiple microbe identification
XX CC sites, each having a unique address indicative of the position of that
XX CC microbe identification site on the substrate and groups of nucleic acid
XX CC probes disposed at the microbe identification sites, each group being
XX CC complementary to a target nucleic acid to provide a detectable signal at
XX CC one or more microbe identification sites. The apparatus is useful for
XX CC detecting the presence of one or more microbes in a sample, such as virus
XX CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
XX CC microbe. The apparatus is particularly useful for clinical diagnosis,
XX CC research, epidemiological surveillance, bioterrorism countermeasures,
XX CC environmental pathogen surveys, and monitoring food contaminants. Current
XX CC testing procedures or devices, such as radioimmunoassays and ELISA, are
XX CC difficult to implement, time consuming, expensive, outdated, and
XX CC typically rely on the use of agents that recognise and bind to membrane
XX CC bound proteins or carbohydrates of the pathogen. These further cannot
XX CC assay multiple pathogens. The new apparatus or device for detecting
XX CC microbes overcomes these disadvantages. The apparatus is compact,
XX CC sensitive, and quick to detect the presence of any of a number of
XX CC pathogens present in a sample. The present sequence is that of an
XX CC oligonucleotide probe which is related to the microbe detection apparatus
XX CC of the invention.
XX SQ Sequence 70 BP; 13 A; 20 C; 19 G; 18 T; 0 U; 0 Other;
XX Query Match 96.0%; Score 24; DB 12; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
XX Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24
XX RESULT 72
XX ADP05514
XX ID ADP05514 standard; DNA; 70 BP.
XX AC ADP05514;
XX DT 26-AUG-2004 (first entry)
XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID19.
```

XX microbe detection; microbe identification; virus; viral particle;
 KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;
 KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.
 XX Viruses.
 OS
 XX WO2004045365-A2.
 XX
 XX PD 03-JUN-2004.
 XX
 XX PF 23-MAY-2003; 2003WO-US016461.
 XX
 XX PR 15-NOV-2002; 2002US-00295787.
 XX
 XX PA (REGC) UNIV CALIFORNIA.
 XX
 XX PI Jia XY, Berger MA, Tilles JG;
 XX WPI; 2004-449626/42.
 XX
 XX DR New (microarray) apparatus comprising a substrate with attached nucleic
 XX acid probes, useful for detecting one or more microbes in a sample.
 XX PT
 XX PS Claim 16; SEQ ID NO 19; 89pp; English.
 XX
 XX This invention relates to a novel apparatus for detecting a microbe in a
 CC sample which comprises a substrate having multiple microbe identification
 CC sites, each having a unique address indicative of the position of that
 CC microbe identification site on the substrate and groups of nucleic acid
 CC probes disposed at the microbe identification sites, each group being
 CC complementary to a target nucleic acid to provide a detectable signal at
 CC one or more microbe identification sites. The apparatus is useful for
 CC detecting the presence of one or more microbes in a sample, such as virus
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
 CC microbe. The apparatus is particularly useful for clinical diagnosis,
 CC research, epidemiological surveillance, bioterrorism countermeasures,
 CC environmental pathogen surveys, and monitoring food contaminants. Current
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are
 CC difficult to implement, time consuming, expensive, outdated, and
 CC typically rely on the use of agents that recognise and bind to membrane
 CC bound proteins or carbohydrates of the pathogen. These further cannot
 CC assay multiple pathogens. The new apparatus or device for detecting
 CC microbes overcomes these disadvantages. The apparatus is compact,
 CC sensitive, and quick to detect the presence of any of a number of
 CC pathogens present in a sample. The present sequence is that of an
 CC oligonucleotide probe which is related to the microbe detection apparatus
 CC of the invention.
 XX
 XX SQ Sequence 70 BP; 13 A; 19 C; 20 G; 18 T; 0 U; 0 Other;
 Query Match 96.0%; Score 24; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
 Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24
 RESULT 73
 ID ADP05512
 XX ADP05512 standard; DNA; 70 BP.
 XX
 XX AC ADP05512;
 XX
 XX DT 26-AUG-2004 (first entry)
 XX
 XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID17.
 XX
 XX KW microbe detection; microbe identification; virus; viral particle;

KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;
 KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.
 OS Viruses.
 XX
 XX PN WO2004045365-A2.
 XX
 XX PD 03-JUN-2004.
 XX
 XX PF 23-MAY-2003; 2003WO-US016461.
 XX
 XX PR 15-NOV-2002; 2002US-00295787.
 XX
 XX PA (REGC) UNIV CALIFORNIA.
 XX
 XX PI Jia XY, Berger MA, Tilles JG;
 XX WPI; 2004-449626/42.
 XX
 XX DR New (microarray) apparatus comprising a substrate with attached nucleic
 XX acid probes, useful for detecting one or more microbes in a sample.
 XX PT
 XX PS Claim 16; SEQ ID NO 17; 89pp; English.
 XX
 XX This invention relates to a novel apparatus for detecting a microbe in a
 CC sample which comprises a substrate having multiple microbe identification
 CC sites, each having a unique address indicative of the position of that
 CC microbe identification site on the substrate and groups of nucleic acid
 CC probes disposed at the microbe identification sites, each group being
 CC complementary to a target nucleic acid to provide a detectable signal at
 CC one or more microbe identification sites. The apparatus is useful for
 CC detecting the presence of one or more microbes in a sample, such as virus
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
 CC microbe. The apparatus is particularly useful for clinical diagnosis,
 CC research, epidemiological surveillance, bioterrorism countermeasures,
 CC environmental pathogen surveys, and monitoring food contaminants. Current
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are
 CC difficult to implement, time consuming, expensive, outdated, and
 CC typically rely on the use of agents that recognise and bind to membrane
 CC bound proteins or carbohydrates of the pathogen. These further cannot
 CC assay multiple pathogens. The new apparatus or device for detecting
 CC microbes overcomes these disadvantages. The apparatus is compact,
 CC sensitive, and quick to detect the presence of any of a number of
 CC pathogens present in a sample. The present sequence is that of an
 CC oligonucleotide probe which is related to the microbe detection apparatus
 CC of the invention.
 XX
 XX SQ Sequence 70 BP; 9 A; 20 C; 23 G; 18 T; 0 U; 0 Other;
 Query Match 93.6%; Score 23.4; DB 12; Length 70;
 Best Local Similarity 96.0%; Pred. No. 0.25;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
 RESULT 74
 ID ADP05530
 XX ADP05530 standard; DNA; 70 BP.
 XX
 XX AC ADP05530;
 XX
 XX DT 26-AUG-2004 (first entry)
 XX
 XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID35.
 XX
 XX KW microbe detection; microbe identification; virus; viral particle;
 KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;

KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.

OS Viruses.

XX WO2004045365-A2.

XX 03-JUN-2004.

XX 23-MAY-2003; 2003WO-US016461.

XX 15-NOV-2002; 2002US-00295787.

XX (REGC) UNIV CALIFORNIA.

XX Jia XY, Berger MA, Tilles JG;

XX WPI; 2004-449626/42.

XX New (microarray) apparatus comprising a substrate with attached nucleic
 XX acid probes, useful for detecting one or more microbes in a sample.

XX Claim 16; SEQ ID NO 35; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a
 CC sample which comprises a substrate having multiple microbe identification
 CC sites, each having a unique address indicative of the position of that
 CC microbe identification site on the substrate and groups of nucleic acid
 CC probes disposed at the microbe identification sites, each group being
 CC complementary to a target nucleic acid to provide a detectable signal at
 CC one or more microbe identification sites. The apparatus is useful for
 CC detecting the presence of one or more microbes in a sample, such as virus
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
 CC microbe. The apparatus is particularly useful for clinical diagnosis,
 CC research, epidemiological surveillance, bioterrorism countermeasures,
 CC environmental pathogen surveys, and monitoring food contaminants. Current
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are
 CC difficult to implement, time consuming, expensive, outdated, and
 CC typically rely on the use of agents that recognise and bind to membrane
 CC bound proteins or carbohydrates of the pathogen. These further cannot
 CC assay multiple pathogens. The new apparatus or device for detecting
 CC microbes overcomes these disadvantages. The apparatus is compact,
 CC sensitive, and quick to detect the presence of any of a number of
 CC pathogens present in a sample. The present sequence is that of an
 CC oligonucleotide probe which is related to the microbe detection apparatus
 CC of the invention.

XX SQ Sequence 70 BP; 12 A; 21 C; 21 G; 16 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 12; Length 70;

Best Local Similarity 96.0%; Pred. No. 0.25;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 75

ADP05506

ID ADP05506 standard; DNA; 70 BP.

XX AC ADP05506;

XX 26-AUG-2004 (first entry)

XX Novel microbe detection apparatus-related oligonucleotide probe SeqID11.

XX microbe detection; microbe identification; virus; viral particle;
 KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;
 KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX Viruses.

XX WO2004045365-A2.

XX 03-JUN-2004.

XX 23-MAY-2003; 2003WO-US016461.

XX 15-NOV-2002; 2002US-00295787.

XX (REGC) UNIV CALIFORNIA.

XX Jia XY, Berger MA, Tilles JG;

XX WPI; 2004-449626/42.

XX New (microarray) apparatus comprising a substrate with attached nucleic
 XX acid probes, useful for detecting one or more microbes in a sample.

XX Claim 16; SEQ ID NO 11; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a
 CC sample which comprises a substrate having multiple microbe identification
 CC sites, each having a unique address indicative of the position of that
 CC microbe identification site on the substrate and groups of nucleic acid
 CC probes disposed at the microbe identification sites, each group being
 CC complementary to a target nucleic acid to provide a detectable signal at
 CC one or more microbe identification sites. The apparatus is useful for
 CC detecting the presence of one or more microbes in a sample, such as virus
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
 CC microbe. The apparatus is particularly useful for clinical diagnosis,
 CC research, epidemiological surveillance, bioterrorism countermeasures,
 CC environmental pathogen surveys, and monitoring food contaminants. Current
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are
 CC difficult to implement, time consuming, expensive, outdated, and
 CC typically rely on the use of agents that recognise and bind to membrane
 CC bound proteins or carbohydrates of the pathogen. These further cannot
 CC assay multiple pathogens. The new apparatus or device for detecting
 CC microbes overcomes these disadvantages. The apparatus is compact,
 CC sensitive, and quick to detect the presence of any of a number of
 CC pathogens present in a sample. The present sequence is that of an
 CC oligonucleotide probe which is related to the microbe detection apparatus
 CC of the invention.

XX SQ Sequence 70 BP; 13 A; 20 C; 18 G; 19 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 12; Length 70;

Best Local Similarity 96.0%; Pred. No. 0.25;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 76

ADP05522

ID ADP05522 standard; DNA; 70 BP.

XX AC ADP05522;

XX 26-AUG-2004 (first entry)

XX Novel microbe detection apparatus-related oligonucleotide probe SeqID27.

XX microbe detection; microbe identification; virus; viral particle;
 KW pathogenic bacterium; cellular microbe; acellular microbe;
 KW clinical diagnosis; research; epidemiological surveillance;
 KW bioterrorism countermeasure; environmental pathogen survey;
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.

PS Disclosure; SEQ ID NO 40; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX SQ Sequence 117 BP; 25 A; 33 C; 28 G; 31 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 117;

Best Local Similarity 96.0%; Pred. No. 0.27;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCGTTACGA 25

DB 75 TCCGCTGCAGAGTTGCCGTTACGA 51

RESULT 81

AEB56856/c

ID AEB56856 standard; DNA; 173 BP.

XX AC AEB56856;

XX DT 22-SEP-2005 (first entry)

XX Human echovirus 5' untranslated polynucleotide sequence.

DE DNA detection; enteroviral detection; ds.

XX Human echovirus 5.

OS US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; AF188359.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

XX detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX SQ Sequence 173 BP; 36 A; 44 C; 45 G; 48 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 173;

Best Local Similarity 96.0%; Pred. No. 0.28;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCGTTACGA 25

DB 131 TCCGCTGCAGAGTTGCCGTTACGA 107

RESULT 82

AEB56855/c

ID AEB56855 standard; DNA; 173 BP.

XX AC AEB56855;

XX DT 22-SEP-2005 (first entry)

XX Human echovirus 5' untranslated polynucleotide sequence.

DE DNA detection; enteroviral detection; ds.

XX Human echovirus 5.

OS US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; AF188359.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

XX detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

```
XX SQ Sequence 173 BP; 36 A; 45 C; 45 G; 47 T; 0 U; 0 Other;
Query Match 93.6%; Score 23.4; DB 14; Length 173;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25
    |||||
Db 131 TCCGCTGCAGAGTTGCCGTTACGA 107

RESULT 83
AEB56865/c
ID AEB56865 standard; DNA; 198 BP.
XX AC AEB56865;
XX DT 22-SEP-2005 (first entry)
XX DE Human echovirus 12 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human echovirus 2.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11706.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX SQ Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
Query Match 93.6%; Score 23.4; DB 14; Length 198;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25
    |||||
Db 1 TCCGCTGCAGAGTTGCCGTTACGA 67

RESULT 84
AEB56853/c
ID AEB56853 standard; DNA; 198 BP.
XX AC AEB56853;
XX DT 22-SEP-2005 (first entry)
XX DE Human echovirus 2 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human echovirus 2.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11707.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX SQ Sequence 198 BP; 42 A; 53 C; 51 G; 52 T; 0 U; 0 Other;
Query Match 93.6%; Score 23.4; DB 14; Length 198;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25
    |||||
Db 91 TCCGCTGCAGAGTTGCCGTTACGA 67

RESULT 85
AEB56860/c
ID AEB56860 standard; DNA; 198 BP.
XX AC AEB56860;
XX XX
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DT 22-SEP-2005 (first entry)
XX Human echovirus 9 5' untranslated polynucleotide sequence.
DE DNA detection; enteroviral detection; ds.
KW Human echovirus 9.
XX US2005158710-A1.
PN 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
PI WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
PS Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I) (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I) (M1) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX Sequence 198 BP; 39 A; 49 C; 52 G; 58 T; 0 U; 0 Other;
SQ Query Match 93.6%; Score 23.4; DB 14; Length 198;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCGTTACGA 25
DB 91 TCCGCTGCAGAGTTGCCGTTACGA 67
RESULT 86
AEB56811/c
ID AEB56811 standard; DNA; 236 BP.
XX AEB56811;
AC AEB56811;
XX 22-SEP-2005 (first entry)
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:50.
DE DNA detection; enteroviral detection; ds.
KW Unidentified.
XX US2005158710-A1.
PN (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.

XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
PI WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
PS Disclosure; SEQ ID NO 50; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequence. (I) (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I) (M1) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX Sequence 236 BP; 60 A; 52 C; 51 G; 73 T; 0 U; 0 Other;
SQ Query Match 93.6%; Score 23.4; DB 14; Length 236;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCGCTGCAGAGTTGCCGTTACGA 25
DB 75 TCCGCTGCAGAGTTGCCGTTACGA 51
RESULT 87
AEB56810/c
ID AEB56810 standard; DNA; 236 BP.
XX AEB56810;
AC AEB56810;
XX 22-SEP-2005 (first entry)
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:49.
DE DNA detection; enteroviral detection; ds.
KW Unidentified.
XX US2005158710-A1.
PN 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;
 XX WPI; 2005-512251/52.
 XX Novel oligonucleotide comprising sequences for binding and amplifying or
 XX detecting target, useful for detecting enterovirus nucleic acids.
 XX Disclosure; SEQ ID NO 49; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (KI) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) specifically
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 236 BP; 60 A; 52 C; 51 G; 73 T; 0 U; 0 Other;
 SQ

Query Match 93.6%; Score 23.4; DB 14; Length 236;
 Best Local Similarity 96.0%; Pred. No. 0.29;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
 Db 75 TCCGCTGCAGAGTTCGCCATTACGA 51

RESULT 88
 AEB56812/c
 ID AEB56812 standard; DNA; 236 BP.
 AC AEB56812;
 DT 22-SEP-2005 (first entry)
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:51.
 DE DNA detection; enteroviral detection; ds.
 KW Unidentified.
 OS US2005158710-A1.
 XX 21-JUL-2005.
 PD 16-JAN-2004; 2004US-00760048.
 PF 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 TSang S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 Novel oligonucleotide comprising sequences for binding and amplifying or
 detecting target, useful for detecting enterovirus nucleic acids.
 Disclosure; SEQ ID NO 51; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (KI) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) specifically
 CC sensitively and rapidly recognizes the enterovirus genome. (I)
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

XX Sequence 236 BP; 60 A; 52 C; 51 G; 73 T; 0 U; 0 Other;
 SQ

Query Match 93.6%; Score 23.4; DB 14; Length 236;
 Best Local Similarity 96.0%; Pred. No. 0.29;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
 Db 75 TCCGCTGCAGAGTTCGCCATTACGA 51

RESULT 89
 AEB56798/c
 ID AEB56798 standard; DNA; 236 BP.
 XX AEB56798;
 AC AEB56798;
 DT 22-SEP-2005 (first entry)
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:37.
 DE DNA detection; enteroviral detection; ds.
 KW Unidentified.
 OS US2005158710-A1.
 XX 21-JUL-2005.
 PD 16-JAN-2004; 2004US-00760048.
 PF 16-JAN-2004; 2004US-00760048.
 XX (TSAN/) TSANG S.
 PA (PRIC/) PRICE J A.
 XX (HELL/) HELLYER T J.
 TSang S, Price JA, Hellyer TJ;
 WPI; 2005-512251/52.
 Novel oligonucleotide comprising sequences for binding and amplifying or
 detecting target, useful for detecting enterovirus nucleic acids.
 Disclosure; SEQ ID NO 37; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the
 CC target binding sequence of an oligonucleotide chosen from any one of the
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
 CC selected amplification or detection reaction. Also described: (1) a kit
 CC (KI) comprising (I), and one or more container that contains (I); and (2)
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying
 CC the target sequence using first amplification primer having a sequence
 CC consisting essentially of target binding sequence of any one of AEB56764
 CC to AEB56771 and optionally a sequence required for selected amplification
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and
 CC (KI) are useful for detecting enterovirus target sequences. (I) specifically
 CC sensitively and rapidly recognizes the enterovirus genome. (I)
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.

CC (K1) are useful for detecting enterovirus target sequences. (I)
 CC specifically and selectively recognizes the enterovirus genome. (I)
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral
 CC genome and allows detection of broad range of enterovirus serotypes. The
 CC present sequence represents a viral 5' untranslated polynucleotide
 CC sequence given in the exemplification of the present invention.
 XX
 SQ Sequence 236 BP; 52 A; 58 C; 57 G; 69 T; 0 U; 0 Other;

```

Query Match      93.68; Score 23.4; DB 14; Length 236;
Best Local Similarity 96.09; Freq. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCATTACGA 51

```

RESULT 90
AEB56805/c
ID ID AEB56805 standard; DNA; 237 BP.
XX
XX AEB56805;
XX AC
XX AC
XX DT 22-SEP-2005 (first entry)
XX DT
XX DT
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:44.

Query Match 93.6%; Score 23.4; DB 14; Length 237;

```

Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
      |||||
Db 75 TCCGCTGCGAGTTGCCCGTTACGA 51

```

RESULT 91
 AEB56806/c
 ID AEB56806 standard; DNA; 237 BP.
 XX
 XX AEB56806;
 XX
 XX
 XX 22-SEP-2005 (first entry)
 XX
 XX
 XX
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:45.

Query Match	93.6%	Score 23.4;	DB 14;	Length 237;
Best Local Similarity	96.0%	Pred. No. 0.29;		
Matches 24;	Conservative	0;	Mismatches 1;	Indels 0

RESULT 92
AEB56861/C

PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
XX	
PT	Novel oligonucleotide comprising sequences for binding and amplifying or
PT	detecting target, useful for detecting enterovirus nucleic acids.
XX	
PS	Disclosure; SEQ ID NO 33; 34pp; English.
XX	
CC	The invention relates to an oligonucleotide (I) consisting of: (a) the
CC	target binding sequence of an oligonucleotide chosen from any one of the
CC	10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC	selected amplification or detection reaction. Also described: (1) a kit
CC	(K1) comprising (I), and one or more container that contains (I); and (2)
CC	detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC	the target sequence using first amplification primer having a sequence
CC	consisting essentially of target binding sequence of any one of AEB56764
CC	to AEB56771 and optionally a sequence required for selected amplification
CC	reaction; and (b) detecting the amplified target sequence. (I), (M1) and
CC	(K1) are useful for detecting enterovirus target sequences. (I)
CC	specifically and selectively recognizes the enterovirus genome. (I)
CC	sensitively and rapidly detects fewer than 500 copies of enteroviral
CC	genome and allows detection of broad range of enterovirus serotypes. The
CC	present sequence represents a viral 5' untranslated polynucleotide
CC	sequence given in the exemplification of the present invention.
XX	
SQ	Sequence 238 BP; 59 A; 53 C; 53 G; 73 T; 0 U; 0 Other;
	Query Match 93.6%; Score 23.4; DB 14; Length 238;
	Best Local Similarity 96.0%; Pred. No. 0.29;
	Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 TCGCTGCAGAGTTGCCGTTACGA 25
Dd	75 TCGCTGCAGAGTTACCGTTACGA 51
	RESULT 95
ID	AEB56867/c
AC	AEB56867 standard; DNA; 238 BP.
XX	
AC	AEB56867;
XX	
DT	22-SEP-2005 (first entry)
XX	
DE	Human echovirus 12 5' untranslated polynucleotide sequence.
XX	
KW	DNA detection; enteroviral detection; ds.
OS	Human echovirus 12.
XX	
PN	US2005158710-A1.
XX	
PD	21-JUL-2005.
XX	
PF	16-JAN-2004; 2004US-00760048.
XX	
PR	16-JAN-2004; 2004US-00760048.
XX	
PA	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;
XX	
DR	WPI; 2005-512251/52.
DR	GEBANK; X79047.
PR	16-JAN-2004; 2004US-00760048.
XX	(TSAN/) TSANG S.
PA	(PRIC/) PRICE J A.
PA	(HELL/) HELLYER T J.
XX	
PI	Tsang S, Price JA, Hellyer TJ;

selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (i), and one or more container that contains (i); and (2) detecting (M1) an enterovirus target sequence, involving; (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (i), (M1) and (K1) are useful for detecting enterovirus target sequences. (i) specifically and selectively recognizes the enterovirus genome. (i) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;
Query Match 93.6%; Score 23.4; DB 14; Length 238;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TCCGCTGCAGAGTTGCCCGTTACGA 25
131 TCCGCTGCAGAGTTGCCCATACGA 107

RESULT 97
ABL53113/C
ID ABL53113 standard; DNA; 525 BP.

ABL53113;
07-AUG-2003 (revised)
25-JUN-2002 (first entry)
Micro-organism detection probe #55.
Probe; microorganism detection; microbiological quality;
water purification; ss.
Echovirus sp.
WO200202811-A2.
10-JAN-2002.
06-JUL-2001; 2001WO-FR002191.
06-JUL-2000; 2000FR-00008839.
(INNR) BIO MERIEUX.
Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;
Armand M, Laffaire P;
WPI; 2002-148021/19.
Monitoring microbiological quality of water, useful particularly for
controlling water purification, uses oligonucleotide probes to detect at
least three representative microbes.
Claim 24; Page 76; 85pp; French.

The present invention relates to a method for monitoring microbiological quality of an aqueous environmental medium that potentially contains many different microorganisms. A reference set of at least three microorganisms is chosen that, separately or collectively, represent microbiological quality. The test medium is treated, then any microorganisms, or their fragments, in the treated medium is contacted with a set of at least three probes for specific identification and multiple determination of selected microorganisms. This determination represents the level of microbiological quality. The method is useful for identifying and quantifying microorganisms in water and provides results that are used to control water purification/production processes. The

present sequence is a probe which was used to illustrate the invention.
(Updated on 07-AUG-2003 to correct OS field.)

Sequence 525 BP; 117 A; 142 C; 135 G; 131 T; 0 U; 0 Other;
Query Match 93.6%; Score 23.4; DB 6; Length 525;
Best Local Similarity 96.0%; Pred. No. 0.32;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TCCGCTGCAGAGTTGCCCGTTACGA 25
475 TCCGCTGCAGAGTTGCCCATACGA 451

RESULT 98
AAC85153/C
ID AAC85153 standard; RNA; 646 BP.

AAC85153;
08-MAY-2001 (first entry)
Echo virus (ECV12) 5' non-translated region (NTR) sequence.
Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
Coxsackievirus B3; CVB3; NTR; non-translated region; echo virus; ds.
Echo virus.

Key Location/Qualifiers
stem_loop 2..87
/*tag= a
/note= "Domain I"
stem_loop 103..180
/*tag= b
/note= "Domain II"
stem_loop 183..232
/*tag= c
/note= "Domain III"
stem_loop 240..443
/*tag= d
/note= "Domain IV"
stem_loop 451..559
/*tag= e
/note= "Domain V"
stem_loop 586..622
/*tag= f
/note= "Domain VI"
stem_loop 623..643
/*tag= g
/note= "Domain VII"

WO200104136-A1.

18-JAN-2001.

08-JUL-2000; 2000WO-US018681.

09-JUL-1999; 99US-0143104P.

(UYNE-) UNIV NEBRASKA.

Romero JR, Bradrick SS, Dunn JJ;

WPI; 2001-138310/14.

Recombinant enterovirus genome for use as vector or vaccine, modified by replacing a part or all of its 5' non-translated region by 5'NTR of enterovirus genome that encodes virus modified in tropism or virulence.
Disclosure; Fig 2; 49pp; English.

The invention provides an enterovirus genome (I) for use as a vector or

CC vaccine, modified to produce a virus (V1) having a restricted or altered
 CC species or tissue tropism, compared to an equivalent unmodified virus, or
 CC modified to produce an attenuated virus (V2), by replacing a part or all
 CC of the 5' non-translated region (5'NTR) of (1) with a 5'NTR of an
 CC enterovirus genome that encodes V1 or V2. (1) is useful as vaccine or
 CC vector in targeting genes of interest to specific cells or tissues. (1)
 CC is also useful for diagnostic purposes, e.g. to identify virulent, versus
 CC nonvirulent strains of an enterovirus. The present sequence represents
 CC the 5' NTR (non-translated region) sequence of echo virus (ECV12)
 XX

SQ Sequence 646 BP; 145 A; 176 C; 163 G; 0 T; 162 U; 0 Other;
 Query Match 93.6%; Score 23.4; DB 4; Length 646;
 Best Local Similarity 96.0%; Pred. No. 0.33;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
 |||||
 Db 538 TCCGCTGCAGAGTTCGCCGTTACGA 514

RESULT 99
 AAZ98719/c
 ID AAZ98719 standard; cDNA; 7400 BP.
 XX
 AC AAZ98719;
 XX
 DT 20-JUN-2000 (first entry)
 XX
 DE Swine vesicular disease virus (SVDV) N3 mutant strain gene sequence.
 XX
 KW Swine vesicular disease virus; SVDV; swine vesicular disease;
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
 KW differentiation; vaccine; prevent; ss.
 XX
 OS Swine vesicular disease virus.

FH Key Location/Qualifiers
 FT misc_feature 2693..2710
 FT /*tag= a
 FT /note= "Nucleotides in this position replace the wild-
 FT type nucleotide sequence of strain Taiwan Yu-Li (see
 FT AAZ98717)"
 XX

PN EP982403-A1.
 XX
 PD 01-MAR-2000.
 XX
 PF 14-AUG-1998; 98EP-00306486.
 XX
 PR 14-AUG-1998; 98EP-00306486.
 XX
 PA (BIOT-) DEV CENT BIOTECHNOLOGY.
 XX
 PI Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;
 XX WPI; 2000-258616/23.
 XX
 DR Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
 PT to prevent swine vesicular disease.
 XX
 PS Claim 4; Page; 66pp; English.

XX This sequence represents the full length Swine vesicular disease virus
 CC (SVDV) gene sequence from the SVDV strain N3. SVDV is the causative agent
 CC of swine vesicular disease, which is very similar to foot and mouth
 CC disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA
 CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
 CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
 CC prophylaxis of swine vesicular disease. The invention also includes a
 CC method for differentiating the mutant SVDV nucleotide sequences from the
 CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
 CC virus through the use of polymerase chain reaction. Note: This sequence

CC is not present in the specification, but has been derived from the wild-
 CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
 CC 34-38 of the specification

SQ Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;
 Query Match 93.6%; Score 23.4; DB 3; Length 7400;
 Best Local Similarity 96.0%; Pred. No. 0.43;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
 |||||
 Db 538 TCCGCTGCAGAGTTCGCCGTTACGA 514

RESULT 100
 AAZ98717/c
 ID AAZ98717 standard; cDNA; 7400 BP.
 XX

AC AAZ98717;
 XX
 DT 20-JUN-2000 (first entry)
 XX
 DE Swine vesicular disease virus (SVDV) gene sequence.
 XX

KW Swine vesicular disease virus; SVDV; swine vesicular disease;
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
 KW differentiation; vaccine; prevent; ss.

OS Swine vesicular disease virus.

PN EP982403-A1.

PD 01-MAR-2000.

PF 14-AUG-1998; 98EP-00306486.

PR 14-AUG-1998; 98EP-00306486.

PA (BIOT-) DEV CENT BIOTECHNOLOGY.

PI Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;

XX WPI; 2000-258616/23.

XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
 PT to prevent swine vesicular disease.

PS Claim 1; Page 34-38; 66pp; English.

XX This sequence represents the full length Swine vesicular disease virus
 CC (SVDV) gene sequence from the SVDV strain Taiwan Yu-Li. SVDV is the
 CC causative agent of swine vesicular disease, which is very similar to foot
 CC and mouth disease. The invention relates to the wild-type Taiwan Yu-Li
 CC strain cDNA sequence, and the gene sequences of the mutant SVDV strains
 CC N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a
 CC vaccine for the prophylaxis of swine vesicular disease. The invention
 CC also includes a method for differentiating the mutant SVDV nucleotide
 CC sequences from the wild type strain of SVDV, coxsackievirus and foot-and-
 CC mouth disease virus through the use of polymerase chain reaction

SQ Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 3; Length 7400;
 Best Local Similarity 96.0%; Pred. No. 0.43;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
 |||||
 Db 538 TCCGCTGCAGAGTTCGCCGTTACGA 514

Search completed: March 9, 2006, 00:30:40

Job time : 264.485 secs

